

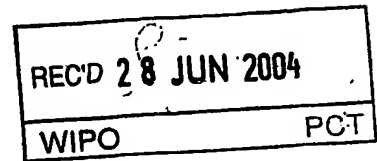
06. 05. 2004



Europäisches
Patentamt

European
Patent Office

Office européen
des brevets



Bescheinigung

Certificate

Attestation

Die angehefteten Unterla-
gen stimmen mit der
ursprünglich eingereichten
Fassung der auf dem näch-
sten Blatt bezeichneten
europäischen Patentanmel-
dung überein.

The attached documents
are exact copies of the
European patent application
described on the following
page, as originally filed.

Les documents fixés à
cette attestation sont
conformes à la version
initialement déposée de
la demande de brevet
européen spécifiée à la
page suivante.

Patentanmeldung Nr. Patent application No. Demande de brevet n°

03450112.2

**PRIORITY
DOCUMENT**
SUBMITTED OR TRANSMITTED IN
COMPLIANCE WITH RULE 17.1(a) OR (b)

Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
p.o.

R C van Dijk



Anmeldung Nr:
Application no.: 03450112.2
Demande no:

Anmeldetag:
Date of filing: 07.05.03
Date de dépôt:

Anmelder/Applicant(s)/Demandeur(s):

Intercell Biomedizinische Forschungs- und
Entwicklungs AG
Campus Vienna Biocenter 6
1030 Vienna
AUTRICHE

Bezeichnung der Erfindung/Title of the invention/Titre de l'invention:
(Falls die Bezeichnung der Erfindung nicht angegeben ist, siehe Beschreibung.
If no title is shown please refer to the description.
Si aucun titre n'est indiqué se référer à la description.)

Streptococcus agalactiae antigens

In Anspruch genommene Priorität(en) / Priority(ies) claimed / Priorité(s)
revendiquée(s)

Staat/Tag/Aktenzeichen/State/Date/File no./Pays/Date/Numéro de dépôt:

Internationale Patentklassifikation/International Patent Classification/
Classification internationale des brevets:

C07K14/00

Am Anmeldetag benannte Vertragsstaaten/Contracting states designated at date of
filing/Etats contractants désignées lors du dépôt:

AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LU MC NL
PT RO SE SI SK TR LI

The present invention relates to isolated nucleic acid molecules, which encode antigens for *Streptococcus agalactiae*, which are suitable for use in preparation of pharmaceutical medicaments for the prevention and treatment of bacterial infections caused by *Streptococcus agalactiae*.

Streptococcus agalactiae is a gram-positive bacterium, and belongs to the Group B Streptococci (GBS) based on its hemolysis pattern in blood agar. The organism is encapsulated, and capsule is an important element of pathogenicity. Capsules are antigenic and form the basis for classifying GBS by serotypes. Nine distinct GBS serotypes have been identified: Ia, Ib, II, III, IV, V, VI, VII and VIII. Most *S. agalactiae* serotypes have been shown to cause serious disease, and the two most common serotypes - type III and V - are estimated to account for the majority of invasive disease worldwide. The ranking and serotype prevalence differs by age group and geographic area. In the US, GBS type III causes more than 50% of infant disease, type V about 40% of nonpregnant adult disease, and type Ia about a third of disease in any patient population.

Streptococcus agalactiae is an important agent of human disease at the extremities of age and in those who have underlying disease. Group B *Streptococci* are the major cause of generalized and focal infections in the newborn infant. GBS is the predominant pathogen in newborns in the US since the 1970's. Bacterial infection can lead to life threatening diseases, such as sepsis, pneumonia and meningitis. Survivors can become permanently handicapped with hearing, learning and visual disabilities. Newborns usually acquire the organism intrapartum or during delivery from their GBS-colonized mothers. In addition, GBS are also a frequent cause of infections in pregnant women and in chronically ill and elderly patients, such as those suffering from diabetes, malignancies, immunodeficiencies, etc., (reviewed by Balter, S. et al. in Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 154-160).

10-35% of pregnant women are colonized with GBS, but are asymptomatic. However, GBS colonization is important because of the risk of vertical transmission. 50-70% of neonates born to colonized women - that is 5-15% of all newborns - become colonized by GBS during delivery. Colonization is a prerequisite for infection and disease. The most preterm infants are at the highest risk for invasive disease due to low maternal transfer of antibodies and immature immune system. GBS carriage during pregnancy may be chronic, intermittent, or transient. It is difficult to assess the duration of carriage, since women are screened once during a prenatal visit from the late trimester. Several studies suggest that there is a correlation (~90%) between the colonization status in the third trimester and at the time of delivery. Serotyping of the isolates indicates that persistence of the same type is most common (reviewed by Balter, S. et al. in Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 154-160).

Without preventive intervention, 1 to 2% of all neonates and 15% of neonates born to heavily colonized women develop invasive disease (sepsis, pneumonia and/or meningitis). In the US, GBS infections affect 1-5 newborns/1000 live birth. About 17,000 cases of invasive GBS disease occurred in the US annually, and 7,500 occurred in newborns before prevention. GBS is the most common cause of bacterial meningitis accounting for ~ 40 % of all cases reported in this age group. The overall incidence of invasive GBS disease is 0.2-0.7/100,000 in the US. It is somewhat lower in Europe. Mortality without preventive intervention is 6% with invasive disease, every 16. infected newborn dies and 20% of survivors become permanently handicapped.

The rates of serious group B strep infections are much higher among newborns than among any other age group. Nonetheless, serious group B strep infections occur in other age groups in both men and women. Among non-pregnant adults, rates of serious disease range from 4.1 to 7.2 cases per 100,000 populations. The average death rate for invasive infections (infections where the bacteria have entered a part of the body that is normally not exposed to bacteria) is 8-10% for adult's ages 18-64 and 15-25% for adults 65 years of age and over. Mortality rates are lower among younger adults, and adults who do not have other medical conditions. The rate of serious group B strep disease increases with age. The average age of cases

in non-pregnant adults is about 60 years old. Most adult group B strep disease occurs in adults who have serious medical conditions. These include: diabetes mellitus; liver disease; history of stroke; history of cancer; or bedsores. Among the elderly, rates of serious group B strep disease are more common among residents of nursing facilities, and among bedridden hospitalized patients. Group B strep disease among non-pregnant adults may often be acquired after recent trauma, or after having certain invasive hospital procedures like surgery ([Farley, M., 2001]; [Jackson, L. et al., 1995]; www.cdc.gov/groupbstrep/).

Direct medical costs of neonatal disease before prevention were \$294 million annually and GBS continues to pose a considerable economic burden.

A definitive diagnosis of infection with *Streptococcus agalactiae* generally relies on isolation of the organism from cervical swabs, blood or other normally sterile body sites. Tests are also available to detect capsular polysaccharide antigen in body fluids.

Penicillin G is the treatment of choice for established cases of GBS. Ten days of treatment is recommended for bacteremia, pneumonia and soft tissue infections, while 2-3 weeks is recommended for meningitis and 3-4 weeks for osteomyelitis.

Prevention has been established since 1994 in North America by screening pregnant women for carriage of GBS, taking vaginal and anorectal swabs at 35-37 weeks' gestation, or by identifying risk factors at admission for delivery without cultures. Women who are candidates for prophylaxis are given intrapartum antibiotic therapy during labor to prevent early-onset neonatal disease. This prevention method has decreased the incidence of GBS disease from 1.7 to 0.4/1000 live births between 1993 and 1999 in the US. Although most neonatal GBS disease can be prevented through intrapartum prophylaxis (Penicillin G or Ampicillin), currently available strategies are not ideal, especially for the prevention of late-onset (>7 days of age) infections and disease in premature babies. There are always individuals who escape of screening for carriage due to several reasons, such as intermittent carriers, who are tested negative at wks 32-35, but become positive during delivery, unattendance, negligence, or delivery before screening date (32-35 wks).

In the long run, widespread use of antibiotics usually induces resistant strains that appear after a period of time. Extensive use of Penicillin (every 3-5th women are treated with high dose), and other antibiotics has already been shown to steadily increase the percentage of antibiotic resistant clinical isolates (ref). Moreover, efficiency of antibiotic based prevention is not that effective for late onset disease, as it is for early onset (within 48 hrs after delivery). An additional concern is that prevention in susceptible adult populations has not been addressed.

Vaccine development is hindered by the lack of sufficient knowledge about the elements of protective immunity against GBS carriage and disease. The relationship of carriage to the development of natural immunity is poorly understood. In addition, the immunologic mechanism that allows disease to occur in a carrier is ill defined. However, it is suggested that the maternal serum levels of pathogen-specific antibodies are correlated with neonatal GBS disease. It has been firmly established that there is an inverse correlation between maternal anti-capsular polysaccharide antibody levels at delivery and the frequency of invasive neonatal diseases [Campbell, J. et al., 2000].

Although the group B carbohydrate antigen is common to all strains of GBS, unfortunately, it is not strongly immunogenic and antibodies are not protective from lethal challenge in experimental models. The GBS capsule itself that is made of polysaccharides, is immunogenic and is able to induce protective antibodies. However, this protection is type-specific. Although capsular specific antibodies have been shown to be highly protective, it remains unclear what concentration of these serotype-specific antibodies protect against disease and more recently it has become clear that opsonic activity and avidity of these

antibodies are more critical determinants of protection than concentration.

The importance of surface proteins in human immunity to *S. agalactiae* already has been appreciated. It is apparent that all serotypes express surface proteins with activity relevant to host immune defense. The alpha C protein, beta C protein, Rib and Sip proteins are well-characterized biochemically and genetically, and have also been shown to be immunogenic and protective in animal models ([Michel, J. et al., 1991]; [Brodeur, B. et al., 2000]; [Larsson, C. et al., 1999]; [Cheng, Q. et al., 2002]). The major problem with these proteins as vaccine candidates seems to be their variability in prevalence among the different clinical isolates of GBS. The Rib protein for example is present in serotype III GBS, but missing from type V, which is responsible for a significant portion of disease worldwide. Some other surface proteins are characterized as being immunogenic, but there is a limited systematic work done to identify most of the immunogenic proteins of GBS.

Thus, there remains a need for an effective treatment to prevent or ameliorate GBS infections. A vaccine could not only prevent infections by GBS, but more specifically prevent or ameliorate colonization of host tissues (esp. in the birth canal), thereby reducing the incidence of transmission from mother to fetus. Reducing the incidence of acute infection and carriage of the organism would lead to prevention of invasive diseases in newborns - pneumonia, bacteremia, meningitis, and sepsis. Vaccines capable of showing cross-protection against the majority of *S. agalactiae* strains causing human infections could also be useful to prevent or ameliorate infections caused by all other streptococcal species, namely groups A, C and G.

A vaccine can contain a whole variety of different antigens. Examples of antigens are whole-killed or attenuated organisms, subfractions of these organisms/tissues, proteins, or, in their most simple form, peptides. Antigens can also be recognized by the immune system in form of glycosylated proteins or peptides and may also be or contain polysaccharides or lipids. Short peptides can be used since for example cytotoxic T-cells (CTL) recognize antigens in form of short usually 8-11 amino acids long peptides in conjunction with major histocompatibility complex (MHC). B-cells can recognize linear epitopes as short as 4-5 amino acids, as well as three-dimensional structures (conformational epitopes). In order to obtain sustained, antigen-specific immune responses, adjuvants need to trigger immune cascades that involve all cells of the immune system. Primarily, adjuvants are acting, but are not restricted in their mode of action, on so-called antigen presenting cells (APCs). These cells usually first encounter the antigen(s) followed by presentation of processed or unmodified antigen to immune effector cells. Intermediate cell types may also be involved. Only effector cells with the appropriate specificity are activated in a productive immune response. The adjuvant may also locally retain antigens and co-injected factors. In addition, the adjuvant may act as a chemoattractant for other immune cells or may act locally and/or systemically as a stimulating agent for the immune system.

Vaccine development since the late 1970s has focused on the capsular polysaccharides, but a safe, effective product is still not available. However, vaccine against *S. agalactiae* is ranked as one of the most important for development and administration to infants and high-risk adults. Currently vaccines against this infection are only in the research stages of development. Efforts are focused on using capsular polysaccharide (CPS) as immunogens, either with or without conjugation to protein [Paoletti, L. et al., 2002]. However, there are several arguments against the use of polysaccharide-based vaccine. Polysaccharides induce IgG2 antibodies, which cross the placenta less efficiently than IgG1 or IgG3 antibodies. It is especially a problem for the most susceptible neonates, the still-borns since placental antibody transfer is low before weeks 32-34. It is estimated that ~10% of deliveries occur before the 34th pregnancy week.

Protein conjugate vaccines are no doubt a great new addition to the armamentarium in the battle against GBS disease, but the vaccine can contain only a limited number of GBS serotypes and given adequate ecological pressure, replacement disease by non-vaccine serotypes remains a real threat, particularly in

areas with very high disease burden. Moreover polysaccharide antigens used for active immunization do not provide immunological memory in humans. Conjugation of CPS to non-GBS related immunogenic protein carriers (e.g. tetanus toxoid, cholera toxin B subunit, etc.) has been shown to be beneficial in inducing higher concentrations of antibodies in vaccinees, but it does not provide pathogen-specific B cell and T cell epitopes which would recruit memory B and T cells during a real infection to support the most effective host response. To be able to supplement the CPS vaccines with proteins fulfilling these criteria it is necessary to identify conserved immunogenic GBS-specific surface proteins.

All these insufficiencies suggest that there is a need to develop new generation vaccines composed of proteins, or their derivatives, expressed by all strains under *in vivo* conditions with the ability to induce opsonizing and/or neutralizing antibodies in humans.

There is a great potential for passive antibody-based therapy. There have been already attempts to use human intravenous immunoglobulin (IVIG) preparations for prevention. Recent advances in the technology of monoclonal antibody production provide the means to generate human antibody reagents and reintroduce antibody therapies, while avoiding the toxicities associated with serum therapy. Immunoglobulins are an extremely versatile class of antimicrobial proteins that can be used to prevent and treat emerging infectious diseases. Antibody therapy has been effective against a variety of diverse microorganisms (reviewed in [Burnie, J. et al., 1998]). Anti-GBS mAbs could be given therapeutically to every newborn that develop invasive diseases or preventively to low birth-weight and premature neonates.

During the last decade the immunogenicity and protective capacity of several GBS proteins have been described in animal models and these are now being explored for the development of species-common protein based vaccines. Such proteins are the GBS surface proteins Sip [Brodeur, B. et al., 2000], rib, e-protein and [Michel, J. et al., 1991].

Certain proteins or enzymes displayed on the surface of gram-positive organisms significantly contribute to pathogenesis, are involved in the disease process caused by these pathogens. Often, these proteins are involved in direct interactions with host tissues or in concealing the bacterial surface from the host defense mechanisms [Navarre, W. et al., 1999]. *S. agalactiae* is not an exception in this regard. Several surface proteins are characterized as virulence factors, important for GBS pathogenicity ((reviewed in [Paoletti L.C. et al. in Gram positive pathogens, ed. by Fischetti V.A et al., ASM Press 2000, pp 137-153]; [Paoletti, L. et al., 2002])). If antibodies to these proteins could offer better protection to humans then polysaccharides, they could provide the source of a novel, protein-based GBS vaccine to be used in conjunction with or in place of the more traditional capsular polysaccharide vaccine. The use of some of the above-described proteins as antigens for a potential vaccine as well as a number of additional candidates resulted mainly from a selection based on easiness of identification or chance of availability. There is a demand to identify relevant antigens for *S. agalactiae* in a more comprehensive way.

The present inventors have developed a method for identification, isolation and production of hyperimmune serum reactive antigens from a specific pathogen, especially from *Staphylococcus aureus* and *Staphylococcus epidermidis* (WO 02/059148). However, given the differences in biological property, pathogenic function and genetic background, *Streptococcus agalactiae* is distinctive from *Staphylococcus* strains. Importantly, the selection of sera for the identification of antigens from *S. agalactiae* is different from that applied to the *S. aureus* screens. Four major types of human antibody sources were collected for that purpose. First, healthy pregnant women who were tested negative for cervical and anorectal carriage of GBS. This donor group represents the most important source of antibodies. In addition to their serum samples, human cervical secretions collected with cervical wicks, containing secretory IgA (sIgA) were also used for antigen identification and validation. The main value of this collection is that sIgA can be considered the major immune effector molecule on mucosal surfaces. Second, healthy pregnant women

colonized with GBS whose newborn remained GBS-free (although with antibiotic prevention). Third, adults below <45 years of age without clinical disease. Four, naïve individuals, young children between 5 and 10 months of age, after they already lost maternal antibodies and have not acquired GBS-specific ones due to the lack of GBS disease.

To be able to select for relevant serum sources, a series of ELISAs and immunoblotting experiments measuring anti-*S. agalactiae* IgG and IgA antibody levels were performed with bacterial lysates and culture supernatant proteins. Sera from high titer carriers and non-carriers were included in the genomic-based antigen identification. This approach for selection of human sera is basically very different from that used for *S. aureus*, where carriage or non-carriage state couldn't be associated with antibody levels.

The present invention uses high throughput genomic method to identify *in vivo* expressed pathogen-specific proteins with the ability to induce antibodies in humans during the course of infections and colonization.

The genomes of the two bacterial species *S. agalactiae* and *S. aureus* by itself show a number of important differences. The genome of *S. agalactiae* contains app. 2.2 Mb, while *S. aureus* harbours 2.85 Mb. They have an average GC content of 35.7 and 33%, respectively and approximately 30 to 45% of the encoded genes are not shared between the two pathogens. In addition, the two bacterial species require different growth conditions and media for propagation. A list of the most important diseases, which can be inflicted by the two pathogens is presented below. *S. aureus* causes mainly nosocomial, opportunistic infections: impetigo, folliculitis, abscesses, boils, infected lacerations, endocarditis, meningitis, septic arthritis, pneumonia, osteomyelitis, scalded skin syndrome (SSS), toxic shock syndrome. *S. agalactiae* causes mainly neonatal infections and diseases in elderly, such as bacteremia, sepsis, wound infection, osteomyelitis and meningitis.

The complete genome sequence of a capsular serotype III isolate of *S. agalactiae*, designated NEM316 (ATCC 12403) was determined by the random shotgun sequencing strategy (GenBank accession number AL732656; see www.tigr.org/tigrscripts/CMR2/CMRHomePage.spl). (Glaser, P. et al., 2002).

The problem underlying the present invention was to provide means for the development of medicaments such as vaccines against *S. agalactiae* infection. More particularly, the problem was to provide an efficient, relevant and comprehensive set of nucleic acid molecules or hyperimmune serum reactive antigens from *S. agalactiae* that can be used for the manufacture of said medicaments.

Therefore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:

- a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from Seq ID No 14, 90, 157-216.
- b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
- c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
- d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
- e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

According to a preferred embodiment of the present invention the sequence identity is at least 80%, preferably at least 95%, especially 100%.

Furthermore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune

serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of

- a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from Seq ID No 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448.
- b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
- c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
- d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
- e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

According to another aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

- a) a nucleic acid molecule selected from Seq ID No 32, 86, 91, 101, 127.
- b) a nucleic acid molecule which is complementary to the nucleic acid of a),
- c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

Preferably, the nucleic acid molecule is DNA or RNA.

According to a preferred embodiment of the present invention, the nucleic acid molecule is isolated from a genomic DNA, especially from a *S. agalactiae* genomic DNA.

According to the present invention a vector comprising a nucleic acid molecule according to any of the present invention is provided.

In a preferred embodiment the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragments thereof encoded by the nucleic acid molecule according to the present invention.

The present invention also provides a host cell comprising the vector according to the present invention.

According to another aspect the present invention further provides a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to the present invention.

In a preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of Seq ID No 231, 307, 374-433.

In another preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of Seq ID No 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462.

In a further preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of Seq ID No 249, 303, 308, 318, 344.

According to a further aspect the present invention provides fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1A, especially peptides comprising amino acid 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-

213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of Seq ID No 218; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of Seq ID No 219; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of Seq ID No 220; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of Seq ID No 221; 29-38, 44-64, 70-76, 78-87, 94-100, 102-112, 119-134, 140-149, 163-173, 178-186, 188-194, 207-234, 247-262, 269-290 and 73-92 of Seq ID No 222; 10-28, 36-63, 77-87, 103-119, 127-136, 141-169, 171-183, 195-200, 207-232, 236-246, 251-265, 268-283, 287-297, 314-322, 335-343, 354-363, 384-390, 405-411, 419-436, 443-455, 467-473, 480-513, 518-529, 550-557, 565-585, 602-608, 616-625, 632-660, 665-677, 685-701, 726-736, 738-747, 752-761, 785-796, 801-813, 838-853, 866-871 and 757-774 of Seq ID No 223; 31-38, 61-66, 74-81, 90-115, 123-145, 154-167, 169-179, 182-193, 200-206, 238-244, 267-272 and 235-251 of Seq ID No 224; 19-25, 38-54, 56-64, 66-72, 74-92, 94-100, 116-129, 143-149, 156-183, 204-232, 253-266, 269-275, 294-307 and 241-313 of Seq ID No 225; 5-34, 50-56, 60-65, 74-85, 89-97, 108-119, 159-165, 181-199, 209-225, 230-240, 245-251, 257-262, 274-282, 300-305 and 64-75 of Seq ID No 226; 5-13, 16-21, 27-42, 45-52, 58-66, 74-87, 108-114, 119-131 and 39-51 of Seq ID No 227; 6-23, 46-54, 59-65, 78-84, 100-120, 128-133, 140-146, 159-165, 171-183, 190-204, 224-232, 240-248, 250-259, 274-280, 288-296, 306-315 and 267-274 of Seq ID No 228; 5-12, 15-24, 26-36, 42-65, 68-80, 82-104, 111-116, 125-144, 159-167, 184-189, 209-218, 235-243, 254-265, 269-283, 287-300, 306-316, 318-336, 338-352, 374-392 and 162-174 of Seq ID No 229; 30-42, 45-54 and 25-37 of Seq ID No 230; 10-30, 53-59, 86-95, 116-130, 132-147, 169-189, 195-201, 212-221, 247-256, 258-265, 278-283, 291-298, 310-316, 329-339, 341-352, 360-367, 388-396, 398-411, 416-432, 443-452, 460-466, 506-512, 515-521, 542-548 and 419-431 of Seq ID No 231; 4-27, 30-53, 60-67, 70-90, 92-151, 159-185, 189-195, 198-210, 215-239 and 173-189 of Seq ID No 232; 4-26, 41-54, 71-78, 116-127, 140-149, 151-158, 161-175, 190-196, 201-208, 220-226, 240-252, 266-281, 298-305, 308-318, 321-329, 344-353, 372-378, 384-405, 418-426, 429-442, 457-463, 494-505, 514-522 and 174-188 of Seq ID No 233; 17-25, 27-39, 61-67, 81-89, 99-110, 120-131, 133-139, 147-161, 167-172, 179-185, 192-198, 203-213, 226-238, 243-258, 261-267, 284-290, 296-307, 311-328, 340-352, 356-371 and 239-256 of Seq ID No 234; 8-30, 40-49, 67-80, 114-123, 126-142, 152-162, 188-194 and 57-70 of Seq ID No 235; 4-23, 28-34, 36-47, 50-61, 76-81, 89-94, 96-104, 112-119, 126-146, 155-181, 195-200, 208-214, 220-229, 244-260, 263-276, 282-288, 292-300, 317-323, 336-351, 353-359, 363-375, 382-399, 415-432, 444-455, 458-471, 476-481, 484-492, 499-517, 522-529, 535-541, 543-568, 572-584, 586-600, 607-617, 626-637, 656-675 and 282-297 of Seq ID No 236; 6-24, 30-35, 38-45, 63-91, 134-140, 146-160, 167-188, 214-220, 226-234, 244-250, 260-270, 286-301, 316-329, 340-371, 429-446, 448-459, 474-481, 485-491, 512-526, 537-544, 550-565, 573-583, 596-613, 621-630, 652-658 and 87-97 of Seq ID No 237; 8-20, 26-48, 56-67, 76-86, 94-109, 115-121, 123-129, 143-160, 178-186, 191-198, 201-208, 221-236, 238-244, 260-268 and 237-247 of Seq ID No 238; 4-40, 42-57, 73-87, 98-117, 126-135, 150-156, 166-174, 196-217, 231-236, 248-258, 276-284, 293-301, 307-313, 339-347, 359-365, 375-387, 395-402, 428-440, 445-456, 485-490, 497-505, 535-541, 547-555, 610-625, 648-656, 665-671 and 448-528 of Seq ID No 239; 10-18, 39-45, 51-61, 80-96, 98-106, 110-115, 158-172, 174-183, 191-200, 220-237, 249-255, 274-289, 308-324, 331-341, 372-381, 384-397, 405-414 and 322-338 of Seq ID No 240; 30-36, 38-56, 85-108, 134-147, 149-160, 163-183, 188-201, 206-211, 219-238, 247-254 and 5-13 of Seq ID No 241; 11-40, 98-103, 110-115, 133-145, 151-159, 172-179, 192-201, 204-212, 222-228, 235-245, 258-268, 283-296, 298-309, 322-329, 342-351, 354-362, 372-378, 385-393, 407-418, 495-516 and 1-148 of Seq ID No 242; 5-19, 21-36, 73-94, 112-119, 122-137, 139-145, 152-167, 184-190, 198-204, 208-224, 249-265, 267-281, 299-304, 309-317, 326-333, 356-364, 368-374, 381-389, 391-414, 419-425, 430-435 and 113-140 of Seq ID No 243; 45-54, 59-67, 78-91 and 15-23 of Seq ID No 244; 11-22, 33-47, 52-80, 88-112, 124-129 and 6-25 of Seq ID No 245; 26-41, 51-63, 80-89, 93-115, 150-163, 187-193, 220-237, 240-249, 286-294, 296-306, 316-329, 345-353, 361-370, 407-425, 428-437, 474-482, 484-494, 504-517, 533-541, 549-558, 595-613, 616-625, 660-668, 673-685, 711-726, 736-744, 749-761, 787-802, 812-820, 825-837, 863-878, 888-896, 901-913, 939-954, 964-972, 977-989, 1003-1008, 1016-1022, 1028-1034, 1041-1053, 1059-1074, 1101-1122, 420-511 and 581-704 of Seq ID No 246; 18-25, 27-55, 71-83, 89-95, 102-113, 120-146, 150-156, 174-185 and 159-175 of Seq ID No 247; 24-30,

38-56, 63-68, 87-93, 136-142, 153-164, 183-199, 213-219, 226-234, 244-261, 269-278, 283-289, 291-297, 320-328, 330-336, 340-346, 348-356, 358-366, 382-387, 401-408, 414-419, 449-455, 468-491, 504-512, 531-537, 554-560, 597-608, 621-627, 632-643, 650-662, 667-692, 703-716, 724-737, 743-758, 783-794, 800-818, 846-856 and 806-884 of Seq ID No 248; 4-14, 21-39, 86-92, 99-107, 121-131, 136-144, 147-154, 158-166, 176-185, 193-199, 207-222, 224-230 and 117-136 of Seq ID No 249; 65-76, 85-97, 103-109, 115-121, 125-146, 163-169, 196-205, 212-219, 228-237, 241-247, 254-262, 269-288, 294-303, 305-313, 328-367, 395-401, 405-412, 418-429, 437-447, 481-488, 506-513, 519-524, 530-541, 546-557 and 266-284 of Seq ID No 250; 5-14, 37-42, 49-71, 78-92, 97-112, 127-136, 147-154, 156-163, 186-198, 216-225, 233-243, 248-253, 295-307, 323-332, 359-366, 368-374, 380-398 and 194-223 of Seq ID No 251; 4-11, 33-39, 45-72, 100-113, 119-129, 136-144, 169-175, 177-185, 200-208, 210-219, 262-276, 278-297, 320-326, 336-344, 347-362, 381-394, 443-453 and 438-454 of Seq ID No 252; 4-29, 31-52, 55-61, 95-110, 138-158, 162-171, 179-187, 202-229, 239-248, 251-256, 262-267, 269-285, 304-310, 351-360, 362-368, 381-388, 415-428, 435-440, 448-458 and 161-178 of Seq ID No 253; 4-17, 19-28, 32-43, 47-59, 89-110, 112-126, 128-134, 140-148, 152-161, 169-184, 191-204, 230-235, 255-264, 328-338, 341-347, 401-409, 413-419, 433-441, 449-458, 463-468, 476-482, 486-492, 500-506, 529-545 and 305-381 of Seq ID No 254; 10-29, 38-45, 53-61, 134-145, 152-160, 163-170, 202-208, 219-229, 248-258, 266-275, 282-288, 315-320, 328-334, 377-385, 392-402, 418-424, 447-453, 460-471, 479-487, 491-497, 500-507, 531-537, 581-594, 615-623, 629-635, 644-652, 659-666, 668-678, 710-717, 719-728, 736-741, 747-760, 766-773, 784-789, 794-800, 805-817, 855-861, 866-887 and 698-715 of Seq ID No 255; 16-26, 29-37, 44-58, 62-68, 74-80, 88-95, 97-120, 125-144, 165-196 and 58-72 of Seq ID No 256; 14-21, 23-46, 49-60, 63-74, 78-92, 96-103, 117-129, 134-161, 169-211, 217-231, 239-248, 252-281, 292-299, 313-343 and 243-257 of Seq ID No 257; 11-27, 46-52, 67-72, 76-84, 91-112, 116-153, 160-175, 187-196, 202-211, 213-220 and 43-76 of Seq ID No 258; 5-29, 37-56, 78-86, 108-118, 152-161 and 120-130 of Seq ID No 259; 8-14, 19-41, 52-66, 75-82, 87-92, 106-121, 127-133, 136-143, 158-175, 180-187, 196-204, 221-228, 239-245, 259-265, 291-306, 318-323, 328-340, 352-358, 361-368, 375-381, 391-399, 411-418, 431-442, 446-455, 484-496, 498-510, 527-533, 541-549, 558-565, 575-585, 587-594, 644-655, 661-668, 671-677 and 184-196 of Seq ID No 260; 4-22, 29-38, 55-62, 75-81, 102-107, 110-134, 143-150, 161-167, 172-179, 191-215, 223-233, 241-247, 251-264, 266-272, 288-309, 340-352, 354-366, 394-402, 414-438 and 198-218 of Seq ID No 261; 24-44, 49-70, 80-91, 105-118, 128-136, 140-154 and 77-92 of Seq ID No 262; 5-22, 31-36, 41-47, 67-74, 83-90, 105-122, 135-143, 160-167 and 118-129 of Seq ID No 263; 4-25, 33-73, 81-93, 96-106, 114-120, 122-128, 130-172, 179-208, 210-241, 251-283, 296-301 and 92-100 of Seq ID No 264; 14-24, 29-38, 43-50, 52-72, 86-97, 101-107, 110-125, 127-141, 145-157, 168-175, 177-184, 186-195, 205-226, 238-250, 255-261, 284-290, 293-304, 307-314, 316-323, 325-356, 363-371, 383-390, 405-415, 423-432, 442-454, 466-485, 502-511, 519-527, 535-556, 558-565, 569-574, 612-634, 641-655, 672-686, 698-709, 715-722, 724-732, 743-753, 760-769, 783-792, 818-825, 830-839, 842-849, 884-896, 905-918, 926-940, 957-969, 979-1007, 1015-1021, 1049-1057 and 336-349 of Seq ID No 265; 6-16, 26-31, 33-39, 62-73, 75-85, 87-100, 113-123, 127-152, 157-164, 168-181, 191-198, 208-214, 219-226, 233-254, 259-266, 286-329 and 181-195 of Seq ID No 266; 4-13, 32-39, 53-76, 99-108, 110-116, 124-135, 137-146, 149-157, 162-174, 182-190, 207-231, 242-253, 255-264, 274-283, 291-323, 334-345, 351-360, 375-388, 418-425, 456-474, 486-492, 508-517, 520-536, 547-560, 562-577, 31-45 and 419-443 of Seq ID No 267; 15-26, 30-37, 42-49, 58-90, 93-99, 128-134, 147-154, 174-179, 190-197, 199-205, 221-230, 262-274, 277-287, 300-314, 327-333, 343-351, 359-377, 388-396, 408-413, 416-425, 431-446 and 246-256 of Seq ID No 268; 5-26, 34-42, 47-54, 61-67, 71-104, 107-115, 131-138, 144-153, 157-189, 196-202, 204-210, 228-245, 288-309, 316-329, 332-341, 379-386, 393-399, 404-412, 414-421, 457-468, 483-489, 500-506, 508-517, 523-534, 543-557, 565-580, 587-605, 609-617, 619-627, 631-636, 640-646, 662-668, 675-682, 705-710, 716-723, 727-732, 750-758, 784-789, 795-809, 869-874, 14-138, 166-286, 372-503, 674-696 and 754-859 of Seq ID No 269; 5-17, 32-38, 40-47, 80-89, 113-119, 125-137, 140-154, 157-163, 170-177, 185-199, 213-225, 228-236, 242-248, 277-290, 292-305, 323-333, 347-353, 364-370, 385-394, 399-406, 423-433, 441-451, 462-474, 477-487 and 116-124 of Seq ID No 270; 7-16, 18-30, 32-49, 53-61, 63-85, 95-101, 105-115, 119-134, 143-150, 159-178, 185-202, 212-229, 236-250, 254-265, 268-294 and 63-72 of Seq ID No 271; 4-12, 19-47, 73-81, 97-103, 153-169, 188-198, 207-213, 217-223, 236-242, 255-265, 270-278, 298-305, 309-317, 335-347, 354-363, 373-394, 419-424, 442-465, 486-492, 500-507, 542-549, 551-558, 560-572, 580-589, 607-614, 617-623, 647-653, 666-676, 694-704, 706-714, 748-754, 765-772, 786-792, 795-806 and 358-370 of Seq ID No 272; 18-28, 30-38, 40-46, 49-55, 69-78, 82-98, 104-134, 147-153, 180-190, 196-202, 218-236, 244-261, 266-273, 275-286, 290-295, 301-314, 378-387, 390-395, 427-434 and 290-305 of Seq ID No 273; 4-13, 20-31, 39-51, 54-61, 69-84, 87-105, 117-124 and 108-125 of Seq ID No 274; 24-34, 43-54, 56-66, 68-79 and 50-

69 of Seq ID No 275; 5-43, 71-77, 102-131, 141-148, 150-156, 159-186, 191-207, 209-234, 255-268, 280-286, 293-299, 317-323, 350-357, 363-372, 391-397, 406-418, 428-435, 455-465, 484-497, 499-505, 525-531, 575-582, 593-607, 621-633, 638-649, 655-673, 684-698, 711-725, 736-741, 743-752, 759-769, 781-793, 813-831, 843-853, 894-905, 908-916, 929-946, 953-963, 970-978, 1001-1007, 1011-1033, 165-178 and 818-974 of Seq ID No 276; 16-44, 63-86, 98-108, 185-191, 222-237, 261-274, 282-294, 335-345, 349-362, 374-384, 409-420, 424-430, 440-447, 453-460, 465-473, 475-504, 522-534, 538-551, 554-560, 567-582, 598-607, 611-619, 627-640, 643-653, 655-661, 669-680, 684-690, 701-707, 715-731, 744-750, 756-763, 768-804, 829-837, 845-853, 855-879, 884-890, 910-928, 77-90, 144-212, 279-355, 434-536, 782-810 and 875-902 of Seq ID No 277; 4-22, 29-41, 45-51, 53-66, 70-77, 86-95, 98-104, 106-124, 129-135, 142-151, 153-161, 169-176, 228-251, 284-299, 331-337, 339-370, 380-387, 393-398, 406-411, 423-433, 440-452, 461-469, 488-498, 501-516, 523-530, 532-559, 562-567, 570-602, 612-628, 630-645, 649-659, 666-672, 677-696, 714-723, 727-747 and 212-227 of Seq ID No 278; 4-9, 17-31, 35-41, 56-61, 66-75, 81-87, 90-124, 133-138, 149-163, 173-192, 213-219, 221-262, 265-275, 277-282, 292-298, 301-307, 333-346, 353-363, 371-378, 419-430, 435-448, 456-469, 551-570, 583-599, 603-612 and 275-291 of Seq ID No 279; 28-34, 53-58, 72-81, 100-128, 145-154, 159-168, 172-189, 217-225, 227-249, 256-263, 299-309, 322-330, 361-379, 381-388, 392-401, 404-417, 425-436, 440-446, 451-464, 469-487, 502-511, 543-551, 559-564, 595-601, 606-612, 615-626, 633-642, 644-650, 664-670, 674-684, 692-701, 715-723, 726-734, 749-756, 763-771, 781-787, 810-843, 860-869, 882-889, 907-917, 931-936, 941-948, 951-958, 964-971, 976-993, 1039-1049, 1051-1065, 1092-1121, 1126-1132, 1145-1151, 1158-1173, 1181-1192, 1194-1208, 1218-1223, 1229-1243, 1249-1254, 1265-1279, 1287-1297, 1303-1320, 1334-1341, 1343-1358, 1372-1382, 1406-1417, 1419-1425, 1428-1434, 1441-1448, 1460-1473, 1494-1504, 1509-1514, 1529-1550, 654-669 and 1400-1483 of Seq ID No 280; 10-16, 20-25, 58-65, 97-109, 118-132, 134-146, 148-155, 186-195, 226-233, 244-262, 275-284, 295-310, 317-322, 330-339, 345-351, 366-375, 392-403, 408-415, 423-430, 435-444, 446-457, 467-479, 486-499, 503-510, 525-537, 540-585, 602-612, 614-623, 625-634, 639-645, 650-669, 700-707, 717-724, 727-739, 205-230 and 733-754 of Seq ID No 281; 5-22, 37-43, 72-81, 105-113, 128-133, 148-160, 188-194, 204-230, 238-245, 251-257 and 194-213 of Seq ID No 282; 16-21, 35-41, 56-72, 74-92, 103-109 and 62-68 of Seq ID No 283; 4-15, 17-82, 90-104, 107-159, 163-170, 188-221, 234-245, 252-265 and 220-235 of Seq ID No 284; 16-22, 36-46, 61-75, 92-107, 113-121, 139-145, 148-160 and 30-42 of Seq ID No 285; 4-12, 20-26, 43-49, 55-62, 66-78, 121-127, 135-141, 146-161, 164-170, 178-189, 196-205, 233-238, 269-279, 288-318, 325-332, 381-386, 400-407 and 328-346 of Seq ID No 286; 5-12, 31-49, 57-63, 69-79, 89-97, 99-114, 116-127, 134-142, 147-154, 160-173, 185-193, 199-204, 211-222, 229-236, 243-249, 256-274 and 58-68 of Seq ID No 287; 10-20, 28-34, 39-53, 68-79, 84-90, 99-106 and 73-79 of Seq ID No 288; 14-37, 45-50, 61-66, 77-82, 93-98, 109-114, 125-130, 141-146, 157-162, 173-178, 189-194, 205-210, 221-226, 237-242, 253-258, 269-274, 285-290, 301-306, 316-332, 349-359, 371-378, 385-406, 34-307 and 312-385 of Seq ID No 289; 4-10, 17-38, 50-85, 93-99, 109-116, 128-185, 189-197, 199-210, 223-256, 263-287, 289-312, 327-337, 371-386, 389-394, 406-419, 424-432, 438-450, 458-463, 475-502, 507-513, 519-526, 535-542, 550-567 and 361-376 of Seq ID No 290; 10-39, 42-93, 100-144, 155-176, 178-224, 230-244, 246-255, 273-282, 292-301, 308-325, 332-351, 356-361, 368-379, 386-393, 400-421 and 138-155 of Seq ID No 291; 5-11, 17-34, 40-45, 50-55, 72-80, 101-123, 145-151, 164-172, 182-187, 189-195, 208-218, 220-241, 243-252, 255-270, 325-331, 365-371, 391-398, 402-418, 422-428, 430-435, 443-452, 463-469, 476-484, 486-494, 503-509, 529-553, 560-565, 570-590, 608-614, 619-627, 654-661, 744-750, 772-780, 784-790, 806-816, 836-853, 876-885, 912-918, 926-933, 961-975, 980-987, 996-1006, 1016-1028, 1043-1053, 1057-1062, 994-1003 and 1033-1056 of Seq ID No 292; 17-45, 64-71, 73-81, 99-109, 186-192, 223-238, 262-275, 283-295, 336-346, 350-363, 375-385, 410-421, 425-431, 441-448, 454-463, 468-474, 476-512, 523-537, 539-552, 568-583, 599-608, 612-620, 628-641, 644-654, 656-662, 670-681, 685-695, 702-708, 716-723, 725-735, 757-764, 769-798, 800-806, 808-816, 826-840, 846-854, 856-862, 874-881, 885-902, 907-928, 274-350 and 443-513 of Seq ID No 293; 4-22, 29-41, 45-51, 53-61, 70-76, 85-92, 99-104, 111-122, 134-140, 142-154, 163-174, 224-232, 255-265, 273-279, 283-297, 330-335, 337-348, 356-367, 373-385, 391-396, 421-431, 442-455, 475-485, 493-505, 526-538, 544-561, 587-599, 605-620, 622-651, 662-670, 675-681, 687-692, 697-712, 714-735 and 252-262 of Seq ID No 294; 4-12, 15-35, 40-46, 50-59, 67-94, 110-128, 143-169, 182-188, 207-215, 218-228, 238-250 and 74-90 of Seq ID No 295; 9-18, 42-58, 78-85, 88-95, 97-106, 115-122, 128-134, 140-145, 154-181, 186-202, 204-223, 261-267, 269-278, 284-293, 300-336, 358-368 and 12-29 of Seq ID No 296; 7-34, 46-53, 62-72, 82-88, 100-105, 111-117, 132-137, 144-160, 166-180, 183-189, 209-221, 231-236, 246-253, 268-282, 286-293, 323-336, 364-372, 378-392, 422-433 and 388-405 of Seq ID No 297; 21-27, 34-50, 72-77, 80-95, 164-177, 192-198, 202-220, 226-236, 239-247, 270-279, 285-292, 315-320, 327-334, 348-355, 364-371, 388-397, 453-476, 488-

497, 534-545, 556-576, 582-588, 601-607, 609-616, 642-662, 674-681, 687-697, 709-715, 721-727, 741-755 and 621-739 of Seq ID No 298; 4-14, 16-77, 79-109 and 25-99 of Seq ID No 299; 4-9, 17-23, 30-37, 44-55, 65-72, 77-93, 102-121, 123-132, 146-153 and 17-29 of Seq ID No 300; 4-18, 25-41, 52-60, 83-92, 104-112, 117-123, 149-155, 159-167, 170-192, 201-210, 220-227, 245-250 and 124-137 of Seq ID No 301; 8-25, 50-55, 89-95, 138-143, 148-153, 159-169, 173-179, 223-238, 262-268, 288-295, 297-308, 325-335, 403-409, 411-417, 432-446, 463-475, 492-501, 524-530, 542-548, 561-574, 576-593, 604-609, 612-622, 637-654, 665-672, 678-685, 720-725, 731-739, 762-767, 777-783, 820-838, 851-865, 901-908, 913-920, 958-970, 1000-1006, 1009-1015, 1020-1026, 1043-1052, 1055-1061, 1-128, 252-341, 771-793 and 1043-1058 of Seq ID No 302; 16-26, 33-46 and 64-76 of Seq ID No 303; 4-27, 69-77, 79-101, 117-123, 126-142, 155-161, 171-186, 200-206, 213-231, 233-244, 267-273, 313-329, 335-344, 347-370, 374-379, 399-408, 422-443, 445-453, 461-468, 476-482, 518-534, 544-553, 556-567, 578-595, 601-620, 626-636, 646-658, 666-681, 715-721, 762-768, 778-785, 789-803, 809-819, 22-108, 153-318, 391-527 and 638-757 of Seq ID No 304; 6-21, 32-43, 62-92, 104-123, 135-141, 145-152, 199-216, 218-226, 237-247, 260-269, 274-283, 297-303, 1-72 and 127-211 of Seq ID No 305; 6-26, 50-56, 83-89, 108-114, 123-131, 172-181, 194-200, 221-238, 241-247, 251-259, 263-271, 284-292, 304-319, 321-335, 353-358, 384-391, 408-417, 424-430, 442-448, 459-466, 487-500, 514-528, 541-556, 572-578, 595-601, 605-613, 620-631, 635-648, 660-670, 673-679, 686-693, 702-708, 716-725, 730-735, 749-755, 770-777, 805-811, 831-837, 843-851, 854-860, 863-869, 895-901, 904-914, 922-929, 933-938, 947-952, 956-963, 1000-1005, 1008-1014, 1021-1030, 1097-1103, 1120-1130, 1132-1140, 1-213, 269-592 and 992-1120 of Seq ID No 306; 9-16, 33-39, 47-59, 65-79, 81-95, 103-108, 115-123, 138-148, 163-171, 176-185, 191-196, 205-211, 213-221, 224-256, 261-276, 294-302, 357-363, 384-390, 95-111 and 161-189 of Seq ID No 307; 21-27, 35-45, 70-76, 92-105, 129-143, 145-155, 161-166, 170-191, 204-211, 214-231, 234-246, 249-255, 259-275 and 1-18 of Seq ID No 308; 21-35, 45-53, 56-64, 69-97 and 1-16 of Seq ID No 309; 25-33, 41-47, 61-68, 86-101, 106-114, 116-129, 134-142, 144-156, 163-176, 181-190, 228-251, 255-261, 276-292, 295-305, 334-357, 368-380, 395-410, 424-429, 454-460, 469-482, 510-516, 518-527, 531-546, 558-570, 579-606, 628-636, 638-645, 651-656, 668-674, 691-698, 717-734, 742-754, 765-770, 792-797, 827-835, 847-859, 874-881, 903-909, 926-933, 942-961, 964-977, 989-1004, 1010-1028, 1031-1047, 1057-1075, 1081-1095, 1108-1117, 1138-1144, 1182-1189, 1193-1206, 1220-1229, 1239-1246, 1257-1267, 1271-1279, 1284-1301, 1312-1320, 1329-1335, 1341-1347, 1358-1371, 1399-1404, 1417-1426, 1458-1463, 1468-1476, 1478-1485, 1493-1506, 1535-1541, 1559-1574, 1583-1590, 1595-1601, 1603-1611, 1622-1628, 1634-1644, 1671-1685, 1689-1696, 1715-1720, 1734-1746, 1766-1775, 1801-1806, 1838-1844, 1858-1871, 1910-1917, 1948-1955, 1960-1974, 2000-2015, 2019-2036, 2041-2063, 748-847 and 1381-1391 of Seq ID No 310; 5-12, 18-24, 27-53, 56-63, 96-113, 119-124, 131-136, 157-163, 203-209, 215-223, 233-246, 264-273, 311-316, 380-389, 393-399, 425-433, 445-450, 457-462, 464-470, 475-482, 507-513, 527-535, 542-548, 550-565, 591-602, 607-613, 627-642, 644-664, 673-712, 714-732, 739-764, 769-782, 812-818, 826-838, 848-854, 860-871, 892-906, 930-938, 940-954, 957-973, 990-998, 1002-1021, 1024-1033, 1037-1042, 1050-1060, 1077-1083, 1085-1092, 1100-1129, 1144-1161, 1169-1175, 1178-1189, 1192-1198, 1201-1207, 1211-1221, 1229-1239, 1250-1270, 1278-1292, 1294-1300, 1314-1335, 1344-1352, 1360-1374, 1394-1405, 1407-1414, 1416-1424, 1432-1452, 1456-1462, 1474-1497, 1500-1510, 1516-1522, 1534-1542, 1550-1559, 1584-1603, 1608-1627, 187-273 and 306-441 of Seq ID No 311; 70-80, 90-97, 118-125, 128-140, 142-148, 154-162, 189-202, 214-222, 224-232, 254-260, 275-313, 317-332, 355-360, 392-398, 425-432, 448-456, 464-470, 476-482, 491-505, 521-528, 533-546, 560-567, 592-597, 605-614, 618-626, 637-644, 646-653, 660-666, 677-691 and 207-227 of Seq ID No 312; 5-19, 26-34, 37-55, 57-66, 69-83, 86-102, 115-134, 138-143, 154-172, 178-195, 209-246, 251-257, 290-302, 306-311 and 256-266 of Seq ID No 313; 10-20, 22-28, 35-57, 72-79, 87-103, 108-128, 130-144, 158-171, 190-198, 225-242, 274-291, 301-315, 317-324, 374-385 and 353-365 of Seq ID No 314; 4-9, 17-30, 34-54, 59-66, 73-94, 118-130, 135-150, 158-171, 189-198, 219-239, 269-275, 283-301, 89-106 and 176-193 of Seq ID No 315; 14-20, 22-74, 77-86, 89-99, 104-109, 126-135, 154-165, 181-195, 197-212, 216-224, 264-275 and 107-118 of Seq ID No 316; 4-18, 21-38, 63-72, 101-109, 156-162, 165-179, 183-192, 195-210, 212-218, 230-239, 241-256, 278-290, 299-311, 313-322, 332-341, 348-366, 386-401, 420-426, 435-450, 455-460, 468-479, 491-498, 510-518, 532-538, 545-552, 557-563, 567-573, 586-595, 599-609, 620-626, 628-636, 652-657, 665-681 and 1-198 of Seq ID No 317; 4-10, 16-38, 51-68, 73-79, 94-115, 120-125, 132-178, 201-208, 216-223, 238-266, 269-295, 297-304, 337-342, 347-356, 374-401, 403-422, 440-447, 478-504, 510-516, 519-530, 537-544 and 191-206 of Seq ID No 318; 12-40, 42-48, 66-71, 77-86, 95-102, 113-120, 129-137, 141-148, 155-174, 208-214, 218-225, 234-240, 256-267, 275-283, 300-306, 313-321, 343-350, 359-367, 370-383, 398-405, 432-439, 443-461, 492-508, 516-526, 528-535 and 370-478 of Seq ID No 319; 6-14, 20-37, 56-62, 90-95, 97-113, 118-125, 140-145, 161-170, 183-202,

237-244, 275-284, 286-305, 309-316, 333-359, 373-401, 405-412 and 176-187 of Seq ID No 320; 33-44, 50-55, 59-80, 86-101, 129-139, 147-153, 157-163, 171-176, 189-201, 203-224, 239-245, 257-262, 281-287, 290-297, 304-320, 322-331, 334-350, 372-390, 396-401, 71-88 and 353-372 of Seq ID No 321; 5-11, 15-24, 26-33, 40-47, 75-88, 95-103, 105-112 and 17-30 of Seq ID No 322; 5-11, 16-39, 46-54, 62-82, 100-107, 111-124, 126-150, 154-165, 167-183, 204-238, 245-295, 301-313, 316-335 and 8-16 of Seq ID No 323; 4-19, 34-48, 69-74, 79-107, 115-127, 129-135, 143-153, 160-169, 171-182 and 142-153 of Seq ID No 324; 4-30, 65-74, 82-106, 110-120, 124-132, 135-140, 146-175, 179-184, 190-196, 217-223, 228-233, 250-267, 275-292, 303-315, 322-332 and 174-186 of Seq ID No 325; 9-16, 29-41, 47-57, 68-84, 87-109, 113-119, 162-180, 186-193, 195-201, 203-208, 218-230, 234-243, 265-271, 281-292, 305-312, 323-332, 341-347, 349-363, 368-374, 383-390, 396-410, 434-440, 446-452, 455-464, 466-473, 515-522, 529-542, 565-570, 589-600, 602-613, 618-623, 637-644, 1019-1027, 1238-1244, 1258-1264, 1268-1276, 1281-1292, 1296-1302 and 883-936 of Seq ID No 326; 10-17, 23-32, 39-44, 54-72, 75-81, 88-111, 138-154, 160-167, 178-185, 201-210, 236-252, 327-334, 336-342, 366-376, 388-400, 410-430, 472-482, 493-526, 552-558, 586-592, 598-603, 612-621, 630-635, 641-660 and 384-393 of Seq ID No 327; 4-22, 24-39, 50-59, 73-84, 100-105, 111-117, 130-138, 155-161, 173-178, 182-189, 205-215, 266-284, 308-313, 321-328, 330-337, 346-363, 368-374, 388-395, 397-405, 426-434, 453-459, 482-492, 501-507, 509-515, 518-523, 527-544, 559-590, 598-612, 614-629, 646-659, 663-684, 686-694, 698-721 and 445-461 of Seq ID No 328; 14-22, 27-33 and 3-17 of Seq ID No 329; 29-41, 66-73, 81-87, 90-108, 140-146, 150-159, 165-184, 186-196, 216-226, 230-238, 247-253, 261-269 and 126-140 of Seq ID No 330; 5-12, 16-25, 27-33, 36-45, 60-68, 83-88, 103-126 and 86-101 of Seq ID No 331; 14-23, 36-47, 56-66, 84-89, 94-105, 111-127, 140-153, 160-174, 176-183, 189-203, 219-225, 231-237, 250-257 and 194-227 of Seq ID No 332; 4-25, 54-60, 64-71, 73-82, 89-106, 117-124, 157-169, 183-188, 199-210, 221-232, 236-244, 255-264 and 58-98 of Seq ID No 333; 13-19, 26-36, 41-53, 55-71, 77-84, 86-108, 114-135, 157-172, 177-183, 187-194, 208-213, 218-226, 110-125 and 156-170 of Seq ID No 334; 5-24, 63-69, 77-85, 94-112, 120-137, 140-146, 152-159, 166-172, 179-187, 193-199, 206-212, 222-228, 234-240, 244-252, 257-264, 270-289, 298-309, 316-328, 337-348, 363-375, 1-56 and 340-352 of Seq ID No 335; 18-39, 42-71, 78-120, 124-144, 152-173, 179-189, 199-209, 213-222, 228-258, 269-304, 329-361, 364-372, 374-389, 396-441 and 313-327 of Seq ID No 336; 19-25, 91-98, 108-120, 156-162, 168-174, 191-204, 211-216, 232-266, 272-278, 286-308, 316-321, 327-333, 344-355, 358-364, 384-391, 395-428, 464-476, 487-495, 497-511, 544-561, 563-573, 575-582, 588-594, 10-25 and 322-338 of Seq ID No 337; 14-26, 32-49, 51-57, 59-72, 80-91, 102-112, 119-125, 147-161, 164-173, 175-183, 188-213, 217-222, 246-254, 260-276, 282-303, 308-318, 321-328, 333-350, 352-359, 371-378, 392-401, 407-414, 416-443, 448-463, 471-484, 490-497, 501-514, 519-527, 539-551, 557-570, 578-590, 592-598, 600-610, 618-629, 633-647, 654-667, 676-689, 702-709, 718-726, 728-737, 741-760, 764-780, 786-795, 808-826, 836-842, 845-852, 865-874, 881-887, 931-945, 949-957, 968-974, 979-986, 1003-1009, 1023-1029 and 90-103 of Seq ID No 338; 11-16, 37-56, 60-66, 69-77, 80-88, 93-106, 117-139, 166-171 and 72-90 of Seq ID No 339; 59-84, 123-133, 145-150, 161-167, 178-189 and 115-128 of Seq ID No 340; 15-33, 39-46, 52-64, 74-87, 108-124, 127-144, 150-156, 173-179, 184-194, 201-208, 219-236, 243-269, 272-295, 302-309, 343-349, 356-361, 370-379, 405-411, 414-423, 430-451, 457-464, 466-475, 477-483, 496-502, 507-522, 541-548, 557-563, 571-577, 579-585, 590-605, 626-642, 650-662, 671-691, 704-710, 751-769, 775-781, 786-791, 794-829, 851-858, 868-878, 884-904, 913-919, 931-939 and 132-142 of Seq ID No 341; 33-58, 64-71, 74-80, 83-88, 96-120, 122-139, 146-157, 167-177, 207-213, 220-225, 236-242, 264-279, 300-305, 326-336, 340-347, 350-360, 97-115 and 199-211 of Seq ID No 342; 4-26, 43-57, 70-99, 102-117, 121-133, 142-148, 151-168, 170-183, 192-220, 235-249, 258-279 and 30-41 of Seq ID No 343; 34-42, 48-58, 70-94, 110-130, 154-160, 164-172, 178-183, 195-203, 211-222, 229-250, 256-261, 274-284, 286-292, 312-323 and 222-233 of Seq ID No 344; 4-9, 15-36, 38-45, 49-74, 78-88, 100-112, 136-191, 211-220, 226-233, 239-246, 254-274, 287-307, 316-322, 342-353, 356-366, 373-378, 384-393, 405-431, 449-457, 459-468, 487-511, 515-524, 529-541, 544-552, 562-568, 571-576 and 208-280 of Seq ID No 345; 10-27, 31-37, 39-54, 71-108, 124-143 and 2-107 of Seq ID No 346; 16-27, 38-57, 64-70, 90-102, 104-113, 116-137, 160-166 and 1-80 of Seq ID No 347; 13-21, 31-36, 56-67, 127-136, 153-171, 173-180, 184-200, 214-222, 225-231, 239-263, 267-273 and 135-159 of Seq ID No 348; 12-27, 31-51, 68-74, 77-87, 94-101, 108-114, 117-123, 127-134, 138-168, 173-196, 201-207, 212-217, 227-237, 247-257, 264-280 and 205-223 of Seq ID No 349; 17-22, 25-54, 70-76, 92-100 and 98-110 of Seq ID No 350; 7-29, 40-50, 60-67, 87-96, 105-111, 119-164, 172-199, 206-212, 220-227, 237-259, 272-279, 282-293, 295-309, 313-319, 321-328, 345-363, 376-386 and 159-176 of Seq ID No 351; 4-19, 24-30, 36-43, 50-68, 71-89, 93-106, 141-152, 154-172, 179-197, 199-215, 229-239, 246-252, 255-263, 281-298, 319-325, 329-356, 358-368, 374-390, 397-409, 420-429, 432-444, 450-456, 459-475, 483-494, 496-502, 520-528, 532-

556 and 362-377 of Seq ID No 352; 18-25, 40-62, 77-85, 91-97, 105-116, 123-133, 139-184, 189-197 and 122-140 of Seq ID No 353; 4-49, 52-58, 62-70, 79-105, 109-133, 142-150, 163-168, 206-214, 220-228, 233-240, 243-254, 274-281, 303-311, 327-338, 357-373, 378-396, 403-413, 420-436, 441-453, 461-467, 475-481, 484-498, 506-512, 514-521, 523-529, 562-579, 589-595, 598-603, 615-648, 714-722, 728-742, 749-758, 777-792, 795-807 and 643-658 of Seq ID No 354; 8-27, 37-48, 51-56, 72-79, 87-106, 120-138, 140-147, 167-176, 187-197, 205-216, 222-229, 234-239, 243-249, 277-288, 292-315, 334-343, 347-353, 363-391, 398-404, 430-447, 461-467, 478-492, 498-507 and 456-470 of Seq ID No 355; 5-12, 18-24, 59-69, 80-93, 95-109, 119-125, 130-137, 139-147, 158-163, 168-176, 182-202, 206-215, 222-239, 241-249, 267-277, 291-298, 311-318, 321-327, 338-344, 348-355, 373-386, 393-406, 411-417, 434-443, 446-465, 473-484, 514-521, 532-553, 584-594 and 221-237 of Seq ID No 356; 4-14, 27-34, 50-58, 63-72, 79-106, 109-114, 121-142, 146-154, 161-167, 169-175, 178-201, 223-238, 249-254, 259-264, 278-292, 294-312, 319-330 and 167-191 of Seq ID No 357; 7-28, 36-42, 50-61, 63-80, 122-152, 161-174, 176-191 and 140-190 of Seq ID No 358; 20-57, 59-65, 70-78, 86-102, 119-133, 142-161, 163-173, 177-188, 192-202, 204-220, 222-236, 240-253, 279-319, 326-331, 337-383, 390-399, 406-412, 420-427, 431-438 and 381-395 of Seq ID No 359; 13-18, 28-34, 37-43, 50-59, 75-81, 83-97, 105-121, 139-147, 200-206, 209-227, 231-247, 260-271, 318-327, 366-381, 388-394, 399-406 and 182-201 of Seq ID No 360; 6-29, 37-43, 51-56, 70-77, 82-102, 110-119, 127-143, 178-190, 201-209, 216-243, 261-269, 281-292, 305-313, 327-339, 341-354, 356-373, 391-397, 423-429, 438-445, 450-478 and 21-314 of Seq ID No 361; 4-12, 15-21, 32-41, 59-76, 80-89, 96-104 and 90-103 of Seq ID No 362; 9-28, 30-41, 44-54, 69-74, 77-82, 90-97, 104-123, 125-135, 149-155, 164-173, 177-184, 217-226, 230-235, 238-244, 258-272, 282-297, 300-305, 309-315, 317-322, 327-336, 348-362, 368-374, 380-387, 400-411, 414-424, 451-458, 460-466, 483-494, 497-503, 506-511, 521-528, 540-553, 569-587, 598-606, 628-642, 661-681, 688-700, 718-733, 740-749, 752-764, 769-783, 823-834, 848-854, 862-872, 878-884, 886-898, 915-920, 938-951, 954-961, 963-972, 982-989, 996-1003, 1010-1016, 1021-1032, 1038-1044, 1047-1057, 1060-1070, 1079-1088, 1094-1102, 1117-1127, 1129-1135, 1142-1153, 1158-1204, 1212-1229, 1234-1263, 1269-1277, 1308-1313, 1327-1338, 1344-1376, 1400-1415, 1436-1443, 1448-1458, 1497-1504, 1511-1522, 1544-1566, 3-82 and 509-576 of Seq ID No 363; 8-36, 40-64, 71-79, 88-94, 102-109, 118-127, 138-148, 151-159, 163-174, 192-198, 200-206, 220-233, 268-273, 290-301, 304-309, 316-323, 331-349, 378-391, 414-420, 427-437, 455-475, 494-510, 541-547, 549-555, 616-640, 1-60, 55-139, 212-308, 386-458 and 458-624 of Seq ID No 364; 16-31, 35-42, 70-77, 91-101, 120-130, 132-140, 143-153, 185-190, 195-202, 215-222, 228-238, 241-251, 257-264, 268-277, 288-302, 312-324, 326-333, 341-348, 364-382, 415-429, 438-454, 458-466, 491-499, 501-521 and 273-281 of Seq ID No 365; 8-14, 32-57, 74-149, 155-177, 179-212, 221-266, 271-296, 304-324, 329-346, 349-359, 368-401, 413-419, 426-454, 465-478, 493-510 and 466-490 of Seq ID No 366; 22-28, 33-51, 64-89, 96-119, 126-132, 138-146, 152-159, 161-169, 172-179, 193-198, 205-211, 221-231, 235-254, 273-280, 297-303, 312-320, 328-346, 351-373, 378-384, 391-398, 448-454, 460-468, 470-481, 516-558, 574-593, 597-602, 613-623, 626-646, 649-656, 668-673, 675-683, 696-708, 715-722, 724-739, 745-751, 759-777, 780-804, 816-822 and 102-113 of Seq ID No 367; 12-28, 41-91, 98-107, 112-120, 125-131, 151-193, 215-221, 240-250, 263-280 and 128-138 of Seq ID No 368; 16-24, 32-38, 46-62, 68-81, 90-105, 127-133, 144-150, 160-166, 178-184, 186-202, 210-219, 232-240, 252-258, 264-273, 293-324, 337-344, 349-357, 360-369, 385-398, 410-416, 419-427, 441-449, 458-476, 508-515, 523-539, 544-549, 562-569, 571-579, 96-109 and 127-139 of Seq ID No 369; 19-25, 28-34, 56-61, 85-97, 110-116 and 39-53 of Seq ID No 370; 4-37, 41-50, 62-72, 91-97, 99-109, 114-125, 136-141, 149-158, 160-166, 201-215 and 27-225 of Seq ID No 371; 15-31, 44-51, 96-105, 122-130, 149-157, 162-168, 178-183, 185-192, 198-204, 206-213, 221-234, 239-245, 248-255, 257-266, 289-335, 349-357, 415-422, 425-441, 448-454, 462-468 and 463-481 of Seq ID No 372; 5-31, 39-55, 63-72, 76-99, 106-155, 160-177, 179-199, 207-217, 223-240, 245-255, 261-267, 294-316, 321-343, 354-378, 382-452, 477-488, 529-536, 555-569, 584-591, 593-612, 620-627, 632-640, 647-654, 671-680, 698-704, 723-730, 732-750, 769-775, 781-788, 822-852 and 505-525 of Seq ID No 373; 3-18 of Seq ID No 374; 4-14 and 12-24 of Seq ID No 375; 4-11, 22-30 and 12-25 of Seq ID No 376; 5-12 and 4-18 of Seq ID No 377; 4-28 and 7-14 of Seq ID No 378; 6-16 and 8-16 of Seq ID No 379; 4-15, 18-33 and 24-36 of Seq ID No 380; 4-10, 16-21 and 20-31 of Seq ID No 381; 6-19 of Seq ID No 382; 11-18 and 3-10 of Seq ID No 383; 13-24 and 3-15 of Seq ID No 384; 15-27 and 7-16 of Seq ID No 385; 11-16 and 1-15 of Seq ID No 386; 4-16 and 9-21 of Seq ID No 387; 4-24, 40-48, 54-67 and 22-39 of Seq ID No 388; 6-30, 34-55, 62-68, 78-106 and 68-74 of Seq ID No 389; 3-14 of Seq ID No 390; 9-19 and 6-21 of Seq ID No 391; 4-17 and 1-9 of Seq ID No 392; 5-30 and 1-8 of Seq ID No 393; 4-16, 23-46, 51-56 and 45-55 of Seq ID No 394; 7-16 of Seq ID No 395; 2-14 of Seq ID No 396; 4-36, 43-65 and 50-62 of Seq ID No 397; 10-30 and 14-21 of Seq ID No 398; 9-17 and 1-10 of Seq ID No 399; 4-12

and 3-16 of Seq ID No 400; 4-15 and 5-23 of Seq ID No 401; 10-21 of Seq ID No 402; 6-16 of Seq ID No 403; 4-29, 31-38 and 2-14 of Seq ID No 404; 4-35 and 33-42 of Seq ID No 405; 2-17 of Seq ID No 406; 9-18, 30-35 and 15-33 of Seq ID No 407; 4-9 and 6-12 of Seq ID No 408; 3-17 of Seq ID No 409; 12-21, 37-44, 52-61, 72-80 and 38-48 of Seq ID No 410; 4-10, 29-44, 54-61, 69-78 and 13-27 of Seq ID No 411; 13-23, 36-53 and 2-15 of Seq ID No 412; 4-25, 28-46, 56-72, 81-99, 120-132, 134-142, 154-160 and 129-141 of Seq ID No 413; 4-15, 24-33, 35-41, 64-86 and 21-33 of Seq ID No 414; 9-15 and 4-13 of Seq ID No 415; 4-11, 13-19, 34-48 and 15-32 of Seq ID No 416; 4-21 and 11-31 of Seq ID No 417; 23-57 and 38-50 of Seq ID No 418; 4-32 and 3-13 of Seq ID No 419; 4-10, 13-25, 32-42, 56-68, 72-84 and 26-38 of Seq ID No 420; 4-20, 31-48, 52-58, 65-71, 80-93, 99-108, 114-123 and 37-49 of Seq ID No 421; 6-12, 14-20 and 3-25 of Seq ID No 422; 14-25, 27-38 and 5-14 of Seq ID No 423; 4-41, 57-105, 109-118, 123-136, 144-152 and 86-99 of Seq ID No 424; 6-19 of Seq ID No 425; 2-19 of Seq ID No 426; 14-47 and 1-14 of Seq ID No 427; 4-21, 29-44 and 2-18 of Seq ID No 428; 23-29 and 10-28 of Seq ID No 429; 6-16, 22-36 and 11-22 of Seq ID No 430; 4-19, 30-44 and 18-27 of Seq ID No 431; 5-15, 37-45, 58-65 and 38-47 of Seq ID No 432; 4-15, 23-34 and 4-15 of Seq ID No 433; 30-36, 44-54, 79-85, 101-114, 138-152, 154-164, 170-175, 179-200, 213-220, 223-240, 243-255, 258-264, 268-284 and 10-28 of Seq ID No 434; the peptides comprising amino acid sequences of column "Identical region" of the Table 1B, especially peptides comprising amino acid 210-226 and 738-753 of Seq ID No 449; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 450; 893-906 of Seq ID No 451; 51-69 of Seq ID No 452; 110-125 of Seq ID No 453; 291-305 of Seq ID No 454; 210-226 and 738-753 of Seq ID No 455; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 456; 893-906 of Seq ID No 457; 51-69 of Seq ID No 458; 110-125 of Seq ID No 459; 291-305 of Seq ID No 460; 32-44 of Seq ID No 461; 399-410 of Seq ID No 462; the serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 2, especially peptides comprising amino acid 120-143, 138-161 and 156-179 of Seq ID No 218; 110-129 and 168-184 of Seq ID No 219; 74-90 of Seq ID No 222; 759-773 of Seq ID No 223; 237-260 of Seq ID No 224; 265-284 of Seq ID No 225; 65-74 of Seq ID No 226; 41-50 of Seq ID No 227; 163-174 of Seq ID No 229; 26-37 of Seq ID No 230; 174-189 of Seq ID No 232; 240-256 of Seq ID No 234; 285-297 of Seq ID No 236; 238-247 of Seq ID No 238; 491-519 of Seq ID No 239; 114-140 of Seq ID No 243; 267-284 of Seq ID No 250; 439-453 of Seq ID No 252; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 60-71 of Seq ID No 256; 244-257 of Seq ID No 257; 44-63 and 57-76 of Seq ID No 258; 185-196 of Seq ID No 260; 119-129 of Seq ID No 263; 182-195 of Seq ID No 266; 32-44 and 424-442 of Seq ID No 267; 247-256 of Seq ID No 268; 678-694, 785-805, 55-77 and 72-94 of Seq ID No 269; 210-226 of Seq ID No 281; 37-59 of Seq ID No 289; 13-29 of Seq ID No 296; 136-159 of Seq ID No 348; 205-222 of Seq ID No 349; 99-110 of Seq ID No 350; 160-176 of Seq ID No 351; 457-470 of Seq ID No 355; 221-237 of Seq ID No 356; 167-190 of Seq ID No 357; 96-120 of Seq ID No 361; 399-417, 503-519 and 544-563 of Seq ID No 364; 46-68, 159-183 and 184-198 of Seq ID No 371; 463-481 of Seq ID No 372; the immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 4; especially peptides comprising amino acid 110-129 and 168-184 of Seq ID No 219; 877-901, 333-354, 326-344 and 801-809 of Seq ID No 277; 1-54 of Seq ID No 347; 544-563, 31-51, 107-119, 399-417 and 503-519 of Seq ID No 364; 120-198 of Seq ID No 218; 20-35 of Seq ID No 219; 118-201 of Seq ID No 221; 48-132 of Seq ID No 242; 118-136 of Seq ID No 249; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 50-76 of Seq ID No 258; 785-819 and 44-128 of Seq ID No 269; 90-128 of Seq ID No 274; 314-384 of Seq ID No 289; 327-349 of Seq ID No 293; 242-314, 405-478 and 23-100 of Seq ID No 304; 129-210 of Seq ID No 305; 162-188 of Seq ID No 307; 750-772 of Seq ID No 310; 1-56 of Seq ID No 335; 322-337 of Seq ID No 337; 72-90 of Seq ID No 339; 374-395 of Seq ID No 345; 136-159 of Seq ID No 348; 141-164 of Seq ID No 358; 96-157 of Seq ID No 361; 1-82 of Seq ID No 363; 489-556 of Seq ID No 364; 159-183 and 49-133 of Seq ID No 371.

The present invention also provides a process for producing a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising expressing one or more of the nucleic acid molecules according to the present invention in a suitable expression system.

Moreover, the present invention provides a process for producing a cell, which expresses a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention

comprising transforming or transfecting a suitable host cell with the vector according to the present invention.

According to the present invention a pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof as defined in the present invention or a nucleic acid molecule as defined in the present invention is provided.

In a preferred embodiment the pharmaceutical composition further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, especially KLKLSKLK, neuroactive compounds, especially human growth hormone, alum, Freund's complete or incomplete adjuvants or combinations thereof.

In a more preferred embodiment the immunostimulatory substance is a combination of either a polycationic polymer and immunostimulatory deoxynucleotides or of a peptide containing at least two LysLeuLys motifs and immunostimulatory deoxynucleotides.

In a still more preferred embodiment the polycationic polymer is a polycationic peptide, especially polyarginine.

According to the present invention the use of a nucleic acid molecule according to the present invention or a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *S. agalactiae* infection, is provided.

Also an antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to the present invention, is provided herewith.

In a preferred embodiment the antibody is a monoclonal antibody.

In another preferred embodiment the effective part of the antibody comprises Fab fragments.

In a further preferred embodiment the antibody is a chimeric antibody.

In a still preferred embodiment the antibody is a humanized antibody.

The present invention also provides a hybridoma cell line, which produces an antibody according to the present invention.

Moreover, the present invention provides a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administering an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the invention, to said animal,
- removing an antibody containing body fluid from said animal, and
- producing the antibody by subjecting said antibody containing body fluid to further purification steps.

Accordingly, the present invention also provides a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administering an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the present invention, to said animal,

- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

The antibodies provided or produced according to the above methods may be used for the preparation of a medicament for treating or preventing *S. agalactiae* infections.

According to another aspect the present invention provides an antagonist, which binds to a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention.

Such an antagonist capable of binding to a hyperimmune serum-reactive antigen or fragment thereof according to the present invention may be identified by a method comprising the following steps:

- a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to the present invention with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
- b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

An antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention to its interaction partner may be identified by a method comprising the following steps:

- a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to the present invention,
- b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to the present invention,
- c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form an interaction complex,
- d) providing a candidate antagonist,
- e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
- f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

The hyperimmune serum reactive antigens or fragments thereof according to the present invention may be used for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

The present invention also provides a process for *in vitro* diagnosing a disease related to expression of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

The present invention also provides a process for *in vitro* diagnosis of a bacterial infection, especially a *S. agalactiae* infection, comprising analyzing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the

presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

Moreover, the present invention provides the use of a hyperimmune serum reactive antigen or fragment thereof according to the present invention for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is an anticaline.

The present invention also provides the use of a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

The nucleic acid molecule according to the present invention may also be used for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

The present invention advantageously provides an efficient, relevant and comprehensive set of isolated nucleic acid molecules and their encoded hyperimmune serum reactive antigens or fragments thereof identified from *S. agalactiae* using an antibody preparation from multiple human plasma pools and surface expression libraries derived from the genome of *S. agalactiae*. Thus, the present invention fulfils a widely felt demand for *S. agalactiae* antigens, vaccines, diagnostics and products useful in procedures for preparing antibodies and for identifying compounds effective against *S. agalactiae* infection.

An effective vaccine should be composed of proteins or polypeptides, which are expressed by all strains and are able to induce high affinity, abundant antibodies against cell surface components of *S. agalactiae*. The antibodies should be IgG1 and/or IgG3 for opsonization, and any IgG subtype and IgA for neutralisation of adherence and toxin action. A chemically defined vaccine must be definitely superior compared to a whole cell vaccine (attenuated or killed), since components of *S. agalactiae*, which cross-react with human tissues or inhibit opsonization can be eliminated, and the individual proteins inducing protective antibodies and/or a protective immune response can be selected.

The approach, which has been employed for the present invention, is based on the interaction of GBS proteins or peptides with the antibodies present in human sera. The antibodies produced against *S. agalactiae* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. In addition, the antigenic proteins as identified by the bacterial surface display expression libraries using pools of pre-selected sera, are processed in a second and third round of screening by individual selected or generated sera. Thus the present invention supplies an efficient, relevant, comprehensive set of GBS antigens as a pharmaceutical composition, especially a vaccine preventing infection by *S. agalactiae*.

In the antigen identification program for identifying a comprehensive set of antigens according to the present invention, at least two different bacterial surface expression libraries are screened with several serum pools or plasma fractions or other pooled antibody containing body fluids (antibody pools). The antibody pools are derived from a serum collection, which has been tested against antigenic compounds of *S. agalactiae*, such as whole cell extracts and culture supernatant proteins. Preferably, three distinct serum collections are used, obtained ad 1. from healthy pregnant women tested negative for cervical and anorectal carriage of GBS, ad 2. healthy pregnant women tested positive for cervical and/or anorectal carriage of GBS who's newborn remained GBS-free (although with antibiotic prevention), ad 3. from adults below <45 years of age without clinical disease. Sera have to react with multiple GBS-specific antigens in order to be considered hyperimmune and therefore relevant in the screening method applied for the present invention.

The expression libraries as used in the present invention should allow expression of all potential antigens,

e.g. derived from all secreted and surface proteins of *S. agalactiae*. Bacterial surface display libraries will be represented by a recombinant library of a bacterial host displaying a (total) set of expressed peptide sequences of *S. agalactiae* on two selected outer membrane proteins (LamB and FhuA) at the bacterial host membrane [Georgiou, G., 1997]; [Etz, H. et al., 2001]. One of the advantages of using recombinant expression libraries is that the identified hyperimmune serum-reactive antigens may be instantly produced by expression of the coding sequences of the screened and selected clones expressing the hyperimmune serum-reactive antigens without further recombinant DNA technology or cloning steps necessary.

The comprehensive set of antigens identified by the described program according to the present invention is analysed further by one or more additional rounds of screening. Therefore individual antibody preparations or antibodies generated against selected peptides, which were identified as immunogenic are used. According to a preferred embodiment the individual antibody preparations for the second round of screening are derived from pregnant women and non-pregnant adults who show an antibody titer above a certain minimum level, for example an antibody titer being higher than 80 percentile, preferably higher than 90 percentile, especially higher than 95 percentile of the human (patient or healthy individual) sera tested. Using such high titer individual antibody preparations in the second screening round allows a very selective identification of the hyperimmune serum-reactive antigens and fragments thereof from *S. agalactiae*.

Following the comprehensive screening procedure, the selected antigenic proteins, expressed as recombinant proteins or *in vitro* translated products, in case it can not be expressed in prokaryotic expression systems, or the identified antigenic peptides (produced synthetically) are tested in a second screening by a series of ELISA and Western blotting assays for the assessment of their immunogenicity with a large human serum collection (minimum ~150 healthy and patients sera).

It is important that the individual antibody preparations (which may also be the selected serum) allow a selective identification of the most promising candidates of all the hyperimmune serum-reactive antigens from all the promising candidates from the first round. Therefore, preferably at least 10 individual antibody preparations (i.e. antibody preparations (e.g. sera) from at least 10 different individuals having suffered from an infection to the chosen pathogen) should be used in identifying these antigens in the second screening round. Of course, it is possible to use also less than 10 individual preparations, however, selectivity of the step may not be optimal with a low number of individual antibody preparations. On the other hand, if a given hyperimmune serum-reactive antigen (or an antigenic fragment thereof) is recognized by at least 10 individual antibody preparations, preferably at least 30, especially at least 50 individual antibody preparations, identification of the hyperimmune serum-reactive antigen is also selective enough for a proper identification. Hyperimmune serum-reactivity may of course be tested with as many individual preparations as possible (e.g. with more than 100 or even with more than 1,000).

Therefore, the relevant portion of the hyperimmune serum-reactive antibody preparations according to the method of the present invention should preferably be at least 10, more preferred at least 30, especially at least 50 individual antibody preparations. Alternatively (or in combination) hyperimmune serum-reactive antigens may preferably be also identified with at least 20%, preferably at least 30%, especially at least 40% of all individual antibody preparations used in the second screening round.

According to a preferred embodiment of the present invention, the sera from which the individual antibody preparations for the second round of screening are prepared (or which are used as antibody preparations), are selected by their titer against *S. agalactiae* (e.g. against a preparation of this pathogen, such as a lysate, cell wall components and recombinant proteins). Preferably, some are selected with a total IgA titer above 300 U, especially above 500 U, and/or an IgG titer above 5,000 U, especially above 10,000 U (U = units, calculated from the OD_{405nm} reading at a given dilution) when the whole organism

(total lysate or whole cells) is used as antigen in the ELISA.

The antibodies produced against streptococci by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. The recognition of linear epitopes recognized by serum antibodies can be based on sequences as short as 4-5 amino acids. Of course it does not necessarily mean that these short peptides are capable of inducing the given antibody *in vivo*. For that reason the defined epitopes, polypeptides and proteins are further to be tested in animals (mainly in mice) for their capacity to induce antibodies against the selected proteins *in vivo*.

The preferred antigens are located on the cell surface or secreted, and are therefore accessible extracellularly. Antibodies against cell wall proteins are expected to serve multiple purposes: to inhibit adhesion, to interfere with nutrient acquisition, to inhibit immune evasion and to promote phagocytosis (Hornef, M. et al., 2002). Antibodies against secreted proteins are beneficial in neutralisation of their function as toxin or virulence component. It is also known that bacteria communicate with each other through secreted proteins. Neutralizing antibodies against these proteins will interrupt growth-promoting cross-talk between or within streptococcal species. Bioinformatic analyses (signal sequences, cell wall localisation signals, transmembrane domains) proved to be very useful in assessing cell surface localisation or secretion. The experimental approach includes the isolation of antibodies with the corresponding epitopes and proteins from human serum, and the generation of immune sera in mice against (poly) peptides selected by the bacterial surface display screens. These sera are then used in a third round of screening as reagents in the following assays: cell surface staining of *S. agalactiae* grown under different conditions (FACS or microscopy), determination of neutralizing capacity (toxin, adherence), and promotion of opsonization and phagocytosis (*in vitro* phagocytosis assay).

For that purpose, bacterial *E. coli* clones are directly injected into mice and immune sera are taken and tested in the relevant *in vitro* assay for functional opsonic or neutralizing antibodies. Alternatively, specific antibodies may be purified from human or mouse sera using peptides or proteins as substrate.

Host defence against *S. agalactiae* relies mainly on opsonophagocytic killing mechanism. Inducing high affinity antibodies of the opsonic and neutralizing type by vaccination helps the innate immune system to eliminate bacteria and toxins. This makes the method according to the present invention an optimal tool for the identification of GBS antigenic proteins.

The skin and mucous membranes are formidable barriers against invasion by streptococci. However, once the skin or the mucous membranes are breached the first line of non-adaptive cellular defence begins its co-ordinate action through complement and phagocytes, especially the polymorphonuclear leukocytes (PMNs). These cells can be regarded as the cornerstones in eliminating invading bacteria. As *Streptococcus agalactiae* is a primarily extracellular pathogen, the major anti-streptococcal adaptive response comes from the humoral arm of the immune system, and is mediated through three major mechanisms: promotion of opsonization, toxin neutralisation, and inhibition of adherence. It is believed that opsonization is especially important, because of its requirement for an effective phagocytosis. For efficient opsonization the microbial surface has to be coated with antibodies and complement factors for recognition by PMNs through receptors to the Fc fragment of the IgG molecule or to activated C3b. After opsonization, streptococci are phagocytosed and killed. Antibodies bound to specific antigens on the cell surface of bacteria serve as ligands for the attachment to PMNs and to promote phagocytosis. The very same antibodies bound to the adhesins and other cell surface proteins are expected to neutralize adhesion and prevent colonization. The selection of antigens as provided by the present invention is thus well suited to identify those that will lead to protection against infection in an animal model or in humans.

According to the antigen identification method used herein, the present invention can surprisingly provide a set of comprehensive novel nucleic acids and novel hyperimmune serum reactive antigens and

fragments thereof of *S. agalactiae*, among other things, as described below. According to one aspect, the invention particularly relates to the nucleotide sequences encoding hyperimmune serum reactive antigens which sequences are set forth in the Sequence listing Seq ID No: 1-217 and 435-448 and the corresponding encoded amino acid sequences representing hyperimmune serum reactive antigens are set forth in the Sequence Listing Seq ID No 218-434 and 449-462.

In a preferred embodiment of the present invention, a nucleic acid molecule is provided which exhibits 70% identity over their entire length to a nucleotide sequence set forth with Seq ID No 14, 90, 157-216.. Most highly preferred are nucleic acids that comprise a region that is at least 80% or at least 85% identical over their entire length to a nucleic acid molecule set forth with Seq ID No 14, 90, 157-216. In this regard, nucleic acid molecules at least 90%, 91%, 92%, 93%, 94%, 95%, or 96% identical over their entire length to the same are particularly preferred. Furthermore, those with at least 97% are highly preferred, those with at least 98% and at least 99% are particularly highly preferred, with at least 99% or 99.5% being the more preferred, with 100% identity being especially preferred. Moreover, preferred embodiments in this respect are nucleic acids which encode hyperimmune serum reactive antigens or fragments thereof (polypeptides) which retain substantially the same biological function or activity as the mature polypeptide encoded by said nucleic acids set forth in the Seq ID No 14, 90, 157-216.

Identity, as known in the art and used herein, is the relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Identity can be readily calculated. While there exist a number of methods to measure identity between two polynucleotide or two polypeptide sequences, the term is well known to skilled artisans (e.g. *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity are codified in computer programs. Preferred computer program methods to determine identity between two sequences include, but are not limited to, GCG program package {Devereux, J. et al., 1984}, BLASTP, BLASTN, and FASTA [Altschul, S. et al., 1990].

According to another aspect of the invention, nucleic acid molecules are provided which exhibit at least 96% identity to the nucleic acid sequence set forth with Seq ID No 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448.

According to a further aspect of the present invention, nucleic acid molecules are provided which are identical to the nucleic acid sequences set forth with Seq ID No 32, 86, 91, 101, 127.

The nucleic acid molecules according to the present invention can as a second alternative also be a nucleic acid molecule which is at least essentially complementary to the nucleic acid described as the first alternative above. As used herein complementary means that a nucleic acid strand is base pairing via Watson-Crick base pairing with a second nucleic acid strand. Essentially complementary as used herein means that the base pairing is not occurring for all of the bases of the respective strands but leaves a certain number or percentage of the bases unpaired or wrongly paired. The percentage of correctly pairing bases is preferably at least 70 %, more preferably 80 %, even more preferably 90 % and most preferably any percentage higher than 90 %. It is to be noted that a percentage of 70 % matching bases is considered as homology and the hybridization having this extent of matching base pairs is considered as stringent. Hybridization conditions for this kind of stringent hybridization may be taken from Current Protocols in Molecular Biology (John Wiley and Sons, Inc., 1987). More particularly, the hybridization conditions can be as follows:

- Hybridization performed e.g. in 5 x SSPE, 5 x Denhardt's reagent, 0.1% SDS, 100 g/mL sheared DNA at 68°C

- Moderate stringency wash in 0.2xSSC, 0.1% SDS at 42°C
- High stringency wash in 0.1xSSC, 0.1% SDS at 68°C

Genomic DNA with a GC content of 50% has an approximate T_m of 96°C. For 1% mismatch, the T_m is reduced by approximately 1°C.

In addition, any of the further hybridization conditions described herein are in principle applicable as well.

Of course, all nucleic acid sequence molecules which encode the same polypeptide molecule as those identified by the present invention are encompassed by any disclosure of a given coding sequence, since the degeneracy of the genetic code is directly applicable to unambiguously determine all possible nucleic acid molecules which encode a given polypeptide molecule, even if the number of such degenerated nucleic acid molecules may be high. This is also applicable for fragments of a given polypeptide, as long as the fragments encode a polypeptide being suitable to be used in a vaccination connection, e.g. as an active or passive vaccine.

The nucleic acid molecule according to the present invention can as a third alternative also be a nucleic acid which comprises a stretch of at least 15 bases of the nucleic acid molecule according to the first and second alternative of the nucleic acid molecules according to the present invention as outlined above. Preferably, the bases form a contiguous stretch of bases. However, it is also within the scope of the present invention that the stretch consists of two or more moieties, which are separated by a number of bases.

The present nucleic acids may preferably consist of at least 20, even more preferred at least 30, especially at least 50 contiguous bases from the sequences disclosed herein. The suitable length may easily be optimized due to the planned area of use (e.g. as (PCR) primers, probes, capture molecules (e.g. on a (DNA) chip), etc.). Preferred nucleic acid molecules contain at least a contiguous 15 base portion of one or more of the predicted immunogenic amino acid sequences listed in tables 1 and 2, especially the sequences of table 2 with scores of more than 10, preferably more than 20, especially with a score of more than 25. Specifically preferred are nucleic acids containing a contiguous portion of a DNA sequence of any sequence in the sequence protocol of the present application which shows 1 or more, preferably more than 2, especially more than 5, non-identical nucleic acid residues compared to the published *Streptococcus agalactiae* strain NEM316 (ATCC 12403) genome ([Glaser, P. et al., 2002]; GenBank accession AL732656) and/or any other published *S. agalactiae* genome sequence or parts thereof, especially of the serotype V 2603 V/R (A909) strain [Tettelin, H. et al., 2002]; GenBank accession AE009948). Specifically preferred non-identical nucleic acid residues are residues, which lead to a non-identical amino acid residue. Preferably, the nucleic acid sequences encode polypeptides having at least 1, preferably at least 2, preferably at least 3 different amino acid residues compared to the published *S. agalactiae* counterparts mentioned above. Also such isolated polypeptides, being fragments of the proteins (or the whole protein) mentioned herein e.g. in the sequence listing, having at least 6, 7, or 8 amino acid residues and being encoded by these nucleic acids are preferred.

The nucleic acid molecule according to the present invention can as a fourth alternative also be a nucleic acid molecule which anneals under stringent hybridisation conditions to any of the nucleic acids of the present invention according to the above outlined first, second, and third alternative. Stringent hybridisation conditions are typically those described herein.

Finally, the nucleic acid molecule according to the present invention can as a fifth alternative also be a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to any of the nucleic acid molecules according to any nucleic acid molecule of the present invention according to the first, second, third, and fourth alternative as outlined above. This kind of nucleic acid molecule refers to

the fact that preferably the nucleic acids according to the present invention code for the hyperimmune serum reactive antigens or fragments thereof according to the present invention. This kind of nucleic acid molecule is particularly useful in the detection of a nucleic acid molecule according to the present invention and thus the diagnosis of the respective microorganisms such as *S. agalactiae* and any disease or diseased condition where this kind of microorganisms is involved. Preferably, the hybridisation would occur or be preformed under stringent conditions as described in connection with the fourth alternative described above.

Nucleic acid molecule as used herein generally refers to any ribonucleic acid molecule or deoxyribonucleic acid molecule, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, nucleic acid molecule as used herein refers to, among other, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and double-stranded regions. In addition, nucleic acid molecule as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term nucleic acid molecule includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "nucleic acid molecule" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are nucleic acid molecule as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term nucleic acid molecule as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of nucleic acid molecule, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells, *inter alia*. The term nucleic acid molecule also embraces short nucleic acid molecules often referred to as oligonucleotide(s). "Polynucleotide" and "nucleic acid" or "nucleic acid molecule" are often used interchangeably herein.

Nucleic acid molecules provided in the present invention also encompass numerous unique fragments, both longer and shorter than the nucleic acid molecule sequences set forth in the sequencing listing of the *S. agalactiae* coding regions, which can be generated by standard cloning methods. To be unique, a fragment must be of sufficient size to distinguish it from other known nucleic acid sequences, most readily determined by comparing any selected *S. agalactiae* fragment to the nucleotide sequences in computer databases such as GenBank.

Additionally, modifications can be made to the nucleic acid molecules and polypeptides that are encompassed by the present invention. For example, nucleotide substitutions can be made which do not affect the polypeptide encoded by the nucleic acid, and thus any nucleic acid molecule which encodes a hyperimmune serum reactive antigen or fragments thereof is encompassed by the present invention.

Furthermore, any of the nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof provided by the present invention can be functionally linked, using standard techniques such as standard cloning techniques, to any desired regulatory sequences, whether a *S. agalactiae* regulatory sequence or a heterologous regulatory sequence, heterologous leader sequence, heterologous marker sequence or a heterologous coding sequence to create a fusion protein.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA or cRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The DNA may be triple-stranded, double-

stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

The present invention further relates to variants of the herein above described nucleic acid molecules which encode fragments, analogs and derivatives of the hyperimmune serum reactive antigens and fragments thereof having a deduced *S. agalactiae* amino acid sequence set forth in the Sequence Listing. A variant of the nucleic acid molecule may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is not known to occur naturally. Such non-naturally occurring variants of the nucleic acid molecule may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells or organisms.

Among variants in this regard are variants that differ from the aforementioned nucleic acid molecules by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Preferred are nucleic acid molecules encoding a variant, analog, derivative or fragment, or a variant, analogue or derivative of a fragment, which have a *S. agalactiae* sequence as set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid(s) is substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *S. agalactiae* polypeptides set forth in the Sequence Listing. Also especially preferred in this regard are conservative substitutions.

The peptides and fragments according to the present invention also include modified epitopes wherein preferably one or two of the amino acids of a given epitope are modified or replaced according to the rules disclosed in e.g. {Tourdot, S. et al., 2000}, as well as the nucleic acid sequences encoding such modified epitopes.

It is clear that also epitopes derived from the present epitopes by amino acid exchanges improving, conserving or at least not significantly impeding the T cell activating capability of the epitopes are covered by the epitopes according to the present invention. Therefore the present epitopes also cover epitopes, which do not contain the original sequence as derived from *S. agalactiae*, but trigger the same or preferably an improved T cell response. These epitopes are referred to as "heteroclitic"; they need to have a similar or preferably greater affinity to MHC/HLA molecules, and the need the ability to stimulate the T cell receptors (TCR) directed to the original epitope in a similar or preferably stronger manner.

Heteroclitic epitopes can be obtained by rational design i.e. taking into account the contribution of individual residues to binding to MHC/HLA as for instance described by {Rammensee, H. et al., 1999}, combined with a systematic exchange of residues potentially interacting with the TCR and testing the resulting sequences with T cells directed against the original epitope. Such a design is possible for a skilled man in the art without much experimentation.

Another possibility includes the screening of peptide libraries with T cells directed against the original epitope. A preferred way is the positional scanning of synthetic peptide libraries. Such approaches have been described in detail for instance by {Hemmer, B. et al., 1999} and the references given therein.

As an alternative to epitopes represented by the present derived amino acid sequences or heteroclitic epitopes, also substances mimicking these epitopes e.g. "peptidomimetics" or "retro-inverso-peptides" can be applied.

Another aspect of the design of improved epitopes is their formulation or modification with substances increasing their capacity to stimulate T cells. These include T helper cell epitopes, lipids or liposomes or preferred modifications as described in WO 01/78767.

Another way to increase the T cell stimulating capacity of epitopes is their formulation with immune stimulating substances for instance cytokines or chemokines like interleukin-2, -7, -12, -18, class I and II interferons (IFN), especially IFN-gamma, GM-CSF, TNF-alpha, flt3-ligand and others.

As discussed additionally herein regarding nucleic acid molecule assays of the invention, for instance, nucleic acid molecules of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to the nucleic acid molecules of the present invention. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 20, at least 25 or at least 30 bases, and may have at least 50 bases. Particularly preferred probes will have at least 30 bases, and will have 50 bases or less, such as 30, 35, 40, 45, or 50 bases.

For example, the coding region of a nucleic acid molecule of the present invention may be isolated by screening a relevant library using the known DNA sequence to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the present invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine to which members of the library the probe hybridizes.

The nucleic acid molecules and polypeptides of the present invention may be employed as reagents and materials for development of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to nucleic acid molecule assays, *inter alia*.

The nucleic acid molecules of the present invention that are oligonucleotides can be used in the processes herein as described, but preferably for PCR, to determine whether or not the *S. agalactiae* genes identified herein in whole or in part are present and/or transcribed in infected tissue such as blood. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. For this and other purposes the arrays comprising at least one of the nucleic acids according to the present invention as described herein, may be used.

The nucleic acid molecules according to the present invention may be used for the detection of nucleic acid molecules and organisms or samples containing these nucleic acids. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease related or linked to the present or abundance of *S. agalactiae*.

Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with *S. agalactiae* may be identifiable by detecting any of the nucleic acid molecules according to the present invention detected at the DNA level by a variety of techniques. Preferred nucleic acid molecules candidates for distinguishing a *S. agalactiae* from other organisms can be obtained.

The invention provides a process for diagnosing disease, arising from infection with *S. agalactiae*, comprising determining from a sample isolated or derived from an individual an increased level of expression of a nucleic acid molecule having the sequence of a nucleic acid molecule set forth in the Sequence Listing. Expression of nucleic acid molecules can be measured using any one of the methods well known in the art for the quantitation of nucleic acid molecules, such as, for example, PCR, RT-PCR, Rnase protection, Northern blotting, other hybridisation methods and the arrays described herein.

Isolated as used herein means separated "by the hand of man" from its natural state; i.e., that, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring nucleic acid molecule or a polypeptide naturally present in a living organism in its natural state is not "isolated," but the same nucleic acid molecule or polypeptide separated from the

coexisting materials of its natural state is "isolated", as the term is employed herein. As part of or following isolation, such nucleic acid molecules can be joined to other nucleic acid molecules, such as DNAs, for mutagenesis, to form fusion proteins, and for propagation or expression in a host, for instance. The isolated nucleic acid molecules, alone or joined to other nucleic acid molecules such as vectors, can be introduced into host cells, in culture or in whole organisms. Introduced into host cells in culture or in whole organisms, such DNAs still would be isolated, as the term is used herein, because they would not be in their naturally occurring form or environment. Similarly, the nucleic acid molecules and polypeptides may occur in a composition, such as a media formulations, solutions for introduction of nucleic acid molecules or polypeptides, for example, into cells, compositions or solutions for chemical or enzymatic reactions, for instance, which are not naturally occurring compositions, and, therein remain isolated nucleic acid molecules or polypeptides within the meaning of that term as it is employed herein.

The nucleic acids according to the present invention may be chemically synthesized. Alternatively, the nucleic acids can be isolated from *S. agalactiae* by methods known to the one skilled in the art.

According to another aspect of the present invention, a comprehensive set of novel hyperimmune serum reactive antigens and fragments thereof are provided by using the herein described antigen identification method. In a preferred embodiment of the invention, a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by any one of the nucleic acids molecules herein described and fragments thereof are provided. In another preferred embodiment of the invention a novel set of hyperimmune serum-reactive antigens which comprises amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 231, 307, 374-433 and fragments thereof are provided. In a further preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462 and fragments thereof are provided. In a still preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 249, 303, 308, 318, 344 and fragments thereof are provided.

The hyperimmune serum reactive antigens and fragments thereof as provided in the invention include any polypeptide set forth in the Sequence Listing as well as polypeptides which have at least 70% identity to a polypeptide set forth in the Sequence Listing, preferably at least 80% or 85% identity to a polypeptide set forth in the Sequence Listing, and more preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide set forth in the Sequence Listing and still more preferably at least 95%, 96%, 97%, 98%, 99% or 99.5% similarity (still more preferably at least 95%, 96%, 97%, 98%, 99%, or 99.5% identity) to a polypeptide set forth in the Sequence Listing and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 4 amino acids and more preferably at least 8, still more preferably at least 30, still more preferably at least 50 amino acids, such as 4, 8, 10, 20, 30, 35, 40, 45 or 50 amino acids.

The invention also relates to fragments, analogs, and derivatives of these hyperimmune serum reactive antigens and fragments thereof. The terms "fragment", "derivative" and "analog" when referring to an antigen whose amino acid sequence is set forth in the Sequence Listing, means a polypeptide which retains essentially the same or a similar biological function or activity as such hyperimmune serum reactive antigen and fragment thereof.

The fragment, derivative or analog of a hyperimmune serum reactive antigen and fragment thereof may be 1) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or 2) one in which one or more of the amino acid residues includes a substituent group, or 3) one in which the mature hyperimmune serum

reactive antigen or fragment thereof is fused with another compound, such as a compound to increase the half-life of the hyperimmune serum reactive antigen and fragment thereof (for example, polyethylene glycol), or 4) one in which the additional amino acids are fused to the mature hyperimmune serum reactive antigen or fragment thereof, such as a leader or secretory sequence or a sequence which is employed for purification of the mature hyperimmune serum reactive antigen or fragment thereof or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

The present invention also relates to antigens of different *S. agalactiae* isolates. Such homologues may easily be isolated based on the nucleic acid and amino acid sequences disclosed herein. There are 9 serotypes distinguished to date and the typing is based on serotype specific antisera. The presence of any antigen can accordingly be determined for every serotype. In addition it is possible to determine the variability of a particular antigen in the various serotypes as described for the *S. pyogenes* sic gene (Hoe, N. et al., 2001). The contribution of the various serotypes to the different GBS infections varies in the different age groups and geographical regions. It is an important aspect that the most valuable protective antigens are expected to be conserved among various clinical strains.

Among the particularly preferred embodiments of the invention in this regard are the hyperimmune serum reactive antigens set forth in the Sequence Listing, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of fragments. Additionally, fusion polypeptides comprising such hyperimmune serum reactive antigens, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of the fragments are also encompassed by the present invention. Such fusion polypeptides and proteins, as well as nucleic acid molecules encoding them, can readily be made using standard techniques, including standard recombinant techniques for producing and expression of a recombinant polynucleic acid encoding a fusion protein.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr.

Further particularly preferred in this regard are variants, analogs, derivatives and fragments, and variants, analogs and derivatives of the fragments, having the amino acid sequence of any polypeptide set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the polypeptide of the present invention. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polypeptides having an amino acid sequence set forth in the Sequence Listing without substitutions.

The hyperimmune serum reactive antigens and fragments thereof of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

Also among preferred embodiments of the present invention are polypeptides comprising fragments of the polypeptides having the amino acid sequence set forth in the Sequence Listing, and fragments of variants and derivatives of the polypeptides set forth in the Sequence Listing.

In this regard a fragment is a polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the afore mentioned hyperimmune serum reactive antigen and fragment thereof, and variants or derivative, analogs, fragments thereof. Such fragments may be "free-

standing", i.e., not part of or fused to other amino acids or polypeptides, or they may be comprised within a larger polypeptide of which they form a part or region. Also preferred in this aspect of the invention are fragments characterised by structural or functional attributes of the polypeptide of the present invention, i.e. fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta-amphipathic regions, flexible regions, surface-forming regions, substrate binding regions, and high antigenic index regions of the polypeptide of the present invention, and combinations of such fragments. Preferred regions are those that mediate activities of the hyperimmune serum reactive antigens and fragments thereof of the present invention. Most highly preferred in this regard are fragments that have a chemical, biological or other activity of the hyperimmune serum reactive antigen and fragments thereof of the present invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *S. agalactiae* or the ability to cause disease in humans. Further preferred polypeptide fragments are those that comprise or contain antigenic or immunogenic determinants in an animal, especially in a human.

An antigenic fragment is defined as a fragment of the identified antigen, which is for itself antigenic or may be made antigenic when provided as a hapten. Therefore, also antigens or antigenic fragments showing one or (for longer fragments) only a few amino acid exchanges are enabled with the present invention, provided that the antigenic capacities of such fragments with amino acid exchanges are not severely deteriorated on the exchange(s), i.e., suited for eliciting an appropriate immune response in an individual vaccinated with this antigen and identified by individual antibody preparations from individual sera.

Preferred examples of such fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1A, especially peptides comprising amino acid 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of Seq ID No 218; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of Seq ID No 219; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of Seq ID No 220; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of Seq ID No 221; 29-38, 44-64, 70-76, 78-87, 94-100, 102-112, 119-134, 140-149, 163-173, 178-186, 188-194, 207-234, 247-262, 269-290 and 73-92 of Seq ID No 222; 10-28, 36-63, 77-87, 103-119, 127-136, 141-169, 171-183, 195-200, 207-232, 236-246, 251-265, 268-283, 287-297, 314-322, 335-343, 354-363, 384-390, 405-411, 419-436, 443-455, 467-473, 480-513, 518-529, 550-557, 565-585, 602-608, 616-625, 632-660, 665-677, 685-701, 726-736, 738-747, 752-761, 785-796, 801-813, 838-853, 866-871 and 757-774 of Seq ID No 223; 31-38, 61-66, 74-81, 90-115, 123-145, 154-167, 169-179, 182-193, 200-206, 238-244, 267-272 and 235-251 of Seq ID No 224; 19-25, 38-54, 56-64, 66-72, 74-92, 94-100, 116-129, 143-149, 156-183, 204-232, 253-266, 269-275, 294-307 and 241-313 of Seq ID No 225; 5-34, 50-56, 60-65, 74-85, 89-97, 108-119, 159-165, 181-199, 209-225, 230-240, 245-251, 257-262, 274-282, 300-305 and 64-75 of Seq ID No 226; 5-13, 16-21, 27-42, 45-52, 58-66, 74-87, 108-114, 119-131 and 39-51 of Seq ID No 227; 6-23, 46-54, 59-65, 78-84, 100-120, 128-133, 140-146, 159-165, 171-183, 190-204, 224-232, 240-248, 250-259, 274-280, 288-296, 306-315 and 267-274 of Seq ID No 228; 5-12, 15-24, 26-36, 42-65, 68-80, 82-104, 111-116, 125-144, 159-167, 184-189, 209-218, 235-243, 254-265, 269-283, 287-300, 306-316, 318-336, 338-352, 374-392 and 162-174 of Seq ID No 229; 30-42, 45-54 and 25-37 of Seq ID No 230; 10-30, 53-59, 86-95, 116-130, 132-147, 169-189, 195-201, 212-221, 247-256, 258-265, 278-

283, 291-298, 310-316, 329-339, 341-352, 360-367, 388-396, 398-411, 416-432, 443-452, 460-466, 506-512, 515-521, 542-548 and 419-431 of Seq ID No 231; 4-27, 30-53, 60-67, 70-90, 92-151, 159-185, 189-195, 198-210, 215-239 and 173-189 of Seq ID No 232; 4-26, 41-54, 71-78, 116-127, 140-149, 151-158, 161-175, 190-196, 201-208, 220-226, 240-252, 266-281, 298-305, 308-318, 321-329, 344-353, 372-378, 384-405, 418-426, 429-442, 457-463, 494-505, 514-522 and 174-188 of Seq ID No 233; 17-25, 27-39, 61-67, 81-89, 99-110, 120-131, 133-139, 147-161, 167-172, 179-185, 192-198, 203-213, 226-238, 243-258, 261-267, 284-290, 296-307, 311-328, 340-352, 356-371 and 239-256 of Seq ID No 234; 8-30, 40-49, 67-80, 114-123, 126-142, 152-162, 188-194 and 57-70 of Seq ID No 235; 4-23, 28-34, 36-47, 50-61, 76-81, 89-94, 96-104, 112-119, 126-146, 155-181, 195-200, 208-214, 220-229, 244-260, 263-276, 282-288, 292-300, 317-323, 336-351, 353-359, 363-375, 382-399, 415-432, 444-455, 458-471, 476-481, 484-492, 499-517, 522-529, 535-541, 543-568, 572-584, 586-600, 607-617, 626-637, 656-675 and 282-297 of Seq ID No 236; 6-24, 30-35, 38-45, 63-91, 134-140, 146-160, 167-188, 214-220, 226-234, 244-250, 260-270, 286-301, 316-329, 340-371, 429-446, 448-459, 474-481, 485-491, 512-526, 537-544, 550-565, 573-583, 596-613, 621-630, 652-658 and 87-97 of Seq ID No 237; 8-20, 26-48, 56-67, 76-86, 94-109, 115-121, 123-129, 143-160, 178-186, 191-198, 201-208, 221-236, 238-244, 260-268 and 237-247 of Seq ID No 238; 4-40, 42-57, 73-87, 98-117, 126-135, 150-156, 166-174, 196-217, 231-236, 248-258, 276-284, 293-301, 307-313, 339-347, 359-365, 375-387, 395-402, 428-440, 445-456, 485-490, 497-505, 535-541, 547-555, 610-625, 648-656, 665-671 and 448-528 of Seq ID No 239; 10-18, 39-45, 51-61, 80-96, 98-106, 110-115, 158-172, 174-183, 191-200, 220-237, 249-255, 274-289, 308-324, 331-341, 372-381, 384-397, 405-414 and 322-338 of Seq ID No 240; 30-36, 38-56, 85-108, 134-147, 149-160, 163-183, 188-201, 206-211, 219-238, 247-254 and 5-13 of Seq ID No 241; 11-40, 98-103, 110-115, 133-145, 151-159, 172-179, 192-201, 204-212, 222-228, 235-245, 258-268, 283-296, 298-309, 322-329, 342-351, 354-362, 372-378, 385-393, 407-418, 495-516 and 1-148 of Seq ID No 242; 5-19, 21-36, 73-94, 112-119, 122-137, 139-145, 152-167, 184-190, 198-204, 208-224, 249-265, 267-281, 299-304, 309-317, 326-333, 356-364, 368-374, 381-389, 391-414, 419-425, 430-435 and 113-140 of Seq ID No 243; 45-54, 59-67, 78-91 and 15-23 of Seq ID No 244; 11-22, 33-47, 52-80, 88-112, 124-129 and 6-25 of Seq ID No 245; 26-41, 51-63, 80-89, 93-115, 150-163, 187-193, 220-237, 240-249, 286-294, 296-306, 316-329, 345-353, 361-370, 407-425, 428-437, 474-482, 484-494, 504-517, 533-541, 549-558, 595-613, 616-625, 660-668, 673-685, 711-726, 736-744, 749-761, 787-802, 812-820, 825-837, 863-878, 888-896, 901-913, 939-954, 964-972, 977-989, 1003-1008, 1016-1022, 1028-1034, 1041-1053, 1059-1074, 1101-1122, 420-511 and 581-704 of Seq ID No 246; 18-25, 27-55, 71-83, 89-95, 102-113, 120-146, 150-156, 174-185 and 159-175 of Seq ID No 247; 24-30, 38-56, 63-68, 87-93, 136-142, 153-164, 183-199, 213-219, 226-234, 244-261, 269-278, 283-289, 291-297, 320-328, 330-336, 340-346, 348-356, 358-366, 382-387, 401-408, 414-419, 449-455, 468-491, 504-512, 531-537, 554-560, 597-608, 621-627, 632-643, 650-662, 667-692, 703-716, 724-737, 743-758, 783-794, 800-818, 846-856 and 806-884 of Seq ID No 248; 4-14, 21-39, 86-92, 99-107, 121-131, 136-144, 147-154, 158-166, 176-185, 193-199, 207-222, 224-230 and 117-136 of Seq ID No 249; 65-76, 85-97, 103-109, 115-121, 125-146, 163-169, 196-205, 212-219, 228-237, 241-247, 254-262, 269-288, 294-303, 305-313, 328-367, 395-401, 405-412, 418-429, 437-447, 481-488, 506-513, 519-524, 530-541, 546-557 and 266-284 of Seq ID No 250; 5-14, 37-42, 49-71, 78-92, 97-112, 127-136, 147-154, 156-163, 186-198, 216-225, 233-243, 248-253, 295-307, 323-332, 359-366, 368-374, 380-398 and 194-223 of Seq ID No 251; 4-11, 33-39, 45-72, 100-113, 119-129, 136-144, 169-175, 177-185, 200-208, 210-219, 262-276, 278-297, 320-326, 336-344, 347-362, 381-394, 443-453 and 438-454 of Seq ID No 252; 4-29, 31-52, 55-61, 95-110, 138-158, 162-171, 179-187, 202-229, 239-248, 251-256, 262-267, 269-285, 304-310, 351-360, 362-368, 381-388, 415-428, 435-440, 448-458 and 161-178 of Seq ID No 253; 4-17, 19-28, 32-43, 47-59, 89-110, 112-126, 128-134, 140-148, 152-161, 169-184, 191-204, 230-235, 255-264, 328-338, 341-347, 401-409, 413-419, 433-441, 449-458, 463-468, 476-482, 486-492, 500-506, 529-545 and 305-381 of Seq ID No 254; 10-29, 38-45, 53-61, 134-145, 152-160, 163-170, 202-208, 219-229, 248-258, 266-275, 282-288, 315-320, 328-334, 377-385, 392-402, 418-424, 447-453, 460-471, 479-487, 491-497, 500-507, 531-537, 581-594, 615-623, 629-635, 644-652, 659-666, 668-678, 710-717, 719-728, 736-741, 747-760, 766-773, 784-789, 794-800, 805-817, 855-861, 866-887 and 698-715 of Seq ID No 255; 16-26, 29-37, 44-58, 62-68, 74-80, 88-95, 97-120, 125-144, 165-196 and 58-72 of Seq ID No 256; 14-21, 23-46, 49-60, 63-74, 78-92, 96-103, 117-129, 134-161, 169-211, 217-231, 239-248, 252-281, 292-299, 313-343 and 243-257 of Seq ID No 257; 11-27, 46-52, 67-72, 76-84, 91-112, 116-153, 160-175, 187-196, 202-211, 213-220 and 43-76 of Seq ID No 258; 5-29, 37-56, 78-86, 108-118, 152-161 and 120-130 of Seq ID No 259; 8-14, 19-41, 52-66, 75-82, 87-92, 106-121, 127-133, 136-143, 158-175, 180-187, 196-204, 221-228, 239-245, 259-265, 291-306, 318-323, 328-340, 352-358, 361-368, 375-381, 391-399, 411-418, 431-442, 446-455, 484-496, 498-510, 527-

533, 541-549, 558-565, 575-585, 587-594, 644-655, 661-668, 671-677 and 184-196 of Seq ID No 260; 4-22, 29-38, 55-62, 75-81, 102-107, 110-134, 143-150, 161-167, 172-179, 191-215, 223-233, 241-247, 251-264, 266-272, 288-309, 340-352, 354-366, 394-402, 414-438 and 198-218 of Seq ID No 261; 24-44, 49-70, 80-91, 105-118, 128-136, 140-154 and 77-92 of Seq ID No 262; 5-22, 31-36, 41-47, 67-74, 83-90, 105-122, 135-143, 160-167 and 118-129 of Seq ID No 263; 4-25, 33-73, 81-93, 96-106, 114-120, 122-128, 130-172, 179-208, 210-241, 251-283, 296-301 and 92-100 of Seq ID No 264; 14-24, 29-38, 43-50, 52-72, 86-97, 101-107, 110-125, 127-141, 145-157, 168-175, 177-184, 186-195, 205-226, 238-250, 255-261, 284-290, 293-304, 307-314, 316-323, 325-356, 363-371, 383-390, 405-415, 423-432, 442-454, 466-485, 502-511, 519-527, 535-556, 558-565, 569-574, 612-634, 641-655, 672-686, 698-709, 715-722, 724-732, 743-753, 760-769, 783-792, 818-825, 830-839, 842-849, 884-896, 905-918, 926-940, 957-969, 979-1007, 1015-1021, 1049-1057 and 336-349 of Seq ID No 265; 6-16, 26-31, 33-39, 62-73, 75-85, 87-100, 113-123, 127-152, 157-164, 168-181, 191-198, 208-214, 219-226, 233-254, 259-266, 286-329 and 181-195 of Seq ID No 266; 4-13, 32-39, 53-76, 99-108, 110-116, 124-135, 137-146, 149-157, 162-174, 182-190, 207-231, 242-253, 255-264, 274-283, 291-323, 334-345, 351-360, 375-388, 418-425, 456-474, 486-492, 508-517, 520-536, 547-560, 562-577, 31-45 and 419-443 of Seq ID No 267; 15-26, 30-37, 42-49, 58-90, 93-99, 128-134, 147-154, 174-179, 190-197, 199-205, 221-230, 262-274, 277-287, 300-314, 327-333, 343-351, 359-377, 388-396, 408-413, 416-425, 431-446 and 246-256 of Seq ID No 268; 5-26, 34-42, 47-54, 61-67, 71-104, 107-115, 131-138, 144-153, 157-189, 196-202, 204-210, 228-245, 288-309, 316-329, 332-341, 379-386, 393-399, 404-412, 414-421, 457-468, 483-489, 500-506, 508-517, 523-534, 543-557, 565-580, 587-605, 609-617, 619-627, 631-636, 640-646, 662-668, 675-682, 705-710, 716-723, 727-732, 750-758, 784-789, 795-809, 869-874, 14-138, 166-286, 372-503, 674-696 and 754-859 of Seq ID No 269; 5-17, 32-38, 40-47, 80-89, 113-119, 125-137, 140-154, 157-163, 170-177, 185-199, 213-225, 228-236, 242-248, 277-290, 292-305, 323-333, 347-353, 364-370, 385-394, 399-406, 423-433, 441-451, 462-474, 477-487 and 116-124 of Seq ID No 270; 7-16, 18-30, 32-49, 53-61, 63-85, 95-101, 105-115, 119-134, 143-150, 159-178, 185-202, 212-229, 236-250, 254-265, 268-294 and 63-72 of Seq ID No 271; 4-12, 19-47, 73-81, 97-103, 153-169, 188-198, 207-213, 217-223, 236-242, 255-265, 270-278, 298-305, 309-317, 335-347, 354-363, 373-394, 419-424, 442-465, 486-492, 500-507, 542-549, 551-558, 560-572, 580-589, 607-614, 617-623, 647-653, 666-676, 694-704, 706-714, 748-754, 765-772, 786-792, 795-806 and 358-370 of Seq ID No 272; 18-28, 30-38, 40-46, 49-55, 69-78, 82-98, 104-134, 147-153, 180-190, 196-202, 218-236, 244-261, 266-273, 275-286, 290-295, 301-314, 378-387, 390-395, 427-434 and 290-305 of Seq ID No 273; 4-13, 20-31, 39-51, 54-61, 69-84, 87-105, 117-124 and 108-125 of Seq ID No 274; 24-34, 43-54, 56-66, 68-79 and 50-69 of Seq ID No 275; 5-43, 71-77, 102-131, 141-148, 150-156, 159-186, 191-207, 209-234, 255-268, 280-286, 293-299, 317-323, 350-357, 363-372, 391-397, 406-418, 428-435, 455-465, 484-497, 499-505, 525-531, 575-582, 593-607, 621-633, 638-649, 655-673, 684-698, 711-725, 736-741, 743-752, 759-769, 781-793, 813-831, 843-853, 894-905, 908-916, 929-946, 953-963, 970-978, 1001-1007, 1011-1033, 165-178 and 818-974 of Seq ID No 276; 16-44, 63-86, 98-108, 185-191, 222-237, 261-274, 282-294, 335-345, 349-362, 374-384, 409-420, 424-430, 440-447, 453-460, 465-473, 475-504, 522-534, 538-551, 554-560, 567-582, 598-607, 611-619, 627-640, 643-653, 655-661, 669-680, 684-690, 701-707, 715-731, 744-750, 756-763, 768-804, 829-837, 845-853, 855-879, 884-890, 910-928, 77-90, 144-212, 279-355, 434-536, 782-810 and 875-902 of Seq ID No 277; 4-22, 29-41, 45-51, 53-66, 70-77, 86-95, 98-104, 106-124, 129-135, 142-151, 153-161, 169-176, 228-251, 284-299, 331-337, 339-370, 380-387, 393-398, 406-411, 423-433, 440-452, 461-469, 488-498, 501-516, 523-530, 532-559, 562-567, 570-602, 612-628, 630-645, 649-659, 666-672, 677-696, 714-723, 727-747 and 212-227 of Seq ID No 278; 4-9, 17-31, 35-41, 56-61, 66-75, 81-87, 90-124, 133-138, 149-163, 173-192, 213-219, 221-262, 265-275, 277-282, 292-298, 301-307, 333-346, 353-363, 371-378, 419-430, 435-448, 456-469, 551-570, 583-599, 603-612 and 275-291 of Seq ID No 279; 28-34, 53-58, 72-81, 100-128, 145-154, 159-168, 172-189, 217-225, 227-249, 256-263, 299-309, 322-330, 361-379, 381-388, 392-401, 404-417, 425-436, 440-446, 451-464, 469-487, 502-511, 543-551, 559-564, 595-601, 606-612, 615-626, 633-642, 644-650, 664-670, 674-684, 692-701, 715-723, 726-734, 749-756, 763-771, 781-787, 810-843, 860-869, 882-889, 907-917, 931-936, 941-948, 951-958, 964-971, 976-993, 1039-1049, 1051-1065, 1092-1121, 1126-1132, 1145-1151, 1158-1173, 1181-1192, 1194-1208, 1218-1223, 1229-1243, 1249-1254, 1265-1279, 1287-1297, 1303-1320, 1334-1341, 1343-1358, 1372-1382, 1406-1417, 1419-1425, 1428-1434, 1441-1448, 1460-1473, 1494-1504, 1509-1514, 1529-1550, 654-669 and 1400-1483 of Seq ID No 280; 10-16, 20-25, 58-65, 97-109, 118-132, 134-146, 148-155, 186-195, 226-233, 244-262, 275-284, 295-310, 317-322, 330-339, 345-351, 366-375, 392-403, 408-415, 423-430, 435-444, 446-457, 467-479, 486-499, 503-510, 525-537, 540-585, 602-612, 614-623, 625-634, 639-645, 650-669, 700-707, 717-724, 727-739, 205-230 and 733-754 of Seq ID No 281; 5-22, 37-43, 72-81, 105-113, 128-

133, 148-160, 188-194, 204-230, 238-245, 251-257 and 194-213 of Seq ID No 282; 16-21, 35-41, 56-72, 74-92, 103-109 and 62-68 of Seq ID No 283; 4-15, 17-82, 90-104, 107-159, 163-170, 188-221, 234-245, 252-265 and 220-235 of Seq ID No 284; 16-22, 36-46, 61-75, 92-107, 113-121, 139-145, 148-160 and 30-42 of Seq ID No 285; 4-12, 20-26, 43-49, 55-62, 66-78, 121-127, 135-141, 146-161, 164-170, 178-189, 196-205, 233-238, 269-279, 288-318, 325-332, 381-386, 400-407 and 328-346 of Seq ID No 286; 5-12, 31-49, 57-63, 69-79, 89-97, 99-114, 116-127, 134-142, 147-154, 160-173, 185-193, 199-204, 211-222, 229-236, 243-249, 256-274 and 58-68 of Seq ID No 287; 10-20, 28-34, 39-53, 68-79, 84-90, 99-106 and 73-79 of Seq ID No 288; 14-37, 45-50, 61-66, 77-82, 93-98, 109-114, 125-130, 141-146, 157-162, 173-178, 189-194, 205-210, 221-226, 237-242, 253-258, 269-274, 285-290, 301-306, 316-332, 349-359, 371-378, 385-406, 34-307 and 312-385 of Seq ID No 289; 4-10, 17-38, 50-85, 93-99, 109-116, 128-185, 189-197, 199-210, 223-256, 263-287, 289-312, 327-337, 371-386, 389-394, 406-419, 424-432, 438-450, 458-463, 475-502, 507-513, 519-526, 535-542, 550-567 and 361-376 of Seq ID No 290; 10-39, 42-93, 100-144, 155-176, 178-224, 230-244, 246-255, 273-282, 292-301, 308-325, 332-351, 356-361, 368-379, 386-393, 400-421 and 138-155 of Seq ID No 291; 5-11, 17-34, 40-45, 50-55, 72-80, 101-123, 145-151, 164-172, 182-187, 189-195, 208-218, 220-241, 243-252, 255-270, 325-331, 365-371, 391-398, 402-418, 422-428, 430-435, 443-452, 463-469, 476-484, 486-494, 503-509, 529-553, 560-565, 570-590, 608-614, 619-627, 654-661, 744-750, 772-780, 784-790, 806-816, 836-853, 876-885, 912-918, 926-933, 961-975, 980-987, 996-1006, 1016-1028, 1043-1053, 1057-1062, 994-1003 and 1033-1056 of Seq ID No 292; 17-45, 64-71, 73-81, 99-109, 186-192, 223-238, 262-275, 283-295, 336-346, 350-363, 375-385, 410-421, 425-431, 441-448, 454-463, 468-474, 476-512, 523-537, 539-552, 568-583, 599-608, 612-620, 628-641, 644-654, 656-662, 670-681, 685-695, 702-708, 716-723, 725-735, 757-764, 769-798, 800-806, 808-816, 826-840, 846-854, 856-862, 874-881, 885-902, 907-928, 274-350 and 443-513 of Seq ID No 293; 4-22, 29-41, 45-51, 53-61, 70-76, 85-92, 99-104, 111-122, 134-140, 142-154, 163-174, 224-232, 255-265, 273-279, 283-297, 330-335, 337-348, 356-367, 373-385, 391-396, 421-431, 442-455, 475-485, 493-505, 526-538, 544-561, 587-599, 605-620, 622-651, 662-670, 675-681, 687-692, 697-712, 714-735 and 252-262 of Seq ID No 294; 4-12, 15-35, 40-46, 50-59, 67-94, 110-128, 143-169, 182-188, 207-215, 218-228, 238-250 and 74-90 of Seq ID No 295; 9-18, 42-58, 78-85, 88-95, 97-106, 115-122, 128-134, 140-145, 154-181, 186-202, 204-223, 261-267, 269-278, 284-293, 300-336, 358-368 and 12-29 of Seq ID No 296; 7-34, 46-53, 62-72, 82-88, 100-105, 111-117, 132-137, 144-160, 166-180, 183-189, 209-221, 231-236, 246-253, 268-282, 286-293, 323-336, 364-372, 378-392, 422-433 and 388-405 of Seq ID No 297; 21-27, 34-50, 72-77, 80-95, 164-177, 192-198, 202-220, 226-236, 239-247, 270-279, 285-292, 315-320, 327-334, 348-355, 364-371, 388-397, 453-476, 488-497, 534-545, 556-576, 582-588, 601-607, 609-616, 642-662, 674-681, 687-697, 709-715, 721-727, 741-755 and 621-739 of Seq ID No 298; 4-14, 16-77, 79-109 and 25-99 of Seq ID No 299; 4-9, 17-23, 30-37, 44-55, 65-72, 77-93, 102-121, 123-132, 146-153 and 17-29 of Seq ID No 300; 4-18, 25-41, 52-60, 83-92, 104-112, 117-123, 149-155, 159-167, 170-192, 201-210, 220-227, 245-250 and 124-137 of Seq ID No 301; 8-25, 50-55, 89-95, 138-143, 148-153, 159-169, 173-179, 223-238, 262-268, 288-295, 297-308, 325-335, 403-409, 411-417, 432-446, 463-475, 492-501, 524-530, 542-548, 561-574, 576-593, 604-609, 612-622, 637-654, 665-672, 678-685, 720-725, 731-739, 762-767, 777-783, 820-838, 851-865, 901-908, 913-920, 958-970, 1000-1006, 1009-1015, 1020-1026, 1043-1052, 1055-1061, 1-128, 252-341, 771-793 and 1043-1058 of Seq ID No 302; 16-26, 33-46 and 64-76 of Seq ID No 303; 4-27, 69-77, 79-101, 117-123, 126-142, 155-161, 171-186, 200-206, 213-231, 233-244, 267-273, 313-329, 335-344, 347-370, 374-379, 399-408, 422-443, 445-453, 461-468, 476-482, 518-534, 544-553, 556-567, 578-595, 601-620, 626-636, 646-658, 666-681, 715-721, 762-768, 778-785, 789-803, 809-819, 22-108, 153-318, 391-527 and 638-757 of Seq ID No 304; 6-21, 32-43, 62-92, 104-123, 135-141, 145-152, 199-216, 218-226, 237-247, 260-269, 274-283, 297-303, 1-72 and 127-211 of Seq ID No 305; 6-26, 50-56, 83-89, 108-114, 123-131, 172-181, 194-200, 221-238, 241-247, 251-259, 263-271, 284-292, 304-319, 321-335, 353-358, 384-391, 408-417, 424-430, 442-448, 459-466, 487-500, 514-528, 541-556, 572-578, 595-601, 605-613, 620-631, 635-648, 660-670, 673-679, 686-693, 702-708, 716-725, 730-735, 749-755, 770-777, 805-811, 831-837, 843-851, 854-860, 863-869, 895-901, 904-914, 922-929, 933-938, 947-952, 956-963, 1000-1005, 1008-1014, 1021-1030, 1097-1103, 1120-1130, 1132-1140, 1-213, 269-592 and 992-1120 of Seq ID No 306; 9-16, 33-39, 47-59, 65-79, 81-95, 103-108, 115-123, 138-148, 163-171, 176-185, 191-196, 205-211, 213-221, 224-256, 261-276, 294-302, 357-363, 384-390, 95-111 and 161-189 of Seq ID No 307; 21-27, 35-45, 70-76, 92-105, 129-143, 145-155, 161-166, 170-191, 204-211, 214-231, 234-246, 249-255, 259-275 and 1-18 of Seq ID No 308; 21-35, 45-53, 56-64, 69-97 and 1-16 of Seq ID No 309; 25-33, 41-47, 61-68, 86-101, 106-114, 116-129, 134-142, 144-156, 163-176, 181-190, 228-251, 255-261, 276-292, 295-305, 334-357, 368-380, 395-410, 424-429, 454-460, 469-482, 510-516, 518-527, 531-546, 558-570, 579-606, 628-636, 638-645,

651-656, 668-674, 691-698, 717-734, 742-754, 765-770, 792-797, 827-835, 847-859, 874-881, 903-909, 926-933, 942-961, 964-977, 989-1004, 1010-1028, 1031-1047, 1057-1075, 1081-1095, 1108-1117, 1138-1144, 1182-1189, 1193-1206, 1220-1229, 1239-1246, 1257-1267, 1271-1279, 1284-1301, 1312-1320, 1329-1335, 1341-1347, 1358-1371, 1399-1404, 1417-1426, 1458-1463, 1468-1476, 1478-1485, 1493-1506, 1535-1541, 1559-1574, 1583-1590, 1595-1601, 1603-1611, 1622-1628, 1634-1644, 1671-1685, 1689-1696, 1715-1720, 1734-1746, 1766-1775, 1801-1806, 1838-1844, 1858-1871, 1910-1917, 1948-1955, 1960-1974, 2000-2015, 2019-2036, 2041-2063, 748-847 and 1381-1391 of Seq ID No 310; 5-12, 18-24, 27-53, 56-63, 96-113, 119-124, 131-136, 157-163, 203-209, 215-223, 233-246, 264-273, 311-316, 380-389, 393-399, 425-433, 445-450, 457-462, 464-470, 475-482, 507-513, 527-535, 542-548, 550-565, 591-602, 607-613, 627-642, 644-664, 673-712, 714-732, 739-764, 769-782, 812-818, 826-838, 848-854, 860-871, 892-906, 930-938, 940-954, 957-973, 990-998, 1002-1021, 1024-1033, 1037-1042, 1050-1060, 1077-1083, 1085-1092, 1100-1129, 1144-1161, 1169-1175, 1178-1189, 1192-1198, 1201-1207, 1211-1221, 1229-1239, 1250-1270, 1278-1292, 1294-1300, 1314-1335, 1344-1352, 1360-1374, 1394-1405, 1407-1414, 1416-1424, 1432-1452, 1456-1462, 1474-1497, 1500-1510, 1516-1522, 1534-1542, 1550-1559, 1584-1603, 1608-1627, 187-273 and 306-441 of Seq ID No 311; 70-80, 90-97, 118-125, 128-140, 142-148, 154-162, 189-202, 214-222, 224-232, 254-260, 275-313, 317-332, 355-360, 392-398, 425-432, 448-456, 464-470, 476-482, 491-505, 521-528, 533-546, 560-567, 592-597, 605-614, 618-626, 637-644, 646-653, 660-666, 677-691 and 207-227 of Seq ID No 312; 5-19, 26-34, 37-55, 57-66, 69-83, 86-102, 115-134, 138-143, 154-172, 178-195, 209-246, 251-257, 290-302, 306-311 and 256-266 of Seq ID No 313; 10-20, 22-28, 35-57, 72-79, 87-103, 108-128, 130-144, 158-171, 190-198, 225-242, 274-291, 301-315, 317-324, 374-385 and 353-365 of Seq ID No 314; 4-9, 17-30, 34-54, 59-66, 73-94, 118-130, 135-150, 158-171, 189-198, 219-239, 269-275, 283-301, 89-106 and 176-193 of Seq ID No 315; 14-20, 22-74, 77-86, 89-99, 104-109, 126-135, 154-165, 181-195, 197-212, 216-224, 264-275 and 107-118 of Seq ID No 316; 4-18, 21-38, 63-72, 101-109, 156-162, 165-179, 183-192, 195-210, 212-218, 230-239, 241-256, 278-290, 299-311, 313-322, 332-341, 348-366, 386-401, 420-426, 435-450, 455-460, 468-479, 491-498, 510-518, 532-538, 545-552, 557-563, 567-573, 586-595, 599-609, 620-626, 628-636, 652-657, 665-681 and 1-198 of Seq ID No 317; 4-10, 16-38, 51-68, 73-79, 94-115, 120-125, 132-178, 201-208, 216-223, 238-266, 269-295, 297-304, 337-342, 347-356, 374-401, 403-422, 440-447, 478-504, 510-516, 519-530, 537-544 and 191-206 of Seq ID No 318; 12-40, 42-48, 66-71, 77-86, 95-102, 113-120, 129-137, 141-148, 155-174, 208-214, 218-225, 234-240, 256-267, 275-283, 300-306, 313-321, 343-350, 359-367, 370-383, 398-405, 432-439, 443-461, 492-508, 516-526, 528-535 and 370-478 of Seq ID No 319; 6-14, 20-37, 56-62, 90-95, 97-113, 118-125, 140-145, 161-170, 183-202, 237-244, 275-284, 286-305, 309-316, 333-359, 373-401, 405-412 and 176-187 of Seq ID No 320; 33-44, 50-55, 59-80, 86-101, 129-139, 147-153, 157-163, 171-176, 189-201, 203-224, 239-245, 257-262, 281-287, 290-297, 304-320, 322-331, 334-350, 372-390, 396-401, 71-88 and 353-372 of Seq ID No 321; 5-11, 15-24, 26-33, 40-47, 75-88, 95-103, 105-112 and 17-30 of Seq ID No 322; 5-11, 16-39, 46-54, 62-82, 100-107, 111-124, 126-150, 154-165, 167-183, 204-238, 245-295, 301-313, 316-335 and 8-16 of Seq ID No 323; 4-19, 34-48, 69-74, 79-107, 115-127, 129-135, 143-153, 160-169, 171-182 and 142-153 of Seq ID No 324; 4-30, 65-74, 82-106, 110-120, 124-132, 135-140, 146-175, 179-184, 190-196, 217-223, 228-233, 250-267, 275-292, 303-315, 322-332 and 174-186 of Seq ID No 325; 9-16, 29-41, 47-57, 68-84, 87-109, 113-119, 162-180, 186-193, 195-201, 203-208, 218-230, 234-243, 265-271, 281-292, 305-312, 323-332, 341-347, 349-363, 368-374, 383-390, 396-410, 434-440, 446-452, 455-464, 466-473, 515-522, 529-542, 565-570, 589-600, 602-613, 618-623, 637-644, 1019-1027, 1238-1244, 1258-1264, 1268-1276, 1281-1292, 1296-1302 and 883-936 of Seq ID No 326; 10-17, 23-32, 39-44, 54-72, 75-81, 88-111, 138-154, 160-167, 178-185, 201-210, 236-252, 327-334, 336-342, 366-376, 388-400, 410-430, 472-482, 493-526, 552-558, 586-592, 598-603, 612-621, 630-635, 641-660 and 384-393 of Seq ID No 327; 4-22, 24-39, 50-59, 73-84, 100-105, 111-117, 130-138, 155-161, 173-178, 182-189, 205-215, 266-284, 308-313, 321-328, 330-337, 346-363, 368-374, 388-395, 397-405, 426-434, 453-459, 482-492, 501-507, 509-515, 518-523, 527-544, 559-590, 598-612, 614-629, 646-659, 663-684, 686-694, 698-721 and 445-461 of Seq ID No 328; 14-22, 27-33 and 3-17 of Seq ID No 329; 29-41, 66-73, 81-87, 90-108, 140-146, 150-159, 165-184, 186-196, 216-226, 230-238, 247-253, 261-269 and 126-140 of Seq ID No 330; 5-12, 16-25, 27-33, 36-45, 60-68, 83-88, 103-126 and 86-101 of Seq ID No 331; 14-23, 36-47, 56-66, 84-89, 94-105, 111-127, 140-153, 160-174, 176-183, 189-203, 219-225, 231-237, 250-257 and 194-227 of Seq ID No 332; 4-25, 54-60, 64-71, 73-82, 89-106, 117-124, 157-169, 183-188, 199-210, 221-232, 236-244, 255-264 and 58-98 of Seq ID No 333; 13-19, 26-36, 41-53, 55-71, 77-84, 86-108, 114-135, 157-172, 177-183, 187-194, 208-213, 218-226, 110-125 and 156-170 of Seq ID No 334; 5-24, 63-69, 77-85, 94-112, 120-137, 140-146, 152-159, 166-172, 179-187, 193-199, 206-212, 222-228, 234-240, 244-252, 257-264, 270-289, 298-309, 316-

328, 337-348, 363-375, 1-56 and 340-352 of Seq ID No 335; 18-39, 42-71, 78-120, 124-144, 152-173, 179-189, 199-209, 213-222, 228-258, 269-304, 329-361, 364-372, 374-389, 396-441 and 313-327 of Seq ID No 336; 19-25, 91-98, 108-120, 156-162, 168-174, 191-204, 211-216, 232-266, 272-278, 286-308, 316-321, 327-333, 344-355, 358-364, 384-391, 395-428, 464-476, 487-495, 497-511, 544-561, 563-573, 575-582, 588-594, 10-25 and 322-338 of Seq ID No 337; 14-26, 32-49, 51-57, 59-72, 80-91, 102-112, 119-125, 147-161, 164-173, 175-183, 188-213, 217-222, 246-254, 260-276, 282-303, 308-318, 321-328, 333-350, 352-359, 371-378, 392-401, 407-414, 416-443, 448-463, 471-484, 490-497, 501-514, 519-527, 539-551, 557-570, 578-590, 592-598, 600-610, 618-629, 633-647, 654-667, 676-689, 702-709, 718-726, 728-737, 741-760, 764-780, 786-795, 808-826, 836-842, 845-852, 865-874, 881-887, 931-945, 949-957, 968-974, 979-986, 1003-1009, 1023-1029 and 90-103 of Seq ID No 338; 11-16, 37-56, 60-66, 69-77, 80-88, 93-106, 117-139, 166-171 and 72-90 of Seq ID No 339; 59-84, 123-133, 145-150, 161-167, 178-189 and 115-128 of Seq ID No 340; 15-33, 39-46, 52-64, 74-87, 108-124, 127-144, 150-156, 173-179, 184-194, 201-208, 219-236, 243-269, 272-295, 302-309, 343-349, 356-361, 370-379, 405-411, 414-423, 430-451, 457-464, 466-475, 477-483, 496-502, 507-522, 541-548, 557-563, 571-577, 579-585, 590-605, 626-642, 650-662, 671-691, 704-710, 751-769, 775-781, 786-791, 794-829, 851-858, 868-878, 884-904, 913-919, 931-939 and 132-142 of Seq ID No 341; 33-58, 64-71, 74-80, 83-88, 96-120, 122-139, 146-157, 167-177, 207-213, 220-225, 236-242, 264-279, 300-305, 326-336, 340-347, 350-360, 97-115 and 199-211 of Seq ID No 342; 4-26, 43-57, 70-99, 102-117, 121-133, 142-148, 151-168, 170-183, 192-220, 235-249, 258-279 and 30-41 of Seq ID No 343; 34-42, 48-58, 70-94, 110-130, 154-160, 164-172, 178-183, 195-203, 211-222, 229-250, 256-261, 274-284, 286-292, 312-323 and 222-233 of Seq ID No 344; 4-9, 15-36, 38-45, 49-74, 78-88, 100-112, 136-191, 211-220, 226-233, 239-246, 254-274, 287-307, 316-322, 342-353, 356-366, 373-378, 384-393, 405-431, 449-457, 459-468, 487-511, 515-524, 529-541, 544-552, 562-568, 571-576 and 208-280 of Seq ID No 345; 10-27, 31-37, 39-54, 71-108, 124-143 and 2-107 of Seq ID No 346; 16-27, 38-57, 64-70, 90-102, 104-113, 116-137, 160-166 and 1-80 of Seq ID No 347; 13-21, 31-36, 56-67, 127-136, 153-171, 173-180, 184-200, 214-222, 225-231, 239-263, 267-273 and 135-159 of Seq ID No 348; 12-27, 31-51, 68-74, 77-87, 94-101, 108-114, 117-123, 127-134, 138-168, 173-196, 201-207, 212-217, 227-237, 247-257, 264-280 and 205-223 of Seq ID No 349; 17-22, 25-54, 70-76, 92-100 and 98-110 of Seq ID No 350; 7-29, 40-50, 60-67, 87-96, 105-111, 119-164, 172-199, 206-212, 220-227, 237-259, 272-279, 282-293, 295-309, 313-319, 321-328, 345-363, 376-386 and 159-176 of Seq ID No 351; 4-19, 24-30, 36-43, 50-68, 71-89, 93-106, 141-152, 154-172, 179-197, 199-215, 229-239, 246-252, 255-263, 281-298, 319-325, 329-356, 358-368, 374-390, 397-409, 420-429, 432-444, 450-456, 459-475, 483-494, 496-502, 520-528, 532-556 and 362-377 of Seq ID No 352; 18-25, 40-62, 77-85, 91-97, 105-116, 123-133, 139-184, 189-197 and 122-140 of Seq ID No 353; 4-49, 52-58, 62-70, 79-105, 109-133, 142-150, 163-168, 206-214, 220-228, 233-240, 243-254, 274-281, 303-311, 327-338, 357-373, 378-396, 403-413, 420-436, 441-453, 461-467, 475-481, 484-498, 506-512, 514-521, 523-529, 562-579, 589-595, 598-603, 615-648, 714-722, 728-742, 749-758, 777-792, 795-807 and 643-658 of Seq ID No 354; 8-27, 37-48, 51-56, 72-79, 87-106, 120-138, 140-147, 167-176, 187-197, 205-216, 222-229, 234-239, 243-249, 277-288, 292-315, 334-343, 347-353, 363-391, 398-404, 430-447, 461-467, 478-492, 498-507 and 456-470 of Seq ID No 355; 5-12, 18-24, 59-69, 80-93, 95-109, 119-125, 130-137, 139-147, 158-163, 168-176, 182-202, 206-215, 222-239, 241-249, 267-277, 291-298, 311-318, 321-327, 338-344, 348-355, 373-386, 393-406, 411-417, 434-443, 446-465, 473-484, 514-521, 532-553, 584-594 and 221-237 of Seq ID No 356; 4-14, 27-34, 50-58, 63-72, 79-106, 109-114, 121-142, 146-154, 161-167, 169-175, 178-201, 223-238, 249-254, 259-264, 278-292, 294-312, 319-330 and 167-191 of Seq ID No 357; 7-28, 36-42, 50-61, 63-80, 122-152, 161-174, 176-191 and 140-190 of Seq ID No 358; 20-57, 59-65, 70-78, 86-102, 119-133, 142-161, 163-173, 177-188, 192-202, 204-220, 222-236, 240-253, 279-319, 326-331, 337-383, 390-399, 406-412, 420-427, 431-438 and 381-395 of Seq ID No 359; 13-18, 28-34, 37-43, 50-59, 75-81, 83-97, 105-121, 139-147, 200-206, 209-227, 231-247, 260-271, 318-327, 366-381, 388-394, 399-406 and 182-201 of Seq ID No 360; 6-29, 37-43, 51-56, 70-77, 82-102, 110-119, 127-143, 178-190, 201-209, 216-243, 261-269, 281-292, 305-313, 327-339, 341-354, 356-373, 391-397, 423-429, 438-445, 450-478 and 21-314 of Seq ID No 361; 4-12, 15-21, 32-41, 59-76, 80-89, 96-104 and 90-103 of Seq ID No 362; 9-28, 30-41, 44-54, 69-74, 77-82, 90-97, 104-123, 125-135, 149-155, 164-173, 177-184, 217-226, 230-235, 238-244, 258-272, 282-297, 300-305, 309-315, 317-322, 327-336, 348-362, 368-374, 380-387, 400-411, 414-424, 451-458, 460-466, 483-494, 497-503, 506-511, 521-528, 540-553, 569-587, 598-606, 628-642, 661-681, 688-700, 718-733, 740-749, 752-764, 769-783, 823-834, 848-854, 862-872, 878-884, 886-898, 915-920, 938-951, 954-961, 963-972, 982-989, 996-1003, 1010-1016, 1021-1032, 1038-1044, 1047-1057, 1060-1070, 1079-1088, 1094-1102, 1117-1127, 1129-1135, 1142-1153, 1158-1204, 1212-1229, 1234-1263, 1269-1277, 1308-1313, 1327-1338, 1344-1376, 1400-

1415, 1436-1443, 1448-1458, 1497-1504, 1511-1522, 1544-1566, 3-82 and 509-576 of Seq ID No 363; 8-36, 40-64, 71-79, 88-94, 102-109, 118-127, 138-148, 151-159, 163-174, 192-198, 200-206, 220-233, 268-273, 290-301, 304-309, 316-323, 331-349, 378-391, 414-420, 427-437, 455-475, 494-510, 541-547, 549-555, 616-640, 1-60, 55-139, 212-308, 386-458 and 458-624 of Seq ID No 364; 16-31, 35-42, 70-77, 91-101, 120-130, 132-140, 143-153, 185-190, 195-202, 215-222, 228-238, 241-251, 257-264, 268-277, 288-302, 312-324, 326-333, 341-348, 364-382, 415-429, 438-454, 458-466, 491-499, 501-521 and 273-281 of Seq ID No 365; 8-14, 32-57, 74-149, 155-177, 179-212, 221-266, 271-296, 304-324, 329-346, 349-359, 368-401, 413-419, 426-454, 465-478, 493-510 and 466-490 of Seq ID No 366; 22-28, 33-51, 64-89, 96-119, 126-132, 138-146, 152-159, 161-169, 172-179, 193-198, 205-211, 221-231, 235-254, 273-280, 297-303, 312-320, 328-346, 351-373, 378-384, 391-398, 448-454, 460-468, 470-481, 516-558, 574-593, 597-602, 613-623, 626-646, 649-656, 668-673, 675-683, 696-708, 715-722, 724-739, 745-751, 759-777, 780-804, 816-822 and 102-113 of Seq ID No 367; 12-28, 41-91, 98-107, 112-120, 125-131, 151-193, 215-221, 240-250, 263-280 and 128-138 of Seq ID No 368; 16-24, 32-38, 46-62, 68-81, 90-105, 127-133, 144-150, 160-166, 178-184, 186-202, 210-219, 232-240, 252-258, 264-273, 293-324, 337-344, 349-357, 360-369, 385-398, 410-416, 419-427, 441-449, 458-476, 508-515, 523-539, 544-549, 562-569, 571-579, 96-109 and 127-139 of Seq ID No 369; 19-25, 28-34, 56-61, 85-97, 110-116 and 39-53 of Seq ID No 370; 4-37, 41-50, 62-72, 91-97, 99-109, 114-125, 136-141, 149-158, 160-166, 201-215 and 27-225 of Seq ID No 371; 15-31, 44-51, 96-105, 122-130, 149-157, 162-168, 178-183, 185-192, 198-204, 206-213, 221-234, 239-245, 248-255, 257-266, 289-335, 349-357, 415-422, 425-441, 448-454, 462-468 and 463-481 of Seq ID No 372; 5-31, 39-55, 63-72, 76-99, 106-155, 160-177, 179-199, 207-217, 223-240, 245-255, 261-267, 294-316, 321-343, 354-378, 382-452, 477-488, 529-536, 555-569, 584-591, 593-612, 620-627, 632-640, 647-654, 671-680, 698-704, 723-730, 732-750, 769-775, 781-788, 822-852 and 505-525 of Seq ID No 373; 3-18 of Seq ID No 374; 4-14 and 12-24 of Seq ID No 375; 4-11, 22-30 and 12-25 of Seq ID No 376; 5-12 and 4-18 of Seq ID No 377; 4-28 and 7-14 of Seq ID No 378; 6-16 and 8-16 of Seq ID No 379; 4-15, 18-33 and 24-36 of Seq ID No 380; 4-10, 16-21 and 20-31 of Seq ID No 381; 6-19 of Seq ID No 382; 11-18 and 3-10 of Seq ID No 383; 13-24 and 3-15 of Seq ID No 384; 15-27 and 7-16 of Seq ID No 385; 11-16 and 1-15 of Seq ID No 386; 4-16 and 9-21 of Seq ID No 387; 4-24, 40-48, 54-67 and 22-39 of Seq ID No 388; 6-30, 34-55, 62-68, 78-106 and 68-74 of Seq ID No 389; 3-14 of Seq ID No 390; 9-19 and 6-21 of Seq ID No 391; 4-17 and 1-9 of Seq ID No 392; 5-30 and 1-8 of Seq ID No 393; 4-16, 23-46, 51-56 and 45-55 of Seq ID No 394; 7-16 of Seq ID No 395; 2-14 of Seq ID No 396; 4-36, 43-65 and 50-62 of Seq ID No 397; 10-30 and 14-21 of Seq ID No 398; 9-17 and 1-10 of Seq ID No 399; 4-12 and 3-16 of Seq ID No 400; 4-15 and 5-23 of Seq ID No 401; 10-21 of Seq ID No 402; 6-16 of Seq ID No 403; 4-29, 31-38 and 2-14 of Seq ID No 404; 4-35 and 33-42 of Seq ID No 405; 2-17 of Seq ID No 406; 9-18, 30-35 and 15-33 of Seq ID No 407; 4-9 and 6-12 of Seq ID No 408; 3-17 of Seq ID No 409; 12-21, 37-44, 52-61, 72-80 and 38-48 of Seq ID No 410; 4-10, 29-44, 54-61, 69-78 and 13-27 of Seq ID No 411; 13-23, 36-53 and 2-15 of Seq ID No 412; 4-25, 28-46, 56-72, 81-99, 120-132, 134-142, 154-160 and 129-141 of Seq ID No 413; 4-15, 24-33, 35-41, 64-86 and 21-33 of Seq ID No 414; 9-15 and 4-13 of Seq ID No 415; 4-11, 13-19, 34-48 and 15-32 of Seq ID No 416; 4-21 and 11-31 of Seq ID No 417; 23-57 and 38-50 of Seq ID No 418; 4-32 and 3-13 of Seq ID No 419; 4-10, 13-25, 32-42, 56-68, 72-84 and 26-38 of Seq ID No 420; 4-20, 31-48, 52-58, 65-71, 80-93, 99-108, 114-123 and 37-49 of Seq ID No 421; 6-12, 14-20 and 3-25 of Seq ID No 422; 14-25, 27-38 and 5-14 of Seq ID No 423; 4-41, 57-105, 109-118, 123-136, 144-152 and 86-99 of Seq ID No 424; 6-19 of Seq ID No 425; 2-19 of Seq ID No 426; 14-47 and 1-14 of Seq ID No 427; 4-21, 29-44 and 2-18 of Seq ID No 428; 23-29 and 10-28 of Seq ID No 429; 6-16, 22-36 and 11-22 of Seq ID No 430; 4-19, 30-44 and 18-27 of Seq ID No 431; 5-15, 37-45, 58-65 and 38-47 of Seq ID No 432; 4-15, 23-34 and 4-15 of Seq ID No 433; 30-36, 44-54, 79-85, 101-114, 138-152, 154-164, 170-175, 179-200, 213-220, 223-240, 243-255, 258-264, 268-284 and 10-28 of Seq ID No 434; the peptides comprising amino acid sequences of column "Identical region" of the Table 1B, especially peptides comprising amino acid 210-226 and 738-753 of Seq ID No 449; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 450; 893-906 of Seq ID No 451; 51-69 of Seq ID No 452; 110-125 of Seq ID No 453; 291-305 of Seq ID No 454; 210-226 and 738-753 of Seq ID No 455; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 456; 893-906 of Seq ID No 457; 51-69 of Seq ID No 458; 110-125 of Seq ID No 459; 291-305 of Seq ID No 460; 32-44 of Seq ID No 461; 399-410 of Seq ID No 462; the serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 2, especially peptides comprising amino acid 120-143, 138-161 and 156-179 of Seq ID No 218; 110-129 and 168-184 of Seq ID No 219; 74-90 of Seq ID No 222; 759-773 of Seq ID No 223; 237-260 of Seq ID No 224;

265-284 of Seq ID No 225; 65-74 of Seq ID No 226; 41-50 of Seq ID No 227; 163-174 of Seq ID No 229; 26-37 of Seq ID No 230; 174-189 of Seq ID No 232; 240-256 of Seq ID No 234; 285-297 of Seq ID No 236; 238-247 of Seq ID No 238; 491-519 of Seq ID No 239; 114-140 of Seq ID No 243; 267-284 of Seq ID No 250; 439-453 of Seq ID No 252; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 60-71 of Seq ID No 256; 244-257 of Seq ID No 257; 44-63 and 57-76 of Seq ID No 258; 185-196 of Seq ID No 260; 119-129 of Seq ID No 263; 182-195 of Seq ID No 266; 32-44 and 424-442 of Seq ID No 267; 247-256 of Seq ID No 268; 678-694, 785-805, 55-77 and 72-94 of Seq ID No 269; 210-226 of Seq ID No 281; 37-59 of Seq ID No 289; 13-29 of Seq ID No 296; 136-159 of Seq ID No 348; 205-222 of Seq ID No 349; 99-110 of Seq ID No 350; 160-176 of Seq ID No 351; 457-470 of Seq ID No 355; 221-237 of Seq ID No 356; 167-190 of Seq ID No 357; 96-120 of Seq ID No 361; 399-417, 503-519 and 544-563 of Seq ID No 364; 46-68, 159-183 and 184-198 of Seq ID No 371; 463-481 of Seq ID No 372; the immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 4; especially peptides comprising amino acid 110-129 and 168-184 of Seq ID No 219; 877-901, 333-354, 326-344 and 801-809 of Seq ID No 277; 1-54 of Seq ID No 347; 544-563, 31-51, 107-119, 399-417 and 503-519 of Seq ID No 364; 120-198 of Seq ID No 218; 20-35 of Seq ID No 219; 118-201 of Seq ID No 221; 48-132 of Seq ID No 242; 118-136 of Seq ID No 249; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 50-76 of Seq ID No 258; 785-819 and 44-128 of Seq ID No 269; 90-128 of Seq ID No 274; 314-384 of Seq ID No 289; 327-349 of Seq ID No 293; 242-314, 405-478 and 23-100 of Seq ID No 304; 129-210 of Seq ID No 305; 162-188 of Seq ID No 307; 750-772 of Seq ID No 310; 1-56 of Seq ID No 335; 322-337 of Seq ID No 337; 72-90 of Seq ID No 339; 374-395 of Seq ID No 345; 136-159 of Seq ID No 348; 141-164 of Seq ID No 358; 96-157 of Seq ID No 361; 1-82 of Seq ID No 363; 489-556 of Seq ID No 364; 159-183 and 49-133 of Seq ID No 371 and fragments comprising at least 6, preferably more than 8, especially more than 10 aa of said sequences. All these fragments individually and each independently form a preferred selected aspect of the present invention.

All linear hyperimmune serum reactive fragments of a particular antigen may be identified by analysing the entire sequence of the protein antigen by a set of peptides overlapping by 1 amino acid with a length of at least 10 amino acids. Subsequently, non-linear epitopes can be identified by analysis of the protein antigen with hyperimmune sera using the expressed full-length protein or domain polypeptides thereof. Assuming that a distinct domain of a protein is sufficient to form the 3D structure independent from the native protein, the analysis of the respective recombinant or synthetically produced domain polypeptide with hyperimmune serum would allow the identification of conformational epitopes within the individual domains of multi-domain proteins. For those antigens where a domain possesses linear as well as conformational epitopes, competition experiments with peptides corresponding to the linear epitopes may be used to confirm the presence of conformational epitopes.

It will be appreciated that the invention also relates to, among others, nucleic acid molecules encoding the aforementioned fragments, nucleic acid molecules that hybridise to nucleic acid molecules encoding the fragments, particularly those that hybridise under stringent conditions, and nucleic acid molecules, such as PCR primers, for amplifying nucleic acid molecules that encode the fragments. In these regards, preferred nucleic acid molecules are those that correspond to the preferred fragments, as discussed above.

The present invention also relates to vectors, which comprise a nucleic acid molecule or nucleic acid molecules of the present invention, host cells which are genetically engineered with vectors of the invention and the production of hyperimmune serum reactive antigens and fragments thereof by recombinant techniques.

A great variety of expression vectors can be used to express a hyperimmune serum reactive antigen or fragment thereof according to the present invention. Generally, any vector suitable to maintain, propagate or express nucleic acids to express a polypeptide in a host may be used for expression in this regard. In accordance with this aspect of the invention the vector may be, for example, a plasmid vector,

a single or double-stranded phage vector, a single or double-stranded RNA or DNA viral vector. Starting plasmids disclosed herein are either commercially available, publicly available, or can be constructed from available plasmids by routine application of well-known, published procedures. Preferred among vectors, in certain respects, are those for expression of nucleic acid molecules and hyperimmune serum reactive antigens or fragments thereof of the present invention. Nucleic acid constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the hyperimmune serum reactive antigens and fragments thereof of the invention can be synthetically produced by conventional peptide synthesizers. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA construct of the present invention.

Host cells can be genetically engineered to incorporate nucleic acid molecules and express nucleic acid molecules of the present invention. Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

The invention also provides a process for producing a *S. agalactiae* hyperimmune serum reactive antigen and a fragment thereof comprising expressing from the host cell a hyperimmune serum reactive antigen or fragment thereof encoded by the nucleic acid molecules provided by the present invention. The invention further provides a process for producing a cell, which expresses a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof comprising transforming or transfecting a suitable host cell with the vector according to the present invention such that the transformed or transfected cell expresses the polypeptide encoded by the nucleic acid contained in the vector.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N- or C-terminus of the polypeptide to improve stability and persistence in the host cell, during purification or during subsequent handling and storage. Also, regions may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability or to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize or purify polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another protein or part thereof. In drug discovery, for example, proteins have been fused with antibody Fc portions for the purpose of high-throughout screening assays to identify antagonists. See for example, {Bennett, D. et al., 1995} and {Johanson, K. et al., 1995}.

The *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography and lectin chromatography.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention can be produced by chemical synthesis as well as by biotechnological means. The latter comprise the transfection or transformation of a host cell with a vector containing a nucleic acid according to the present invention and the cultivation of the transfected or transformed host cell under conditions, which are known to the ones skilled in the art. The production method may also comprise a purification step in

order to purify or isolate the polypeptide to be manufactured. In a preferred embodiment the vector is a vector according to the present invention.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used for the detection of the organism or organisms in a sample containing these organisms or polypeptides derived thereof. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease, most preferably for the diagnosis of a diseases related or linked to the presence or abundance of Gram-positive bacteria, especially bacteria selected from the group comprising streptococci, staphylococci and lactococci. More preferably, the microorganisms are selected from the group comprising *Streptococcus pneumoniae*, *Streptococcus pyogenes* and *Streptococcus mutans*, especially the microorganism is *Streptococcus pyogenes*.

The present invention also relates to diagnostic assays such as quantitative and diagnostic assays for detecting levels of the hyperimmune serum reactive antigens and fragments thereof of the present invention in cells and tissues, including determination of normal and abnormal levels. Thus, for instance, a diagnostic assay in accordance with the invention for detecting over-expression of the polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example, and to identify the infecting organism. Assay techniques that can be used to determine levels of a polypeptide, in a sample derived from a host are well known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays. Among these, ELISAs frequently are preferred. An ELISA assay initially comprises preparing an antibody specific to the polypeptide, preferably a monoclonal antibody. In addition, a reporter antibody generally is prepared which binds to the monoclonal antibody. The reporter antibody is attached to a detectable reagent such as radioactive, fluorescent or enzymatic reagent, such as horseradish peroxidase enzyme.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may also be used for the purpose of or in connection with an array. More particularly, at least one of the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be immobilized on a support. Said support typically comprises a variety of hyperimmune serum reactive antigens and fragments thereof whereby the variety may be created by using one or several of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and/or hyperimmune serum reactive antigens and fragments thereof being different. The characterizing feature of such array as well as of any array in general is the fact that at a distinct or predefined region or position on said support or a surface thereof, a distinct polypeptide is immobilized. Because of this any activity at a distinct position or region of an array can be correlated with a specific polypeptide. The number of different hyperimmune serum reactive antigens and fragments thereof immobilized on a support may range from as little as 10 to several 1000 different hyperimmune serum reactive antigens and fragments thereof. The density of hyperimmune serum reactive antigens and fragments thereof per cm^2 is in a preferred embodiment as little as 10 peptides/polypeptides per cm^2 to at least 400 different peptides/polypeptides per cm^2 and more particularly at least 1000 different hyperimmune serum reactive antigens and fragments thereof per cm^2 .

The manufacture of such arrays is known to the one skilled in the art and, for example, described in US patent 5,744,309. The array preferably comprises a planar, porous or non-porous solid support having at least a first surface. The hyperimmune serum reactive antigens and fragments thereof as disclosed herein, are immobilized on said surface. Preferred support materials are, among others, glass or cellulose. It is also within the present invention that the array is used for any of the diagnostic applications described herein. Apart from the hyperimmune serum reactive antigens and fragments thereof according to the present invention also the nucleic acid molecules according to the present invention may be used for the generation of an array as described above. This applies as well to an array made of antibodies, preferably monoclonal antibodies as, among others, described herein.

In a further aspect the present invention relates to an antibody directed to any of the hyperimmune serum reactive antigens and fragments thereof, derivatives or fragments thereof according to the present invention. The present invention includes, for example, monoclonal and polyclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of a Fab expression library. It is within the present invention that the antibody may be chimeric, i. e. that different parts thereof stem from different species or at least the respective sequences are taken from different species.

Antibodies generated against the hyperimmune serum reactive antigens and fragments thereof corresponding to a sequence of the present invention can be obtained by direct injection of the hyperimmune serum reactive antigens and fragments thereof into an animal or by administering the hyperimmune serum reactive antigens and fragments thereof to an animal, preferably a non-human. The antibody so obtained will then bind the hyperimmune serum reactive antigens and fragments thereof itself. In this manner, even a sequence encoding only a fragment of a hyperimmune serum reactive antigen and fragments thereof can be used to generate antibodies binding the whole native hyperimmune serum reactive antigen and fragments thereof. Such antibodies can then be used to isolate the hyperimmune serum reactive antigens and fragments thereof from tissue expressing those hyperimmune serum reactive antigens and fragments thereof.

For preparation of monoclonal antibodies, any technique known in the art, which provides antibodies produced by continuous cell line cultures can be used (as described originally in {Kohler, G. et al., 1975}.

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention.

Alternatively, phage display technology or ribosomal display could be utilized to select antibody genes with binding activities towards the hyperimmune serum reactive antigens and fragments thereof either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing respective target antigens or from naïve libraries [McCafferty, J. et al., 1990]; [Marks, J. et al., 1992]. The affinity of these antibodies can also be improved by chain shuffling [Clackson, T. et al., 1991].

If two antigen binding domains are present, each domain may be directed against a different epitope – termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the hyperimmune serum reactive antigens and fragments thereof or purify the hyperimmune serum reactive antigens and fragments thereof of the present invention by attachment of the antibody to a solid support for isolation and/or purification by affinity chromatography.

Thus, among others, antibodies against the hyperimmune serum reactive antigens and fragments thereof of the present invention may be employed to inhibit and/or treat infections, particularly bacterial infections and especially infections arising from *S. agalactiae*.

Hyperimmune serum reactive antigens and fragments thereof include antigenically, epitopically or immunologically equivalent derivatives, which form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a hyperimmune serum reactive antigen and fragments thereof or its equivalent which will be specifically recognized by certain antibodies which, when raised to the protein or hyperimmune serum reactive antigen and fragments thereof according to the present invention, interfere with the interaction between pathogen and mammalian host. The term

"immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

The hyperimmune serum reactive antigens and fragments thereof, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof can be used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the hyperimmune serum reactive antigens and fragments thereof. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein, for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively, an antigenic peptide comprising multiple copies of the protein or hyperimmune serum reactive antigen and fragments thereof, or an antigenically or immunologically equivalent hyperimmune serum reactive antigen and fragments thereof, may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized", wherein the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in {Jones, P. et al., 1986} or {Tempest, P. et al., 1991}.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscle, delivery of DNA complexed with specific protein carriers, coprecipitation of DNA with calcium phosphate, encapsulation of DNA in various forms of liposomes, particle bombardment {Tang, D. et al., 1992}, {Eisenbraun, M. et al., 1993} and *in vivo* infection using cloned retroviral vectors {Seeger, C. et al., 1984}.

In a further aspect the present invention relates to a peptide binding to any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such peptides whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art.

Such peptides may be generated by using methods according to the state of the art such as phage display or ribosome display. In case of phage display, basically a library of peptides is generated, in form of phages, and this kind of library is contacted with the target molecule, in the present case a hyperimmune serum reactive antigen and fragments thereof according to the present invention. Those peptides binding to the target molecule are subsequently removed, preferably as a complex with the target molecule, from the respective reaction. It is known to the one skilled in the art that the binding characteristics, at least to a certain extent, depend on the particularly realized experimental set-up such as the salt concentration and the like. After separating those peptides binding to the target molecule with a higher affinity or a bigger force, from the non-binding members of the library, and optionally also after removal of the target molecule from the complex of target molecule and peptide, the respective peptide(s) may subsequently be characterised. Prior to the characterisation optionally an amplification step is realized such as, e. g. by propagating the peptide encoding phages. The characterisation preferably comprises the sequencing of the target binding peptides. Basically, the peptides are not limited in their lengths, however, preferably peptides having a lengths from about 8 to 20 amino acids are preferably obtained in the respective methods. The size of the libraries may be about 10^2 to 10^{18} , preferably 10^8 to 10^{15} different peptides, however, is not limited thereto.

A particular form of target binding hyperimmune serum reactive antigens and fragments thereof are the so-called "anticalines" which are, among others, described in German patent application DE 197 42 706.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably aptamers and spiegelmers.

Aptamers are D-nucleic acids, which are either single stranded or double stranded and which specifically interact with a target molecule. The manufacture or selection of aptamers is, e.g. described in European patent EP 0 533 838. Basically the following steps are realized. First, a mixture of nucleic acids, i. e. potential aptamers, is provided whereby each nucleic acid typically comprises a segment of several, preferably at least eight subsequent randomised nucleotides. This mixture is subsequently contacted with the target molecule whereby the nucleic acid(s) bind to the target molecule, such as based on an increased affinity towards the target or with a bigger force thereto, compared to the candidate mixture. The binding nucleic acid(s) are/is subsequently separated from the remainder of the mixture. Optionally, the thus obtained nucleic acid(s) is amplified using, e.g. polymerase chain reaction. These steps may be repeated several times giving at the end a mixture having an increased ratio of nucleic acids specifically binding to the target from which the final binding nucleic acid is then optionally selected. These specifically binding nucleic acid(s) are referred to as aptamers. It is obvious that at any stage of the method for the generation or identification of the aptamers samples of the mixture of individual nucleic acids may be taken to determine the sequence thereof using standard techniques. It is within the present invention that the aptamers may be stabilized such as, e. g., by introducing defined chemical groups which are known to the one skilled in the art of generating aptamers. Such modification may for example reside in the introduction of an amino group at the 2'-position of the sugar moiety of the nucleotides. Aptamers are currently used as therapeutical agents. However, it is also within the present invention that the thus selected or generated aptamers may be used for target validation and/or as lead substance for the development of medicaments, preferably of medicaments based on small molecules. This is actually done by a competition assay whereby the specific interaction between the target molecule and the aptamer is inhibited by a candidate drug whereby upon replacement of the aptamer from the complex of target and aptamer it may be assumed that the respective drug candidate allows a specific inhibition of the interaction between target and aptamer, and if the interaction is specific, said candidate drug will, at least in principle, be suitable to block the target and thus decrease its biological availability or activity in a respective system comprising such target. The thus obtained small molecule may then be subject to further derivatisation and modification to optimise its physical, chemical, biological and/or medical characteristics such as toxicity, specificity, biodegradability and bioavailability.

Spiegelmers and their generation or manufacture is based on a similar principle. The manufacture of spiegelmers is described in international patent application WO 98/08856. Spiegelmers are L-nucleic acids, which means that they are composed of L-nucleotides rather than D-nucleotides as aptamers are. Spiegelmers are characterized by the fact that they have a very high stability in biological systems and, comparable to aptamers, specifically interact with the target molecule against which they are directed. In the process of generating spiegelmers, a heterogeneous population of D-nucleic acids is created and this population is contacted with the optical antipode of the target molecule, in the present case for example with the D-enantiomer of the naturally occurring L-enantiomer of the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Subsequently, those D-nucleic acids are separated which do not interact with the optical antipode of the target molecule. But those D-nucleic acids interacting with the optical antipode of the target molecule are separated, optionally identified and/or sequenced and subsequently the corresponding L-nucleic acids are synthesized based on the nucleic acid sequence information obtained from the D-nucleic acids. These L-nucleic acids which are identical in terms of sequence with the aforementioned D-nucleic acids interacting with the optical antipode of the target molecule, will specifically interact with the naturally occurring target molecule rather than with the optical antipode thereof. Similar to the method for the generation of aptamers it is

also possible to repeat the various steps several times and thus to enrich those nucleic acids specifically interacting with the optical antipode of the target molecule.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the nucleic acid molecules according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the nucleic acid molecules and their respective sequences according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably ribozymes, antisense oligonucleotides and siRNA.

Ribozymes are catalytically active nucleic acids, which preferably consist of RNA, which basically comprises two moieties. The first moiety shows a catalytic activity whereas the second moiety is responsible for the specific interaction with the target nucleic acid, in the present case the nucleic acid coding for the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Upon interaction between the target nucleic acid and the second moiety of the ribozyme, typically by hybridisation and Watson-Crick base pairing of essentially complementary stretches of bases on the two hybridising strands, the catalytically active moiety may become active which means that it catalyses, either intramolecularly or intermolecularly, the target nucleic acid in case the catalytic activity of the ribozyme is a phosphodiesterase activity. Subsequently, there may be a further degradation of the target nucleic acid, which in the end results in the degradation of the target nucleic acid as well as the protein derived from the said target nucleic acid. Ribozymes, their use and design principles are known to the one skilled in the art, and, for example described in [Doherty, E. et al., 2001] and [Lewin, A. et al., 2001].

The activity and design of antisense oligonucleotides for the manufacture of a medicament and as a diagnostic agent, respectively, is based on a similar mode of action. Basically, antisense oligonucleotides hybridise based on base complementarity, with a target RNA, preferably with a mRNA, thereby activating RNase H. RNase H is activated by both phosphodiester and phosphorothioate-coupled DNA. Phosphodiester-coupled DNA, however, is rapidly degraded by cellular nucleases with the exception of phosphorothioate-coupled DNA. These resistant, non-naturally occurring DNA derivatives do not inhibit RNase H upon hybridisation with RNA. In other words, antisense polynucleotides are only effective as DNA RNA hybriide complexes. Examples for this kind of antisense oligonucleotides are described, among others, in US-patent US 5,849,902 and US 5,989,912. In other words, based on the nucleic acid sequence of the target molecule which in the present case are the nucleic acid molecules for the hyperimmune serum reactive antigens and fragments thereof according to the present invention, either from the target protein from which a respective nucleic acid sequence may in principle be deduced, or by knowing the nucleic acid sequence as such, particularly the mRNA, suitable antisense oligonucleotides may be designed base on the principle of base complementarity.

Particularly preferred are antisense-oligonucleotides, which have a short stretch of phosphorothioate DNA (3 to 9 bases). A minimum of 3 DNA bases is required for activation of bacterial RNase H and a minimum of 5 bases is required for mammalian RNase H activation. In these chimeric oligonucleotides there is a central region that forms a substrate for RNase H that is flanked by hybridising "arms" comprised of modified nucleotides that do not form substrates for RNase H. The hybridising arms of the chimeric oligonucleotides may be modified such as by 2'-O-methyl or 2'-fluoro. Alternative approaches used methylphosphonate or phosphoramidate linkages in said arms. Further embodiments of the antisense oligonucleotide useful in the practice of the present invention are P-methoxyoligonucleotides, partial P-methoxyoligodeoxyribonucleotides or P-methoxyoligonucleotides.

Of particular relevance and usefulness for the present invention are those antisense oligonucleotides as more particularly described in the above two mentioned US patents. These oligonucleotides contain no naturally occurring 5'→3'-linked nucleotides. Rather the oligonucleotides have two types of nucleotides:

2'-deoxyphosphorothioate, which activate RNase H, and 2'-modified nucleotides, which do not. The linkages between the 2'-modified nucleotides can be phosphodiester, phosphorothioate or P-ethoxyphosphodiester. Activation of RNase H is accomplished by a contiguous RNase H-activating region, which contains between 3 and 5 2'-deoxyphosphorothioate nucleotides to activate bacterial RNase H and between 5 and 10 2'-deoxyphosphorothioate nucleotides to activate eucaryotic and, particularly, mammalian RNase H. Protection from degradation is accomplished by making the 5' and 3' terminal bases highly nuclease resistant and, optionally, by placing a 3' terminal blocking group.

More particularly, the antisense oligonucleotide comprises a 5' terminus and a 3' terminus; and from position 11 to 59 5'→3'-linked nucleotides independently selected from the group consisting of 2'-modified phosphodiester nucleotides and 2'-modified P-alkyloxyphosphotriester nucleotides; and wherein the 5'-terminal nucleoside is attached to an RNase H-activating region of between three and ten contiguous phosphorothioate-linked deoxyribonucleotides, and wherein the 3'-terminus of said oligonucleotide is selected from the group consisting of an inverted deoxyribonucleotide, a contiguous stretch of one to three phosphorothioate 2'-modified ribonucleotides, a biotin group and a P-alkyloxyphosphotriester nucleotide.

Also an antisense oligonucleotide may be used wherein not the 5' terminal nucleoside is attached to an RNase H-activating region but the 3' terminal nucleoside as specified above. Also, the 5' terminus is selected from the particular group rather than the 3' terminus of said oligonucleotide.

The nucleic acids as well as the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used as or for the manufacture of pharmaceutical compositions, especially vaccines. Preferably such pharmaceutical composition, preferably vaccine is for the prevention or treatment of diseases caused by, related to or associated with *S. agalactiae*. In so far another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, which comprises inoculating the individual with the hyperimmune serum reactive antigens and fragments thereof of the invention, or a fragment or variant thereof, adequate to produce antibodies to protect said individual from infection, particularly *streptococcal* infection and most particularly *S. agalactiae* infections.

Yet another aspect of the invention relates to a method of inducing an immunological response in an individual which comprises, through gene therapy or otherwise, delivering a nucleic acid functionally encoding hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof, for expressing the hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibodies or a cell mediated T cell response, either cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One-way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise.

A further aspect of the invention relates to an immunological composition which, when introduced into a host capable of having induced within it an immunological response, induces an immunological response in such host, wherein the composition comprises recombinant DNA which codes for and expresses an antigen of the hyperimmune serum reactive antigens and fragments thereof of the present invention. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

The hyperimmune serum reactive antigens and fragments thereof of the invention or a fragment thereof may be fused with a co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing a fused protein which will have immunogenic and protective properties. This fused recombinant protein preferably further comprises an antigenic co-protein, such as Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilise the

protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Also, provided by this invention are methods using the described nucleic acid molecule or particular fragments thereof in such genetic immunization experiments in animal models of infection with *S. agalactiae*. Such fragments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. This approach can allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of *S. agalactiae* infection in mammals, particularly humans.

The hyperimmune serum reactive antigens and fragments thereof may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue and mucosal tissues caused e.g. by viral infection (esp. respiratory, such as the flu) mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The present invention also includes a vaccine formulation, which comprises the immunogenic recombinant protein together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, intradermal intranasal or transdermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in-water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

According to another aspect, the present invention relates to a pharmaceutical composition comprising such a hyperimmune serum-reactive antigen or a fragment thereof as provided in the present invention for *S. agalactiae*. Such a pharmaceutical composition may comprise one or more hyperimmune serum reactive antigens or fragments thereof against *S. agalactiae*. Optionally, such *S. agalactiae* hyperimmune serum reactive antigens or fragments thereof may also be combined with antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *S. agalactiae* and/or other pathogens against which the antigens have been included in the vaccine.

According to a further aspect, the present invention relates to a pharmaceutical composition comprising a nucleic acid molecule encoding a hyperimmune serum-reactive antigen or a fragment thereof as identified above for *S. agalactiae*. Such a pharmaceutical composition may comprise one or more nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof against *S. agalactiae*. Optionally, such *S. agalactiae* nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof may also be combined with nucleic acid molecules encoding antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *S. agalactiae* and/or other pathogens against which the antigens have been included in the vaccine.

The pharmaceutical composition may contain any suitable auxiliary substances, such as buffer substances, stabilisers or further active ingredients, especially ingredients known in connection of pharmaceutical composition and/or vaccine production.

A preferable carrier/or excipient for the hyperimmune serum-reactive antigens, fragments thereof or a coding nucleic acid molecule thereof according to the present invention is an immunostimulatory compound for further stimulating the immune response to the given hyperimmune serum-reactive antigen, fragment thereof or a coding nucleic acid molecule thereof. Preferably the immunostimulatory compound in the pharmaceutical preparation according to the present invention is selected from the group of polycationic substances, especially polycationic peptides, immunostimulatory nucleic acids molecules, preferably immunostimulatory deoxynucleotides, alum, Freund's complete adjuvants, Freund's incomplete adjuvants, neuroactive compounds, especially human growth hormone, or combinations thereof.

It is also within the scope of the present invention that the pharmaceutical composition, especially vaccine, comprises apart from the hyperimmune serum reactive antigens, fragments thereof and/or coding nucleic acid molecules thereof according to the present invention other compounds which are biologically or pharmaceutically active. Preferably, the vaccine composition comprises at least one polycationic peptide. The polycationic compound(s) to be used according to the present invention may be any polycationic compound, which shows the characteristic effects according to the WO 97/30721. Preferred polycationic compounds are selected from basic polypeptides, organic polycations, basic polyamino acids or mixtures thereof. These polyamino acids should have a chain length of at least 4 amino acid residues (WO 97/30721). Especially preferred are substances like polylysine, polyarginine and polypeptides containing more than 20 %, especially more than 50 % of basic amino acids in a range of more than 8, especially more than 20, amino acid residues or mixtures thereof. Other preferred polycations and their pharmaceutical compositions are described in WO 97/30721 (e.g. polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 amino acid residues, especially between 30 and 200 residues.

These polycationic compounds may be produced chemically or recombinantly or may be derived from natural sources.

Cationic (poly)peptides may also be anti-microbial with properties as reviewed in (Ganz, T., 1999). These (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically or recombinantly (WO 02/13857). Peptides may also belong to the class of defensins (WO 02/13857). Sequences of such peptides can be, for example, found in the Antimicrobial Sequences Database under the following internet address:

<http://www.bbcm.univ.trieste.it/~tossi/pag2.html>

Such host defence peptides or defensives are also a preferred form of the polycationic polymer according to the present invention. Generally, a compound allowing as an end product activation (or down-regulation) of the adaptive immune system, preferably mediated by APCs (including dendritic cells) is used as polycationic polymer.

Especially preferred for use as polycationic substances in the present invention are cathelicidin derived antimicrobial peptides or derivatives thereof (International patent application WO 02/13857, incorporated herein by reference), especially antimicrobial peptides derived from mammalian cathelicidin, preferably from human, bovine or mouse.

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from

these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin. For example, mouse cathelin is a peptide which has the amino acid sequence $\text{NH}_2\text{-RLAGLLRKGGEKIGEKLLKKIGOKIKNFFQKLVPQPE-COOH}$. Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20 amino acid residues. Derivations may include the substitution or modification of the natural amino acids by amino acids which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen. These cathelin molecules surprisingly have turned out to be also effective as an adjuvant for an antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further immunactivating substances.

Another preferred polycationic substance to be used according to the present invention is a synthetic peptide containing at least 2 KLK-motifs separated by a linker of 3 to 7 hydrophobic amino acids (International patent application WO 02/32451, incorporated herein by reference).

The pharmaceutical composition of the present invention may further comprise immunostimulatory nucleic acid(s). Immunostimulatory nucleic acids are e. g. neutral or artificial CpG containing nucleic acids, short stretches of nucleic acids derived from non-vertebrates or in form of short oligonucleotides (ODNs) containing non-methylated cytosine-guanine di-nucleotides (CpG) in a certain base context (e.g. described in WO 96/02555). Alternatively, also nucleic acids based on inosine and cytidine as e.g. described in the WO 01/93903, or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448, incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention. Preferably, the mixtures of different immunostimulatory nucleic acids may be used according to the present invention.

It is also within the present invention that any of the aforementioned polycationic compounds is combined with any of the immunostimulatory nucleic acids as aforementioned. Preferably, such combinations are according to the ones as described in WO 01/93905, WO 02/32451, WO 01/54720, WO 01/93903, WO 02/13857 and PCT/EP 02/05448 and the Austrian patent application A 1924/2001, incorporated herein by reference.

In addition or alternatively such vaccine composition may comprise apart from the hyperimmune serum reactive antigens and fragments thereof, and the coding nucleic acid molecules thereof according to the present invention a neuroactive compound. Preferably, the neuroactive compound is human growth factor as, e.g. described in WO 01/24822. Also preferably, the neuroactive compound is combined with any of the polycationic compounds and/or immunostimulatory nucleic acids as afore-mentioned.

In a further aspect the present invention is related to a pharmaceutical composition. Such pharmaceutical composition is, for example, the vaccine described herein. Also a pharmaceutical composition is a pharmaceutical composition which comprises any of the following compounds or combinations thereof: the nucleic acid molecules according to the present invention, the hyperimmune serum reactive antigens and fragments thereof according to the present invention, the vector according to the present invention, the cells according to the present invention, the antibody according to the present invention, the functional nucleic acids according to the present invention and the binding peptides such as the anticalines according to the present invention, any agonists and antagonists screened as described herein. In connection therewith any of these compounds may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a hyperimmune serum reactive antigen and fragments thereof of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not

limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intratracheal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application, for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1 % to about 98 % by weight of the formulation; more usually they will constitute up to about 80 % by weight of the formulation.

In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.05-5 μ g antigen / per kg of body weight, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

With the indicated dose range, no adverse toxicological effects should be observed with the compounds of the invention, which would preclude their administration to suitable individuals.

In a further embodiment the present invention relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. The ingredient(s) can be present in a useful amount, dosage, formulation or combination. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, reflecting approval by the agency of the manufacture, use or sale of the product for human administration.

In connection with the present invention any disease related use as disclosed herein such as, e. g. use of the pharmaceutical composition or vaccine, is particularly a disease or diseased condition which is caused by, linked or associated with Streptococci, more preferably, *S. pyogens* and *pneumoniae*. In connection therewith it is to be noted that *S. agalactiae* comprises several strains including those disclosed herein. A disease related, caused or associated with the bacterial infection to be prevented and/or treated according to the present invention includes besides others bacterial pharyngitis, otitis media, pneumonia, bacteremia, meningitis, peritonitis, wound infection and sepsis in humans.

In a still further embodiment the present invention is related to a screening method using any of the hyperimmune serum reactive antigens or nucleic acids according to the present invention. Screening methods as such are known to the one skilled in the art and can be designed such that an agonist or an antagonist is screened. Preferably an antagonist is screened which in the present case inhibits or prevents the binding of any hyperimmune serum reactive antigen and fragment thereof according to the present

invention to an interaction partner. Such interaction partner can be a naturally occurring interaction partner or a non-naturally occurring interaction partner.

The invention also provides a method of screening compounds to identify those, which enhance (agonist) or block (antagonist) the function of hyperimmune serum reactive antigens and fragments thereof or nucleic acid molecules of the present invention, such as its interaction with a binding molecule. The method of screening may involve high-throughput.

For example, to screen for agonists or antagonists, the interaction partner of the nucleic acid molecule and nucleic acid, respectively, according to the present invention, maybe a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, may be prepared from a cell that expresses a molecule that binds to the hyperimmune serum reactive antigens and fragments thereof of the present invention. The preparation is incubated with labelled hyperimmune serum reactive antigens and fragments thereof in the absence or the presence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule to bind the binding molecule is reflected in decreased binding of the labelled ligand. Molecules which bind gratuitously, i. e., without inducing the functional effects of the hyperimmune serum reactive antigens and fragments thereof, are most likely to be good antagonists. Molecules that bind well and elicit functional effects that are the same as or closely related to the hyperimmune serum reactive antigens and fragments thereof are good agonists.

The functional effects of potential agonists and antagonists may be measured, for instance, by determining the activity of a reporter system following interaction of the candidate molecule with a cell or appropriate cell preparation, and comparing the effect with that of the hyperimmune serum reactive antigens and fragments thereof of the present invention or molecules that elicit the same effects as the hyperimmune serum reactive antigens and fragments thereof. Reporter systems that may be useful in this regard include but are not limited to colorimetric labelled substrate converted into product, a reporter gene that is responsive to changes in the functional activity of the hyperimmune serum reactive antigens and fragments thereof, and binding assays known in the art.

Another example of an assay for antagonists is a competitive assay that combines the hyperimmune serum reactive antigens and fragments thereof of the present invention and a potential antagonist with membrane-bound binding molecules, recombinant binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. The hyperimmune serum reactive antigens and fragments thereof can be labelled such as by radioactivity or a colorimetric compound, such that the molecule number of hyperimmune serum reactive antigens and fragments thereof bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a hyperimmune serum reactive antigen and fragments thereof of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds to the same sites on a binding molecule without inducing functional activity of the hyperimmune serum reactive antigens and fragments thereof of the invention.

Potential antagonists include a small molecule, which binds to and occupies the binding site of the hyperimmune serum reactive antigens and fragments thereof thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules.

Other potential antagonists include antisense molecules (see [Okano, H. et al., 1991];

OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION; CRC Press, Boca Ration, FL (1988), for a description of these molecules).

Preferred potential antagonists include derivatives of the hyperimmune serum reactive antigens and fragments thereof of the invention.

As used herein the activity of a hyperimmune serum reactive antigen and fragment thereof according to the present invention is its capability to bind to any of its interaction partner or the extent of such capability to bind to its or any interaction partner.

In a particular aspect, the invention provides the use of the hyperimmune serum reactive antigens and fragments thereof, nucleic acid molecules or inhibitors of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: i) in the prevention of adhesion of *S. agalactiae* to mammalian extracellular matrix proteins at mucosal surfaces and on in-dwelling devices or to extracellular matrix proteins in wounds; ii) to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins which mediate tissue damage or invasion iii) or lead to evasion of immune defense; iv) to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques, e.g. through inhibiting nutrient acquisition.

Each of the DNA coding sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein upon expression can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The antagonists and agonists may be employed, for instance, to inhibit diseases arising from infection with Streptococcus, especially *S. agalactiae*, such as sepsis.

In a still further aspect the present invention is related to an affinity device such affinity device comprises as least a support material and any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, which is attached to the support material. Because of the specificity of the hyperimmune serum reactive antigens and fragments thereof according to the present invention for their target cells or target molecules or their interaction partners, the hyperimmune serum reactive antigens and fragments thereof allow a selective removal of their interaction partner(s) from any kind of sample applied to the support material provided that the conditions for binding are met. The sample may be a biological or medical sample, including but not limited to, fermentation broth, cell debris, cell preparation, tissue preparation, organ preparation, blood, urine, lymph liquid, liquor and the like.

The hyperimmune serum reactive antigens and fragments thereof may be attached to the matrix in a covalent or non-covalent manner. Suitable support material is known to the one skilled in the art and can be selected from the group comprising cellulose, silicon, glass, aluminium, paramagnetic beads, starch and dextrane.

The present invention is further illustrated by the following figures, examples and the sequence listing, from which further features, embodiments and advantages may be taken. It is to be understood that the present examples are given by way of illustration only and not by way of limitation of the disclosure.

In connection with the present invention

Figure 1 shows the characterization of human antibody sources for *S. agalactiae*.

Figure 2 shows the characterization of the small fragment genomic library, LSAg-70, from *Streptococcus agalactiae* ATCC 12403.

Figure 3 shows the selection of bacterial cells by MACS using biotinylated human IgGs.

Figure 4 shows the serotypes of the applied strains and an example for the gene distribution analysis with one of the identified antigens.

Figure 5 shows examples for induction of epitope-specific antibodies in mice by immunization with *E. coli* lysates.

Figure 6 shows examples for cell surface staining with epitope-specific antisera by flow cytometry.

Figure 7 shows the determination of bactericidal activity of antibodies induced by selected epitopes in an *in vitro* assay.

Table 1A shows the summary of all screens performed with genomic *S. agalactiae* libraries and human serum. Table 1B shows antigenic proteins identified by sequence identity within antigenic regions of the proteins listed in Table 1A.

Table 2 shows the summary of epitope serology analysis with human sera.

Table 3 shows the summary of the gene distribution analysis for the identified antigens in 46 *S. agalactiae* strains.

Table 4 shows the summary of mouse immunogenicity experiments.

The figures to which it might be referred to in the specification are described in the following in more details.

Figure 1 shows the characterization of human sera and cervical secretions for anti-*S. agalactiae* antibodies as measured by immune assays. Total anti-*S. agalactiae* IgG and IgA antibody levels were measured by standard ELISA using total bacterial lysates or culture supernant fractions prepared from *S. agalactiae* serotype III strain ATCC 12403 as coating antigens. (A) Results of representative experiments are shown with healthy adult sera with total bacterial lysate proteins. Data are expressed as ELISA units calculated from absorbance at 405nm at a serum dilution in the linear range of detection (2.000X for IgA, 10,000 for IgG). Selected sera (out of 52) included in the healthy adult non-pregnant serum pool (NSag8-IgG,-IgA) are indicated by bold numbers. (B) Immunoblot analysis was performed on high titer sera selected by ELISA in order to ensure multiple immune reactivity with protein antigens. Results of a representative experiment using total bacterial lysate prepared from *S. agalactiae* serotype III ATCC 12403 strain and selected patients' sera at 5.000X dilution are shown. Blots were developed with anti-human IgG secondary antibody reagent. Low titer sera were included as negative controls. Mw: molecular weight markers. (C) shows selection of cervical secretions from noncolonized pregnant women by immunoblot analysis. Antibodies extracted from cervical wicks were quantitated for IgA content. 2 µg IgA from each preparations were tested for immunoreactivity using total bacterial lysate in a multi-well blotting apparatus. Blots were developed with anti-human IgA secondary antibodies. IgA preparation showing reactivity with GBS proteins (indicated by arrows) were selected and pooled.

Figure 2 (A) shows the fragment size distribution of the *Streptococcus agalactiae* ATCC 12403 small fragment genomic library, LSAg-70. After sequencing 576 randomly selected clones, sequences were trimmed (464) to eliminate vector residues and the numbers of clones with various genomic fragment

sizes were plotted. (B) shows the graphic illustration of the distribution of the same set of randomly sequenced clones of LSAg-70 over the *S. agalactiae* ATCC 12403 chromosome. Rectangles indicate matching sequences to annotated ORFs and diamonds represent fully matched clones to non-coding chromosomal sequences in +/+ or +/- orientation. Circles position all clones with chimeric sequences. Numeric distances in base pairs are indicated over the circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

Figure 3 (A) shows the MACS selection with biotinylated human IgGs. The LSAg-70 library in pMAL9.1 was screened with 15-20 µg biotinylated IgG (PSag11-IgG, purified from human serum). As negative control, no serum was added to the library cells for screening. Number of cells selected after the 1st, 2nd and 3rd elution are shown for each selection round (upper, middle and lower panel, respectively). (B) shows the reactivity of specific clones (1-26) selected by bacterial surface display as analysed by immunoblot analysis with the human serum IgG pool (PSag11-IgG, 4 µg/µl) used for selection by MACS at a dilution of 1:3,000. As a loading control the same blot was also analysed with antibodies directed against the platform protein LamB at a dilution of 1:5,000 of hyperimmune rabbit serum. M, Molecular weight marker; L, Extract from a clone expressing LamB without foreign peptide insert.

Figure 4 (A) shows the representation of different serotypes of *S. agalactiae* clinical isolates analysed for the gene distribution study. A number of the strains were not typable and may represent additional serotypes. (B) shows the PCR analysis for the gene distribution of gbs0061 with the respective oligonucleotides and 46 *S. agalactiae* strains. The predicted size of the PCR fragments is 814 bp. 1-46, *S. agalactiae* strains, clinical isolates as shown under A; -, no genomic DNA added; +, genomic DNA from *S. agalactiae* ATCC 12403, which served as template for library construction.

Figure 5 shows the measurement of epitope-specific mouse serum IgG antibody levels induced by total bacterial lysates of Lamb or FhuA expressing *E. coli* clones with *S. agalactiae*-derived epitopes. (A) shows representative peptide ELISA experiments with three sets of mouse sera (5 mice in each group, 1-5) generated by gbs0428, gbs0628 and gbs632 epitopes, respectively. Sera were tested at two different dilutions: black bars: 100X; grey bars; 1000X. Biotin-labeled synthetic peptides corresponding to the respective epitopes were used in the peptide ELISA. Sera induced with *E. coli* lysate without *S. agalactiae* derived epitopes are indicated as FhuA or Lamb. (B) shows a typical immunoblotting experiment using lysates prepared from individual *E. coli* clones selected for mouse injections. Sera were depleted by *E. coli* lysate not carrying epitope to remove antibodies against *E. coli* proteins. Examples are shown for gbs0918, gbs0428, gbs0628 and gbs632 epitopes. Negative controls (-) are *E. coli* clones with empty platform proteins. Location of platform proteins Lamb and FhuA is indicated by arrows.

Figure 6 shows the detection of specific antibody binding on the cell surface of *Streptococcus agalactiae* by flow cytometry. In Figure 6A preimmune mouse sera and polyclonal sera raised against *S. agalactiae* serotype III lysate were incubated with *S. agalactiae* strain serotype III and analysed by flow cytometry. Control shows the level of non-specific binding of the secondary antibody to the surface of *S. agalactiae* cells. The histograms in figure 5B indicates the increased fluorescence due to specific binding of anti-gbs0031, anti-gbs1925 and anti-gbs0012 antibodies in comparison to the control sera generated against *E. coli* lysate containing only the 'empty' platform protein FhuA.

Figure 7 shows the bactericidal activity of epitope specific antibodies as determined in *in vitro* killing assay. The killing activity of immune sera is measured parallel with and calculated relative to the appropriate control sera. Data are expressed as percentage of killing, that is the reduction on bacterial cfu numbers as a consequence of the presence of specific antibodies. Hyperimmune polyclonal mouse sera generated with *S. agalactiae* lysate and sera from non-immunized mice served as positive and negative controls for the assay, respectively. Immune sera generated with gbs0012, gbs0016, gbs0031, gbs0428, gbs1306 and gbs2018 epitopes were tested for bactericidal activity and data are expressed relative to appropriate controls, such as sera induced with Lamb or FhuA expressing *E. coli* clones without *S.*

agalactiae-derived epitopes. *S. agalactiae* serotype III cells were incubated with mouse phagocytic cells for 60 min, and surviving bacteria were quantified by counting cfus after plating on blood agar.

Table 1: Immunogenic proteins identified by bacterial surface display.

(A) Columns A, 300bp library of *S. agalactiae* ATCC 12403 in *fhuA* with NSag8-IgA (826), B, 300bp library in *fhuA* with PSag10-IgA (768), C, 300bp library in *fhuA* with PSag10-IgG (711), D, 300bp library in *fhuA* with PSag11-IgG (640), E, 70bp library in *lamB* with NSag8-IgA (1057), F, 70bp library in *lamB* with NSag8-IgG (869), G, 70bp library in *lamB* with PSag10-IgA (904), H, 70bp library in *lamB* with PSag10-IgA-adsorbed (493), I, 70bp library in *lamB* with PSag10-IgG (910), J, 70bp library in *lamB* with PSag11-IgA (631), K, 70bp library in *lamB* with PSag11-IgG (926), L, 70bp library in *lamB* with PSag18-IgA (691), M, 70bp library in *lamB* with PSag-sIgA (628); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990). Table 1B lists the immunogenic proteins identified by amino acid sequence identity with peptides identified by bacterial surface display. Antigenic peptides, which have been identified by bacterial surface-display possess identical counterparts in the listed proteins from *S. agalactiae*. The peptides have been shown to react with multiple human sera (see Table 2). Sera directed against these peptides can therefore recognize multiple proteins.

Table 2: Epitope serology with human sera.

Immune reactivity of individual synthetic peptides representing selected epitopes with human sera is shown. Extent of reactivity is expressed as +, ++ or +++, and summed from individual reactivities of peptides with individual sera (13 patient and 9 healthy adult, 22 total). A total score for each peptide was calculated based on ELISA units as the sum of all reactivities. Scores were 2-8 for +, 9-16 for ++ and 17-26 for +++. ELISA units were calculated from OD_{405nm} readings and the serum dilution after correction for background. Location of synthetic peptides within the antigenic ORFs according to the genome annotation of ATCC 12403 strain is given in columns aa from and aa to indicating the first and last amino acid residues, respectively. Peptide names: gbs0012.1 present in annotated ORF: gbs0012.

Table 3: Gene distribution in *S. agalactiae* strains.

Fourty six *S. agalactiae* strains as shown in Figure 4A were tested by PCR with oligonucleotides specific for the genes encoding relevant antigens. The PCR fragment of one selected PCR reaction was sequenced in order to confirm the amplification of the correct DNA fragment. *, number of amino acid substitutions in a serotype IA strain as derived from sequencing as compared to *S. agalactiae* ATCC 12403. #, alternative strain used for sequencing, because gene was not present in the serotype IA strain.

Table 4: Immunogenicity of antigenic epitopes.

S. agalactiae antigens were tested for immunogenicity by immunization with *E. coli* clones harboring plasmids encoding the platform proteins LamB or FhuA fused to *S. agalactiae* peptides. The presence of epitope-specific antibodies were detected and measured by peptide ELISA and/or immunoblotting using the corresponding *E. coli* clone lysate, which served as immunogen. Results are expressed as + to +++++, and calculated for peptide ELISA as the sum of the reactivity of individual mouse sera based on ELISA units (as indicated on Fig. 5A) and for immunoblotting (IB) as the strength of reactivity of pooled (5 individual) mouse sera with the epitope containing platform protein (as indicated on Fig. 5B). Location of synthetic peptides within the antigenic ORFs according to the genome annotation of ATCC 12403 strain is given in columns aa from and aa to indicating the first and last amino acid residues, respectively.

EXAMPLES

Example 1: Characterization and selection of human serum sources based on anti-*S. agalactiae* antibodies, preparation of antibody screening reagents

Experimental procedures

Enzyme linked immune assay (ELISA).

ELISA plates (Maxisorb, Millipore) were coated with 5-10 µg/ml total protein diluted in coating buffer (0.1M sodium carbonate pH 9.2). Three dilutions of sera (2,000X, 10,000X, 50,000X) were made in PBS-BSA. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG or anti-human IgA secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Antigen-antibody complexes were quantified by measuring the conversion of the substrate (ABTS) to colored product based on OD_{405nm} readings by automatic ELIAS reader (TECAN SUNRISE).

Preparation of bacterial antigen extracts

Total bacterial lysate: Bacteria were grown overnight in THB (Todd-Hewitt Broth) and lysed by repeated freeze-thaw cycles: incubation on dry ice/ethanol-mixture until frozen (1 min), then thawed at 37°C (5 min): repeated 3 times. This was followed by sonication and collection of supernatant by centrifugation (3,500 rpm, 15 min, 4°C).

Culture supernatant: After removal of bacteria by centrifugation, the supernatant of overnight grown bacterial cultures was precipitated with ice-cold ethanol by mixing 1 part supernatant with 3 parts absolute ethanol and incubated overnight at -20°C. Precipitates were collected by centrifugation (2,600 g, for 15 min). Dry pellets were dissolved either in PBS for ELISA, or in urea and SDS-sample buffer for SDS-PAGE and immunoblotting. The protein concentration of samples was determined by Bradford assay.

Immunoblotting

Total bacterial lysate and culture supernatant samples were prepared from *in vitro* grown *S. agalactiae* serotype III strain. 10 to 25µg total protein/lane was separated by SDS-PAGE using the BioRad Mini-Protean Cell electrophoresis system and proteins transferred to nitrocellulose membrane (ECL, Amersham Pharmacia). After overnight blocking in 5% milk, human sera were added at 2,000x dilution, and HRPO labeled anti-human IgG was used for detection.

Extraction of antibodies from cervical wicks

Cervical secretions were collected by absorbent cylindrical wicks (Polyfiltronics) which were introduced into the cervical canal during speculum examination and thereafter kept frozen until extraction. Extraction was done according to Hordnes *et al*, 1998 (provider of the samples). Briefly, wicks were mixed with PBS containing protease inhibitors, vortexed and fluid was drained from the tubes containing the wicks. The concentrations of total IgA and IgG antibodies in extracts were determined.

Purification of antibodies for genomic screening. Five sera from both the patient and the healthy group were selected based on the overall anti-GBS titers for serum or cervical secretion pools used in the screening procedure. Antibodies against *E. coli* proteins were removed by incubating the heat-inactivated sera with whole cell *E. coli* cells (DH5alpha, transformed with pHIE11, grown under the same condition as used for bacterial surface display). Highly enriched preparations of IgGs from the pooled, depleted sera were generated by protein G affinity chromatography, according to the manufacturer's instructions (UltraLink Immobilized Protein G, Pierce). IgA antibodies were purified also by affinity chromatography using biotin-labeled anti-human IgA (Southern Biotech) immobilized on Streptavidin-agarose (GIBCO BRL). The efficiency of depletion and purification was checked by SDS-PAGE, Western blotting, ELISA and protein concentration measurements.

Results

The antibodies produced against *S. agalactiae* by the human immune system and present in human sera

are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. These molecules are essential for the identification of individual antigens in the approach as described in the present invention, which is based on the interaction of the specific anti-GBS antibodies and the corresponding *S. agalactiae* peptides or proteins. To gain access to relevant antibody repertoires, human sera were collected from

- I. healthy pregnant women tested negative for cervical and anorectal carriage of GBS
- II. healthy pregnant women tested positive for cervical and/or anorectal carriage of GBS who's newborn remained GBS-free (although with antibiotic prevention).
- III. adults below <45 years of age without clinical disease.
- IV. naïve individuals, young children between 5 and 10 months of age, after they already lost maternal antibodies and have not acquired GBS-specific ones due to the lack of GBS disease.

In addition cervical secretions were also collected from the first two groups of donors. The extreme value of these antibody sources is mainly the secretory IgA component, which is directly implicated as protective effector molecule on mucosal surfaces.

It is important to screen with antibodies from at least two different populations, pregnant women and nonpregnant adults, since GBS disease affects elderly and immunocompromised adults, as well. Within the pregnant study group, there are again two different patient categories, women who are GBS colonized and those who are noncolonized, to be included in the antigen screen.

Antibodies in serum and other body fluids, such as mucosal secretions induced in individuals exposed to the pathogens are crucial for antigen identification. The exposure to GBS results in asymptomatic colonization, current or past acute or chronic infection. *S. agalactiae* colonization and infections are common, and antibodies are present as a consequence of natural immunization from previous encounters. It is likely that sera from high titer noncolonized individuals contain functional antibodies, which are able to eliminate carriage. At the same time certain antibodies might be induced against GBS components only if the antigen persist. For that reason sera from colonized individuals were also included. It has been shown that colonization is associated with capsular polysaccharide (CPS)-specific antibody responses. However, it is not clear whether sufficient level of antibodies to CPS's would prevent GBS colonization, since there are colonized women with both high and low levels of anti-CPS antibody, and the same is true for noncolonized pregnant women.

However, there are reports that effector function and avidity of antibodies produced during pregnancy might be altered. It is important to recognize that most healthy adults are protected from invasive GBS disease and are less susceptible than newborns and the elderly. Antibodies from these individuals seem to be especially valuable for identification of the corresponding antigens. It is known that anti-GBS antibody levels increase with age.

GBS is a mucosal pathogen and should induce IgA response; for that reason it was important to perform IgA-based screens, as well as IgG-based screens. The fact that some *S. agalactiae* strains express high affinity IgA-binding receptor also points to the importance of IgA in host response. Recently it was reported that not only IgG, but also IgA serum antibodies can be recognized by the FcRIII receptors of PMNs and promote opsonization (Phillips-Quagliata, J. et al., 2000); (Shibuya, A. et al., 2000). The primary role of IgA antibodies is neutralization, mainly at the mucosal surface. The level of serum IgA reflects the quality, quantity and specificity of the dimeric secretory IgA. For that reason the serum collection was not only analyzed for anti-streptococcal IgG, but also for IgA levels. In the ELISA assays highly specific secondary reagents were used to detect antibodies from the high affinity types, such as IgG and IgA, but avoided IgM. Production of IgM antibodies occurs during the primary adaptive humoral response, and results in low affinity antibodies, while IgG and IgA antibodies had already undergone affinity maturation, and are more valuable in fighting or preventing disease.

127 serum samples and 97 cervical secretions from pregnant women and 50 sera from healthy adults were characterized for anti-*S. agalactiae* antibodies by a series of immune assays. Primary characterization was done by ELISA using two different antigen preparations, such as total bacterial extract and culture supernatant proteins prepared from *S. agalactiae* serotype III ATCC 12403 strain. A representative experiment is shown in Fig. 1A using sera from the healthy adult population. Antibody titers were compared at given dilutions where the response was linear. Sera were ranked based on the IgG and IgA reactivity against the two complex antigenic mixtures (including serotype specific type III capsule), and the highest ones were selected for further testing by immunoblotting. This analysis confirmed a high antibody reactivity of the pre-selected sera against multiple GBS proteins, especially when compared to not selected, low-titer sera (Fig 1B). However, ELISA ranking of sera did not always correlated with immunoblot signals suggesting that anti-capsular antibodies were abundant and dominated the ELISA reactivities against total bacterial extracts. Thus the final selection of sera to be included in antibody-pools was based mainly on multiple immunogenic bands in immunoblotting experiments. This extensive antibody characterization approach has led to the unambiguous identification of anti-GBS hyperimmune sera.

The 97 cervical secretions were determined for IgA content, and same amount (2 μ g) was tested for anti-GBS reactivity by immunoblotting. Positively selected sera (as it is shown in Fig. 1C) were divided into colonized and noncolonized IgA pools and used separately in bacterial surface display experiments.

5 sera from both donor groups were selected and pooled for antigen identification by bacterial surface display. Selected sera included in the four pregnant women pools (PSAg10-IgG-IgA, PSAg11-IgG, PSAg18-IgG and PSAg-sIgA) and one healthy adult (non-pregnant) pool (NSAg8-IgG-IgA). IgG and IgA antibodies were purified from pooled sera by affinity chromatography and depleted of *E. coli* -reactive antibodies to avoid background in the bacterial surface display screen.

Example 2: Generation of highly random, frame-selected, small-fragment, genomic DNA libraries of *Streptococcus agalactiae*

Experimental procedures

Preparation of streptococcal genomic DNA. 50 ml Todd-Hewitt Broth medium was inoculated with *S. agalactiae* ATCC 12403 bacteria from a frozen stab and grown with aeration and shaking for 18 h at 37°C. The culture was then harvested, centrifuged with 1,600x g for 15 min and the supernatant was removed. Bacterial pellets were washed 3 x with PBS and carefully re-suspended in 0.5 ml of Lysozyme solution (100 mg/ml). 0.1 ml of 10 mg/ml heat treated RNase A and 20 U of RNase T1 were added, mixed carefully and the solution was incubated for 1 h at 37°C. Following the addition of 0.2 ml of 20 % SDS solution and 0.1 ml of Proteinase K (10 mg/ml) the tube was incubated overnight at 55°C. 1/3 volume of saturated NaCl was then added and the solution was incubated for 20 min at 4°C. The extract was pelleted in a microfuge (13,000 rpm) and the supernatant transferred into a new tube. The solution was extracted with PhOH/CHCl₃/IAA (25:24:1) and with CHCl₃/IAA (24:1). DNA was precipitated at room temperature by adding 0.6x volume of Isopropanol, spooled from the solution with a sterile Pasteur pipette and transferred into tubes containing 80% ice-cold ethanol. DNA was recovered by centrifuging the precipitates with 10-12,000x g, then dried on air and dissolved in ddH₂O.

Preparation of small genomic DNA fragments. Genomic DNA fragments were mechanically sheared into fragments ranging in size between 150 and 300 bp using a cup-horn sonicator (Bandelin Sonoplus UV 2200 sonicator equipped with a BB5 cup horn, 10 sec. pulses at 100 % power output) or into fragments of size between 50 and 70 bp by mild DNase I treatment (Novagen). It was observed that sonication yielded a much tighter fragment size distribution when breaking the DNA into fragments of the 150-300 bp size range. However, despite extensive exposure of the DNA to ultrasonic wave-induced hydromechanical

shearing force, subsequent decrease in fragment size could not be efficiently and reproducibly achieved. Therefore, fragments of 50 to 70 bp in size were obtained by mild DNase I treatment using Novagen's shotgun cleavage kit. A 1:20 dilution of DNase I provided with the kit was prepared and the digestion was performed in the presence of $MnCl_2$ in a 60 μ l volume at 20°C for 5 min to ensure double-stranded cleavage by the enzyme. Reactions were stopped with 2 μ l of 0.5 M EDTA and the fragmentation efficiency was evaluated on a 2% TAE-agarose gel. This treatment resulted in total fragmentation of genomic DNA into near 50-70 bp fragments. Fragments were then blunt-ended twice using T4 DNA Polymerase in the presence of 100 μ M each of dNTPs to ensure efficient flushing of the ends. Fragments were used immediately in ligation reactions or frozen at -20°C for subsequent use.

Description of the vectors. The vector pMAL4.31 was constructed on a pASK-IBA backbone [Skerra, A., 1994] with the beta-lactamase (*bla*) gene exchanged with the Kanamycin resistance gene. In addition the *bla* gene was cloned into the multiple cloning site. The sequence encoding mature beta-lactamase is preceded by the leader peptide sequence of *ompA* to allow efficient secretion across the cytoplasmic membrane. Furthermore a sequence encoding the first 12 amino acids (spacer sequence) of mature beta-lactamase follows the *ompA* leader peptide sequence to avoid fusion of sequences immediately after the leader peptidase cleavage site, since e.g. clusters of positive charged amino acids in this region would decrease or abolish translocation across the cytoplasmic membrane [Kajava, A. et al., 2000]. A *Sma*I restriction site serves for library insertion. An upstream *Fse*I site and a downstream *Not*I site, which were used for recovery of the selected fragment, flank the *Sma*I site. The three restriction sites are inserted after the sequence encoding the 12 amino acid spacer sequence in such a way that the *bla* gene is transcribed in the -1 reading frame resulting in a stop codon 15 bp after the *Not*I site. A +1 bp insertion restores the *bla* ORF so that beta-lactamase protein is produced with a consequent gain of Ampicillin resistance.

The vector pMAL9.1 was constructed by cloning the *lamB* gene into the multiple cloning site of pEH1 [Hashemzadeh-Bonehi, L. et al., 1998]. Subsequently, a sequence was inserted in *lamB* after amino acid 154, containing the restriction sites *Fse*I, *Sma*I and *Not*I. The reading frame for this insertion was constructed in such a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *lamB* and the respective insert.

The vector pHIE11 was constructed by cloning the *fhuA* gene into the multiple cloning site of pEH1. Thereafter, a sequence was inserted in *fhuA* after amino acid 405, containing the restriction site *Fse*I, *Xba*I and *Not*I. The reading frame for this insertion was chosen in a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *fhuA* and the respective insert.

Cloning and evaluation of the library for frame selection. Genomic *S. agalactiae* DNA fragments were ligated into the *Sma*I site of the vector pMAL4.31. Recombinant DNA was electroporated into DH10B electrocompetent *E. coli* cells (GIBCO BRL) and transformants plated on LB-agar supplemented with Kanamycin (50 μ g/ml) and Ampicillin (50 μ g/ml). Plates were incubated over night at 37°C and colonies collected for large scale DNA extraction. A representative plate was stored and saved for collecting colonies for colony PCR analysis and large-scale sequencing. A simple colony PCR assay was used to initially determine the rough fragment size distribution as well as insertion efficiency. From sequencing data the precise fragment size was evaluated, junction intactness at the insertion site as well as the frame selection accuracy (3n+1 rule).

Cloning and evaluation of the library for bacterial surface display. Genomic DNA fragments were excised from the pMAL4.31 vector, containing the *S. agalactiae* library with the restriction enzymes *Fse*I and *Not*I. The entire population of fragments was then transferred into plasmids pMAL9.1 (*LamB*) or pHIE11 (*FhuA*), which have been digested with *Fse*I and *Not*I. Using these two restriction enzymes, which recognise an 8 bp GC rich sequence, the reading frame that was selected in the pMAL4.31 vector is maintained in each of the platform vectors. The plasmid library was then transformed into *E. coli* DH5alpha cells by

electroporation. Cells were plated onto large LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C at a density yielding clearly visible single colonies. Cells were then scraped off the surface of these plates, washed with fresh LB medium and stored in aliquots for library screening at -80°C.

Results

Libraries for frame selection. Two libraries (LSAg-70 and LSAg-300) were generated in the pMAL4.31 vector with sizes of approximately 70 and 300 bp, respectively. For each library, ligation and subsequent transformation of approximately 1 µg of pMAL4.31 plasmid DNA and 50 ng of fragmented genomic *S. agalactiae* DNA yielded 4×10^5 to 2×10^6 clones after frame selection. To assess the randomness of the libraries, approximately 576 randomly chosen clones of LSAg-70 were sequenced. The bioinformatic analysis showed that of these clones only very few were present more than once. Furthermore, it was shown that approximately 80% of the clones fell in the size range between 25 and 100 bp with an average size of approximately 40 bp (Figure 2). Almost all sequences followed the 3n+1 rule, showing that all clones were properly frame selected.

Bacterial surface display libraries. The display of peptides on the surface of *E. coli* required the transfer of the inserts from the LSAg-70 and LSAg-300 libraries from the frame selection vector pMAL4.31 to the display plasmids pMAL9.1 (LamB) or pHIE11 (FhuA). Genomic DNA fragments were excised by *FseI* and *NotI* restriction and ligation of 5ng inserts with 0.1µg plasmid DNA and subsequent transformation into DH5alpha cells resulted in $2\text{--}5 \times 10^6$ clones. The clones were scraped off the LB plates and frozen without further amplification.

Example 3: Identification of highly immunogenic peptide sequences from *S. agalactiae* using bacterial surface displayed genomic libraries and human serum

Experimental procedures

MACS screening. Approximately 2.5×10^8 cells from a given library were grown in 5 ml LB-medium supplemented with 50 µg/ml Kanamycin for 2 h at 37°C. Expression was induced by the addition of 1 mM IPTG for 30 min. Cells were washed twice with fresh LB medium and approximately 2×10^7 cells re-suspended in 100 µl LB medium and transferred to an Eppendorf tube.

10 to 20 µg of biotinylated, human IgGs purified from serum was added to the cells and the suspension incubated overnight at 4°C with gentle shaking. 900 µl of LB medium was added, the suspension mixed and subsequently centrifuged for 10 min at 6,000 rpm at 4°C (For IgA screens, 10 µg of purified IgAs were used and these captured with biotinylated anti-human-IgG secondary antibodies). Cells were washed once with 1 ml LB and then re-suspended in 100 µl LB medium. 10 µl of MACS microbeads coupled to streptavidin (Miltenyi Biotech, Germany) were added and the incubation continued for 20 min at 4°C. Thereafter 900 µl of LB medium was added and the MACS microbead cell suspension was loaded onto the equilibrated MS column (Miltenyi Biotech, Germany) which was fixed to the magnet. (The MS columns were equilibrated by washing once with 1 ml 70% EtOH and twice with 2 ml LB medium.)

The column was then washed three times with 3 ml LB medium. After removal of the magnet, cells were eluted by washing with 2 ml LB medium. After washing the column with 3 ml LB medium, the 2 ml eluate was loaded a second time on the same column and the washing and elution process repeated. The loading, washing and elution process was performed a third time, resulting in a final eluate of 2 ml.

A second and third round of screening was performed as follows. The cells from the final eluate were collected by centrifugation and re-suspended in 1 ml LB medium supplemented with 50 µg/ml Kanamycin. The culture was incubated at 37°C for 90 min and then induced with 1 mM IPTG for 30 min.

Cells were subsequently collected, washed once with 1 ml LB medium and suspended in 10 μ l LB medium. 10 to 20 μ g of human, biotinylated IgGs were added again and the suspension incubated overnight at 4°C with gentle shaking. All further steps were exactly the same as in the first selection round. Cells selected after two rounds of selection were plated onto LB-agar plates supplemented with 50 μ g/ml Kanamycin and grown overnight at 37°C.

Evaluation of selected clones by sequencing and Western blot analysis. Selected clones were grown overnight at 37°C in 3 ml LB medium supplemented with 50 μ g/ml Kanamycin to prepare plasmid DNA using standard procedures. Sequencing was performed at MWG (Germany) or in collaboration with TIGR (U.S.A.).

For Western blot analysis approximately 10 to 20 μ g of total cellular protein was separated by 10% SDS-PAGE and blotted onto HybondC membrane (Amersham Pharmacia Biotech, England). The LamB or FhuA fusion proteins were detected using human serum as the primary antibody at a dilution of approximately 1:3,000 to 1:5,000 and anti-human IgG or IgA antibodies coupled to HRP at a dilution of 1:5,000 as secondary antibodies. Detection was performed using the ECL detection kit (Amersham Pharmacia Biotech, England). Alternatively, rabbit anti-FhuA or rabbit anti-LamB polyclonal immune sera were used as primary antibodies in combination with the respective secondary antibodies coupled to HRP for the detection of the fusion proteins.

Results

Screening of bacterial surface display libraries by magnetic activated cell sorting (MACS) using biotinylated Igs. The libraries LSag-70 in pMAL9.1 and LSag-300 in pHIE11 were screened with pools of biotinylated, human IgGs and IgAs prepared from sera of healthy adults (NSag8-IgG,-IgA) or P10,11,18 (see Example 1: *Preparation of antibodies from human serum*). The selection procedure was performed as described under Experimental procedures. Figure 3A shows a representative example of a screen with the LSag-70 library and PSag11-IgGs. As can be seen from the colony count after the first selection cycle from MACS screening, the total number of cells recovered at the end is drastically reduced from 2×10^7 cells to approximately 2×10^4 cells, but the selection without antibodies added showed a similar reduction in cell numbers (Figure 3A). Therefore a second and third round of selection was performed. At the end of round three, approximately 10^4 cells were recovered with PSag11-IgGs, while only 2×10^3 cells were recovered when no IgGs from human serum were added, clearly showing that selection was dependent on *S. agalactiae* specific antibodies. To evaluate the performance of the screen, 26 selected clones were picked randomly and subjected to immunoblot analysis with screening IgG pool (Figure 3B). This analysis revealed that more than 80% of the selected clones showed reactivity with antibodies present in the relevant serum whereas the control strain expressing LamB without a *S. agalactiae* specific insert did not react with the same serum. In general, the rate of reactivity was observed to lie within the range of 35 to 90%. Colony PCR analysis showed that all selected clones contained an insert in the expected size range.

Subsequent sequencing of a larger number of randomly picked clones (600 to 1200 per screen) led to the identification of the gene and the corresponding peptide or protein sequence that was specifically recognized by the human serum antibodies used for screening. The frequency with which a specific clone is selected reflects at least in part the abundance and/or affinity of the specific antibodies in the serum used for selection and recognizing the epitope presented by this clone. In that regard it is striking that clones derived from some ORFs (e.g. gbs1087, gbs1306, gbs2018) were picked more than 100 times, indicating their highly immunogenic property. Table 1 summarizes the data obtained for all 13 performed screens. All clones that are presented in Table 1 have been verified by immunoblot analysis using whole cellular extracts from single clones to show the indicated reactivity with the pool of human serum used in the respective screen. As can be seen from Table 1, distinct regions of the identified ORF are identified as immunogenic, since variably sized fragments of the proteins are displayed on the surface

by the platform proteins.

It is further worth noticing that most of the genes identified by the bacterial surface display screen encode proteins that are either attached to the surface of *S. agalactiae* and/or are secreted. This is in accordance with the expected role of surface attached or secreted proteins in virulence of *S. agalactiae*.

Example 4: Assessment of the reactivity of highly immunogenic peptide sequences with individual human sera.

Experimental procedures

Peptide synthesis

Peptides were synthesized in small scale (4 mg resin; up to 288 in parallel) using standard F-moc chemistry on a Rink amide resin (PepChem, Tübingen, Germany) using a SyroII synthesizer (MultisynTech, Witten, Germany). After the sequence was assembled, peptides were elongated with Fmoc-epsilon-aminohexanoic acid (as a linker) and biotin (Sigma, St. Louis, MO; activated like a normal amino acid). Peptides were cleaved off the resin with 93%TFA, 5% triethylsilane, and 2% water for one hour. Peptides were dried under vacuum and freeze dried three times from acetonitrile/water (1:1). The presence of the correct mass was verified by mass spectrometry on a Reflex III MALDI-TOF (Bruker, Bremen Germany). The peptides were used without further purification.

Enzyme linked immune assay (ELISA).

Biotin-labeled peptides (at the N-terminus) were coated on Streptavidin ELISA plates (EXICON) at 10 µg/ml concentration according to the manufacturer's instructions. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Sera were tested at two serum dilutions, 200X and 1,000X. Following manual coating, peptide plates were processed and analyzed by the Gemini 160 ELISA robot (TECAN) with a built-in ELISA reader (GENIOS, TECAN).

Results

Following the bioinformatic analysis of selected clones, corresponding peptides were designed and synthesized. In case of epitopes with more than 26 amino acid residues, overlapping peptides were made. All peptides were synthesized with a N-terminal biotin-tag and used as coating reagents on Streptavidin-coated ELISA plates.

The analysis was performed in two steps. First, peptides were selected based on their reactivity with the individual sera, which were included in the serum pools used for preparations of IgG and IgA screening reagents for bacterial surface display. A summary for serum reactivity of 58 peptides representing *S. agalactiae* epitopes from the genomic screen analysed with 22 human sera (from 13 patient and 9 healthy exposed high titer individuals) used for the antigen identification is shown in Table 2. The peptides were compared by the score calculated for each peptide based on the number of positive sera and the extent of reactivity. Peptides range from highly and widely reactive to weakly positive ones.

Example 5: Gene distribution studies with highly immunogenic proteins identified from *S. agalactiae*.

Experimental procedures

Gene distribution of GBS antigens by PCR. An ideal vaccine antigen would be an antigen that is present in all, or the vast majority of strains of the target organism to which the vaccine is directed. In order to

establish whether the genes encoding the identified *Streptococcus agalactiae* antigens occur ubiquitously in *S. agalactiae* strains, PCR was performed on a series of independent *S. agalactiae* isolates with primers specific for the gene of interest. *S. agalactiae* isolates were obtained covering the serotypes most frequently present in patients as shown in Figure 4A. Oligonucleotide sequences as primers were designed for all identified ORFs yielding products of approximately 1,000 bp, if possible covering all identified immunogenic epitopes. Genomic DNA of all *S. agalactiae* strains was prepared as described under Example 2. PCR was performed in a reaction volume of 25 µl using Taq polymerase (1U), 200 nM dNTPs, 10 pMol of each oligonucleotide and the kit according to the manufacturers instructions (Invitrogen, The Netherlands). As standard, 30 cycles (1x: 5min. 95°C, 30x: 30sec. 95°C, 30sec. 56°C, 30sec. 72°C, 1x 4min. 72°C) were performed, unless conditions had to be adapted for individual primer pairs.

Results

Identified genes encoding immunogenic proteins were tested by PCR for their presence in 46 different strains of *S. agalactiae* (Figure 4A). As an example, figure 4B shows the PCR reaction for GBS0061 with all indicated 46 strains. As clearly visible, the gene is present in all strains analysed. The PCR fragment from a type IA strain was sequenced and showed that all 657 bp were identical as compared to the *S. agalactiae* ATCC 12403 strain, indicating a high level of conservation between the two isolates.

From a total of 117 genes analysed, more than 100 were present in all or almost all strains tested, while only 5 genes were absent in more than 10% of the tested 46 strains (Table 3). In addition, only few genes (e.g. GBS0016, GBS1087, GBS1528 and GBS2018) showed variation in size but were present in all or most strain isolates. Sequencing of the generated PCR fragment from one strain and subsequent comparison to the type III strain ATCC 12403 confirmed the amplification of the correct DNA fragment and revealed a degree of sequence divergence as indicated in Table 3. Importantly, many of the identified antigens are well conserved in all strains in sequence and size and are therefore novel vaccine candidates to prevent infections by GBS.

Example 6: Characterization of immune sera obtained from mice immunized with highly immunogenic proteins/peptides from *S. agalactiae* displayed on the surface of *E. coli*.

Experimental procedures

Generation of immune sera from mice

E. coli clones harboring plasmids encoding the platform protein fused to a *S. agalactiae* peptide, were grown in LB medium supplemented with 50µg/ml Kanamycin at 37°C. Overnight cultures were diluted 1:10, grown until an OD₆₀₀ of 0.5 and induced with 0.2 mM IPTG for 2 hours. Pelleted bacterial cells were suspended in PBS buffer and disrupted by sonication on ice, generating a crude cell extract. According to the OD₆₀₀ measurement, an aliquot corresponding to 5x10⁷ cells was injected into NMRI mice i.v., followed by a boost after 2 weeks. Serum was taken 1 week after the second injection. Epitope specific antibody levels were measured by peptide ELISA.

In vitro expression of antigens

Expression of antigens by *in vitro* grown *S. agalactiae* serotype III was tested by immunoblotting. Different growth media and culture conditions were tested to detect the presence of antigens in total lysates and bacterial culture supernatants. Expression was considered confirmed when a specific band corresponding to the predicted molecular weight and electrophoretic mobility was detected.

Cell surface staining

Flow cytometric analysis was carried out as follows. Bacteria were grown under culture conditions, which resulted in expression of the antigen as shown by the immunoblot analysis. Cells were washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1 X 10⁶ CFU in 100µl HBSS, 0.5% BSA. After incubation for 30 to 60 min at 4°C with mouse antisera diluted 50 to

100-fold, unbound antibodies were washed away by centrifugation in excess HBSS, 0.5% BSA. Secondary goat anti-mouse antibody (F(ab')₂ fragment specific) labeled with fluorescein (FITC) was incubated with the cells at 4°C for 30 to 60 min. After washing, cells were fixed with 2% paraformaldehyde. Bound antibodies were detected using a Becton Dickinson FACScan flow cytometer and data further analyzed with the computer program CELLQuest. Negative control sera included mouse pre-immune serum and mouse polyclonal serum generated with lysates prepared from IPTG induced *E. coli* cells transformed with plasmids encoding the genes *lamB* or *fhuA* without *S. agalactiae* genomic insert.

Bactericidal (killing) assay

Murine macrophage cells (RAW246.7 or P388.D1) and bacteria were incubated and the loss of viable bacteria after 60 min was determined by colony counting. In brief, bacteria were washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1×10^5 CFU in 50 μ l HBSS. Bacteria were incubated with mouse sera (up to 25%) and guinea pig complement (up to 5%) in a total volume of 100 μ l for 60 min at 4°C. Pre-opsonized bacteria were mixed with macrophages (murine cell line RAW264.7 or P388.D1; 2×10^6 cells per 100 μ l) at a 1:20 ratio and were incubated at 37°C on a rotating shaker at 500 rpm. An aliquot of each sample was diluted in sterile water and incubated for 5 min at room temperature to lyse macrophages. Serial dilutions were then plated onto Todd-Hewitt Broth agar plates. The plates were incubated overnight at 37°C, and the colonies were counted with the Counterstat flash colony counter (IUL Instruments). Control sera included mouse pre-immune serum and mouse polyclonal serum generated with lysates prepared from IPTG induced *E. coli* transformed with plasmids harboring the genes *lamB* or *fhuA* without *S. agalactiae* genomic insert.

Results

Immunogenicity in mice. The presence of specific antibodies was determined by peptide ELISA and/or immunoblotting using the *E. coli* clone expressing the given epitope embedded in LamB or FhuA platform proteins, as it is exemplified in Fig. 5A and B, respectively, and summarized in Table 4. 31 novel GBS antigens represented by 43 different epitope regions were shown to be immunogenic in mice. Positive sera were then analysed by immunoblotting using total bacterial lysates and culture supernatants prepared from *S. agalactiae* serotype III strain (data not shown). This analysis served as a first step to determine whether the antigenic protein were expressed, and if, under which growth conditions, in order to evaluate surface expression of the polypeptide by FACS analysis. It was anticipated based on literature data that not all proteins would be expressed under *in vitro* conditions.

Cell surface staining of S. agalactiae. Cell surface accessibility for several antigenic proteins was subsequently demonstrated by an assay based on flow cytometry. GBS cells were incubated with preimmune and polyclonal mouse sera raised against *S. agalactiae* lysate or *E. coli* clones harboring plasmids encoding the platform protein fused to a *S. agalactiae* peptide, followed by detection with fluorescently tagged secondary antibody. As shown in Fig. 6A, antisera raised against *S. agalactiae* lysate contains antibodies against surface components, demonstrated by a significant shift in fluorescence of the *S. agalactiae* serotype III cell population. Similar cell surface staining of *S. agalactiae* serotype III cells was observed with polyclonal sera raised against peptides of many of the GBS antigens identified (Fig. 6B). In some instances, a subpopulation of the bacteria was not stained, as indicated by the detection of two peaks in the histograms (Fig. 6B). This phenomenon may be a result of differential expression of the gene products during the growth of the bacterium, insufficient antibody levels or partial inhibition of antibody binding caused by other surface molecules or plasma proteins. Importantly, a well-known protective GBS antigen, Sip/gbs0031 is proved to be also positive in this assay.

In vitro bactericidal activity. Opsonophagocytic killing is the cornerstone of host defense against extracellular bacteria, such as *S. agalactiae*. Cell surface binding of antibodies to bacterial antigens are opsonizing and induce killing (bactericidal) by phagocytic cells (macrophages and neutrophil granulocytes) if the antibodies induced by the particular antigens can bind activated complement

components (C3bi). In Figure 7 data are presented on bactericidal activity measured by antigen-specific antibodies generated in mice with corresponding epitopes. According to these data, several of the novel GBS antigens gbs0012, gbs0016, gbs0428, gbs1306 and gbs2018 induce functional antibodies. Importantly, a well-known protective GBS antigen, Sip/gbs0031 is proved to be strongly positive in the very same assay.

These experiments confirmed the bioinformatic prediction that many of the proteins are exported due to their signal peptide sequence and in addition showed that they are present on the cell surface of *S. agalactiae* serotype III. They also confirm that these proteins are available for recognition by human antibodies with functional properties and make them valuable candidates for the development of a vaccine against GBS diseases.

Table 1A: Immunogenic proteins identified by bacterial surface display.

A, 300bp library of *S.agalactiae* ATCC 12403 in fhuA with IC8-IgA (826), B, 300bp library in fhuA with P10-IgA (768), C, 300bp library in fhuA with P10-IgG (711), D, 300bp library in fhuA with P11-IgG (640), E, 70bp library in lamB with IC8-IgA (1057), F, 70bp library in lamB with IC8-IgG (869), G, 70bp library in lamB with P10-IgA (904), H, 70bp library in lamB with P10-IgA-adsorbed (493), I, 70bp library in lamB with P10-IgG (910), J, 70bp library in lamB with P11-IgA (631), K, 70bp library in lamB with P11-IgG (926), L, 70bp library in lamB with P18-IgA (691), M, 70bp library in lamB with Sekret-IgA (628); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990).

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
gbs0012	weakly similar to beta-lactamase	4-20,35-44,65-70,73-87,92-98,112-137,152-161,177-186,193-200,206-213,229-255,282-294,308-313,320-326,349-355,373-384,388-406,420-425	B:13, C:6	115-199	1, 218
gbs0016	glucan-binding protein B	5-24,35-41,44-70,73-89,103-109,127-143,155-161,185-190,192-207,212-219,246-262,304-336,372-382,384-393,398-407,412-418,438-444	B:12, C:4, D:3, E:5, H:4, I:12, M:2	1-75, 76-161, 164-239	2, 219
gbs0024	phosphoribosylformylgl ycinamide synthase	4-10,16-58,60-71,77-92,100-126,132-146,149-164,166-172,190-209,214-220,223-229,241-256,297-312,314-319,337-343,351-359,378-387,398-418,421-428,430-437,440-448,462-471,510-519,525-536,552-559,561-568,573-582,596-602,608-630,637-649,651-665,681-702,714-732,739-745,757-778,790-805,807-815,821-829,836-842,846-873,880-903,908-914,916-923,931-940,943-948,956-970,975-986,996-1015,1031-1040,1051-1069,1072-1095,1114-1119,1130-1148,1150-1157,1169-1176,1229-1238	F:4	802-812	3, 220
gbs0031	surface immunogenic protein	5-12,14-26,35-47,52-67,72-78,83-98,121-141,152-159,163-183,186-207,209-257,264-277,282-299,301-309,312-318,324-339,358-368,372-378,387-397,425-431	A:17, B:53, C:36, D:4	46-291	4, 221
gbs0048	Hypothetical protein	29-38,44-64,70-76,78-87,94-100,102-112,119-134,140-149,163-173,178-186,188-194,207-234,247-262,269-290	K:13	73-92	5, 222
gbs0053	aldehyde-alcohol	10-28,36-63,77-87,103-119,127-136,141-	B:4	757-774	6, 223

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge- nic region (aa)	Seq. ID (DNA, Prot.)
	dehydrogenase (adhE)	169,171-183,195-200,207-232,236-246,251- 265,268-283,287-297,314-322,335-343,354- 363,384-390,405-411,419-436,443-455,467- 473,480-513,518-529,550-557,565-585,602- 608,616-625,632-660,665-677,685-701,726- 736,738-747,752-761,785-796,801-813,838- 853,866-871			
gbs0061	rplB ribosomal protein L2	31-38,61-66,74-81,90-115,123-145,154- 167,169-179,182-193,200-206,238-244,267- 272	F:2, I:12	235-251	7, 224
gbs0084	DNA-directed RNA polymerase, alpha subunit (rpoA)	19-25,38-54,56-64,66-72,74-92,94-100,116- 129,143-149,156-183,204-232,253-266,269- 275,294-307	C:4, D:6	241-313	8, 225
gbs0107	conserved hypothetical protein	5-34,50-56,60-65,74-85,89-97,108-119,159- 165,181-199,209-225,230-240,245-251,257- 262,274-282,300-305	K:2	64-75	9, 226
gbs0108	deoxyuridine 5'- triphosphate nucleotidohydrolase	5-13,16-21,27-42,45-52,58-66,74-87,108- 114,119-131	L:5	39-51	10, 227
gbs0113	ribose ABC transporter	6-23,46-54,59-65,78-84,100-120,128- 133,140-146,159-165,171-183,190-204,224- 232,240-248,250-259,274-280,288-296,306- 315	R:4	267-274	11, 228
gbs0123	similar to argininosuccinate synthase	5-12,15-24,26-36,42-65,68-80,82-104,111- 116,125-144,159-167,184-189,209-218,235- 243,254-265,269-283,287-300,306-316,318- 336,338-352,374-392	K:17	162-174	12, 229
gbs0127	rpmV 50S ribosomal protein L28	30-42,45-54	F:11	25-37	13, 230
gbs0144	oligopeptide ABC transporter, substrate-binding	10-30,53-59,86-95,116-130,132-147,169- 189,195-201,212-221,247-256,258-265,278- 283,291-298,310-316,329-339,341-352,360- 367,388-396,398-411,416-432,443-452,460- 466,506-512,515-521,542-548	B:7	419-431	14, 231
gbs0183	membrane protein, putative	4-27,30-53,60-67,70-90,92-151,159-185,189- 195,198-210,215-239	F:9	173-189	15, 232
gbs0184	oligopeptide ABC transporter,	4-26,41-54,71-78,116-127,140-149,151- 158,161-175,190-196,201-208,220-226,240-	B:6	174-188	16, 233

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
	oligopeptide-binding	252,266-281,298-305,308-318,321-329,344- 353,372-378,384-405,418-426,429-442,457- 463,494-505,514-522			
gbs0235	glycine betaine/carnitine/chol ine ABC transporter	17-25,27-39,61-67,81-89,99-110,120- 131,133-139,147-161,167-172,179-185,192- 198,203-213,226-238,243-258,261-267,284- 290,296-307,311-328,340-352,356-371	G:8, H:15	239-256	17, 234
gbs0255	conserved hypothetical protein	8-30,40-49,67-80,114-123,126-142,152- 162,188-194	E:2	57-70	18, 235
gbs0260	glycyl-tRNA synthetase (beta subunit)	4-23,28-34,36-47,50-61,76-81,89-94,96- 104,112-119,126-146,155-181,195-200,208- 214,220-229,244-260,263-276,282-288,292- 300,317-323,336-351,353-359,363-375,382- 399,415-432,444-455,458-471,476-481,484- 492,499-517,522-529,535-541,543-568,572- 584,586-600,607-617,626-637,656-675	F:3	282-297	19, 236
gbs0268	transketolase (tkt)	6-24,30-35,38-45,63-91,134-140,146- 160,167-188,214-220,226-234,244-250,260- 270,286-301,316-329,340-371,429-446,448- 459,474-481,485-491,512-526,537-544,550- 565,573-583,596-613,621-630,652-658	E:7	87-97	20, 237
gbs0286	NH ₃ -dependent NAD ⁺ synthetase	8-20,26-48,56-67,76-86,94-109,115-121,123- 129,143-160,178-186,191-198,201-208,221- 236,238-244,260-268	F:12, G:7, H:8	237-247	21, 238
gbs0288	similar to penicillin- binding protein 1A	4-40,42-57,73-87,98-117,126-135,150- 156,166-174,196-217,231-236,248-258,276- 284,293-301,307-313,339-347,359-365,375- 387,395-402,428-440,445-456,485-490,497- 505,535-541,547-555,610-625,648-656,665- 671	D:5, K:3	448-528	22, 239
gbs0343	seryl-tRNA synthetase (serS)	10-18,39-45,51-61,80-96,98-106,110- 115,158-172,174-183,191-200,220-237,249- 255,274-289,308-324,331-341,372-381,384- 397,405-414	E:3	322-338	23, 240
gbs0411	Hypothetical protein	30-36,38-56,85-108,134-147,149-160,163- 183,188-201,206-211,219-238,247-254	F:11	5-13	24, 241
gbs0428	similar to fibrinogen binding protein, putative	11-40,98-103,110-115,133-145,151-159,172- 179,192-201,204-212,222-228,235-245,258- 268,283-296,298-309,322-329,342-351,354-	A:7, B:2, C:31	1-148	25, 242

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
	peptidoglycan linked protein (LPXTG motif)	362,372-378,385-393,407-418,495-516			
gbs0437	glucose-6-phosphate isomerase (pgi)	5-19,21-36,73-94,112-119,122-137,139- 145,152-167,184-190,198-204,208-224,249- 265,267-281,299-304,309-317,326-333,356- 364,368-374,381-389,391-414,419-425,430- 435	E:26	113-140	26, 243
gbs0460	decarboxylase	45-54,59-67,78-91	E:7, K:11	15-23	27, 244
gbs0465	oxydoreductase	11-22,33-47,52-80,88-112,124-129	F:4	6-25	28, 245
gbs0470	similar to alpha protein, putative peptidoglycan linked protein (LPXTG motif)	26-41,51-63,80-89,93-115,150-163,187- 193,220-237,240-249,286-294,296-306,316- 329,345-353,361-370,407-425,428-437,474- 482,484-494,504-517,533-541,549-558,595- 613,616-625,660-668,673-685,711-726,736- 744,749-761,787-802,812-820,825-837,863- 878,888-896,901-913,939-954,964-972,977- 989,1003-1008,1016-1022,1028-1034,1041- 1053,1059-1074,1101-1122	B:4, C:2, D:8	420-511, 581-704	29, 246
gbs0489	acetyltransferase, GNAT family	18-25,27-55,71-83,89-95,102-113,120- 146,150-156,174-185	E:32	159-175	30, 247
gbs0492	gbs0492 valyl-tRNA synthetase	24-30,38-56,63-68,87-93,136-142,153- 164,183-199,213-219,226-234,244-261,269- 278,283-289,291-297,320-328,330-336,340- 346,348-356,358-366,382-387,401-408,414- 419,449-455,468-491,504-512,531-537,554- 560,597-608,621-627,632-643,650-662,667- 692,703-716,724-737,743-758,783-794,800- 818,846-856	A:3	806-884	31, 248
gbs0538	amino acid ABC transporter (ATP- binding protein)	4-14,21-39,86-92,99-107,121-131,136- 144,147-154,158-166,176-185,193-199,207- 222,224-230	G:1	117-136	32, 249
gbs0539	similar to phosphomannomuta se	65-76,85-97,103-109,115-121,125-146,163- 169,196-205,212-219,228-237,241-247,254- 262,269-288,294-303,305-313,328-367,395- 401,405-412,418-429,437-447,481-488,506- 513,519-524,530-541,546-557	K:4	266-284	33, 250
gbs0555	beta-lactam resistance factor	5-14,37-42,49-71,78-92,97-112,127-136,147- 154,156-163,186-198,216-225,233-243,248-	E:3	194-223	34, 251

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
	(fibA)	253,295-307,323-332,359-366,368-374,380-398			
gbs0579	dipeptidase	4-11,33-39,45-72,100-113,119-129,136-144,169-175,177-185,200-208,210-219,262-276,278-297,320-326,336-344,347-362,381-394,443-453	I:4	438-454	35, 252
gbs0580	zinc ABC transporter, zinc-binding adhesion, lipoprotein	4-29,31-52,55-61,95-110,138-158,162-171,179-187,202-229,239-248,251-256,262-267,269-285,304-310,351-360,362-368,381-388,415-428,435-440,448-458	I:11	161-178	36, 253
gbs0628	cell wall surface anchor family protein (IPxTG)	4-17,19-28,32-43,47-59,89-110,112-126,128-134,140-148,152-161,169-184,191-204,230-235,255-264,328-338,341-347,401-409,413-419,433-441,449-458,463-468,476-482,486-492,500-506,529-545	I:9, H:1	305-381	37, 254
gbs0632	cell wall surface anchor family protein, putative (FPKTG motive)	10-29,38-45,53-61,134-145,152-160,163-170,202-208,219-229,248-258,266-275,282-288,315-320,328-334,377-385,392-402,418-424,447-453,460-471,479-487,491-497,500-507,531-537,581-594,615-623,629-635,644-652,659-666,668-678,710-717,719-728,736-741,747-760,766-773,784-789,794-800,805-817,855-861,866-887	H:3	698-715	38, 255
gbs0634	putative surface protein	16-26,29-37,44-58,62-68,74-80,88-95,97-120,125-144,165-196	H:1	58-72	39, 256
gbs0667	regulatory protein, putative, truncation	14-21,23-46,49-60,63-74,78-92,96-103,117-129,134-161,169-211,217-231,239-248,252-281,292-299,313-343	I:2	243-257	40, 257
gbs0672	transcriptional regulator (CntR family)	11-27,46-52,67-72,76-84,91-112,116-153,160-175,187-196,202-211,213-220	G:11	43-76	41, 258
gbs0687	Hypothetical protein	5-29,37-56,78-86,108-118,152-161	I:4	120-130	42, 259
gbs0785	Similar to penicillin binding protein 2B	8-14,19-41,52-66,75-82,87-92,106-121,127-133,136-143,158-175,180-187,196-204,221-228,239-245,259-265,291-306,318-323,328-340,352-358,361-368,375-381,391-399,411-418,431-442,446-455,484-496,498-510,527-533,541-549,558-565,575-585,587-594,644-655,661-668,671-677	K:3	184-196	43, 260

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
gbs0811	beta-glucosidase	4-22,29-38,55-62,75-81,102-107,110- 134,143-150,161-167,172-179,191-215,223- 233,241-247,251-264,266-272,288-309,340- 352,354-366,394-402,414-438	L:13	198-218	44, 261
gbs0828	hypothetical protein	24-44,49-70,80-91,105-118,128-136,140-154	L:3	77-92	45, 262
gbs0851	hypothetical protein	5-22,31-36,41-47,67-74,83-90,105-122,135- 143,160-167	B:2	118-129	46, 263
gbs0865	hypothetical protein	4-25,33-73,81-93,96-106,114-120,122- 128,130-172,179-208,210-241,251-283,296- 301	K:4	92-100	47, 264
gbs0890	exonuclease RexB (rexB)	14-24,29-38,43-50,52-72,86-97,101-107,110- 125,127-141,145-157,168-175,177-184,186- 195,205-226,238-250,255-261,284-290,293- 304,307-314,316-323,325-356,363-371,383- 390,405-415,423-432,442-454,466-485,502- 511,519-527,535-556,558-565,569-574,612- 634,641-655,672-686,698-709,715-722,724- 732,743-753,760-769,783-792,818-825,830- 839,842-849,884-896,905-918,926-940,957- 969,979-1007,1015-1021,1049-1057	E:5	336-349	48, 265
gbs0896	similar to acetoin dehydrogenase	6-16,26-31,33-39,62-73,75-85,87-100,113- 123,127-152,157-164,168-181,191-198,208- 214,219-226,233-254,259-266,286-329	K:2	181-195	49, 266
gbs0898	acetoin dehydrogenase, thymine PPi dependent	4-13,32-39,53-76,99-108,110-116,124- 135,137-146,149-157,162-174,182-190,207- 231,242-253,255-264,274-283,291-323,334- 345,351-360,375-388,418-425,456-474,486- 492,508-517,520-536,547-560,562-577	B:13, F:2, I:2, J:2	31-45, 419- 443	50, 267
gbs0904	phosphoglucosmutase /phosphomannomuta se family protein	15-26,30-37,42-49,58-90,93-99,128-134,147- 154,174-179,190-197,199-205,221-230,262- 274,277-287,300-314,327-333,343-351,359- 377,388-396,408-413,416-425,431-446	L:3	246-256	51, 268
gbs0918	weakly similar to histidine triad protein, putative lipoprotein	5-26,34-42,47-54,61-67,71-104,107-115,131- 138,144-153,157-189,196-202,204-210,228- 245,288-309,316-329,332-341,379-386,393- 399,404-412,414-421,457-468,483-489,500- 506,508-517,523-534,543-557,565-580,587- 605,609-617,619-627,631-636,640-646,662- 668,675-682,705-710,716-723,727-732,750-	B:5, C:11, D:36, E:3, K:3	14-138, 166- 286, 372- 503, 674- 696, 754-859	52, 269

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
		758,784-789,795-809,869-874			
gbs0931	pyruvate kinase	5-17,32-38,40-47,80-89,113-119,125- 137,140-154,157-163,170-177,185-199,213- 225,228-236,242-248,277-290,292-305,323- 333,347-353,364-370,385-394,399-406,423- 433,441-451,462-474,477-487	F:78	116-124	53, 270
gbs0947	similar to L-Lactate Dehydrogenase	7-16,18-30,32-49,53-61,63-85,95-101,105- 115,119-134,143-150,159-178,185-202,212- 229,236-250,254-265,268-294	K:28	63-72	54, 271
gbs0948	DNA gyrase, A subunit (gyrA)	4-12,19-47,73-81,97-103,153-169,188- 198,207-213,217-223,236-242,255-265,270- 278,298-305,309-317,335-347,354-363,373- 394,419-424,442-465,486-492,500-507,542- 549,551-558,560-572,580-589,607-614,617- 623,647-653,666-676,694-704,706-714,748- 754,765-772,786-792,795-806	E:4	358-370	55, 272
gbs0969	similar to unknown plasmid protein	18-28,30-38,40-46,49-55,69-78,82-98,104- 134,147-153,180-190,196-202,218-236,244- 261,266-273,275-286,290-295,301-314,378- 387,390-395,427-434	E:3	290-305	56, 273
gbs0971	similar to putative plasmid replication protein	4-13,20-31,39-51,54-61,69-84,87-105,117- 124	K:17	108-125	57, 274
gbs0972	Hypothetical protein	24-34,43-54,56-66,68-79	E:3	50-69	58, 275
gbs0983	similar to plasmid protein	5-43,71-77,102-131,141-148,150-156,159- 186,191-207,209-234,255-268,280-286,293- 299,317-323,350-357,363-372,391-397,406- 418,428-435,455-465,484-497,499-505,525- 531,575-582,593-607,621-633,638-649,655- 673,684-698,711-725,736-741,743-752,759- 769,781-793,813-831,843-853,894-905,908- 916,929-946,953-963,970-978,1001- 1007,1011-1033	D:11, E:2, F:2, J:10, K:10, L:46, M:3	165-178, 818-974	59, 276
gbs0986	surface antigen proteins, putative peptidoglycan bound	16-44,63-86,98-108,185-191,222-237,261- 274,282-294,335-345,349-362,374-384,409- 420,424-430,440-447,453-460,465-473,475- 504,522-534,538-551,554-560,567-582,598- 607,611-619,627-640,643-653,655-661,669- 680,684-690,701-707,715-731,744-750,756-	B:3, C:12, D:2, E:3, F:20, H:3, I:3, J:5, M:2	77-90, 144- 212, 279- 355, 434- 536, 782- 810, 875-902	60, 277

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge- nic region (aa)	Seq. ID (DNA, Prot.)
		763,768-804,829-837,845-853,855-879,884-890,910-928			
gbs0988	similar to plasmid surface exclusion protein, putative peptidoglycan bound protein (LPXTG motif)	4-22,29-41,45-51,53-66,70-77,86-95,98-104,106-124,129-135,142-151,153-161,169-176,228-251,284-299,331-337,339-370,380-387,393-398,406-411,423-433,440-452,461-469,488-498,501-516,523-530,532-559,562-567,570-602,612-628,630-645,649-659,666-672,677-696,714-723,727-747	J:2	212-227	61, 278
gbs0991	ATP-dependent Clp protease, ATP- binding subunit ClpA	4-9,17-31,35-41,56-61,66-75,81-87,90-124,133-138,149-163,173-192,213-219,221-262,265-275,277-282,292-298,301-307,333-346,353-363,371-378,419-430,435-448,456-469,551-570,583-599,603-612	F:15	275-291	62, 279
gbs0993	similar to plasmid proteins	28-34,53-58,72-81,100-128,145-154,159-168,172-189,217-225,227-249,256-263,299-309,322-330,361-379,381-388,392-401,404-417,425-436,440-446,451-464,469-487,502-511,543-551,559-564,595-601,606-612,615-626,633-642,644-650,664-670,674-684,692-701,715-723,726-734,749-756,763-771,781-787,810-843,860-869,882-889,907-917,931-936,941-948,951-958,964-971,976-993,1039-1049,1051-1065,1092-1121,1126-1132,1145-1151,1158-1173,1181-1192,1194-1208,1218-1223,1229-1243,1249-1254,1265-1279,1287-1297,1303-1320,1334-1341,1343-1358,1372-1382,1406-1417,1419-1425,1428-1434,1441-1448,1460-1473,1494-1504,1509-1514,1529-1550	B:2, F:2, J:4, K:2, M:7	654-669, 1400-1483	63, 280
gbs0995	hypothetical protein	10-16,20-25,58-65,97-109,118-132,134-146,148-155,186-195,226-233,244-262,275-284,295-310,317-322,330-339,345-351,366-375,392-403,408-415,423-430,435-444,446-457,467-479,486-499,503-510,525-537,540-585,602-612,614-623,625-634,639-645,650-669,700-707,717-724,727-739	H:3, I:39, J:3, M:3	205-230, 733-754	64, 281
gbs0997	hypothetical protein	5-22,37-43,72-81,105-113,128-133,148-160,188-194,204-230,238-245,251-257	D:2, F:52	194-213	65, 282

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge- nic region (aa)	Seq. ID (DNA, Prot.)
gbs0998	hypothetical protein	16-21,35-41,56-72,74-92,103-109	I:2	62-68	66, 283
gbs1001	hypothetical protein	4-15,17-82,90-104,107-159,163-170,188- 221,234-245,252-265	G:8	220-235	67, 284
gbs1015	hypothetical protein	16-22,36-46,61-75,92-107,113-121,139- 145,148-160	K:17	30-42	68, 285
gbs1035	conserved hypothetical protein	4-12,20-26,43-49,55-62,66-78,121-127,135- 141,146-161,164-170,178-189,196-205,233- 238,269-279,288-318,325-332,381-386,400- 407	B:3	328-346	69, 286
gbs1041	hypothetical protein	5-12,31-49,57-63,69-79,89-97,99-114,116- 127,134-142,147-154,160-173,185-193,199- 204,211-222,229-236,243-249,256-274	L:2	58-68	70, 287
gbs1066	hypothetical protein	10-20,28-34,39-53,68-79,84-90,99-106	K:2	73-79	71, 288
gbs1087	FbsA	14-37,45-50,61-66,77-82,93-98,109-114,125- 130,141-146,157-162,173-178,189-194,205- 210,221-226,237-242,253-258,269-274,285- 290,301-306,316-332,349-359,371-378,385- 406	A:7, B:2, C:4, E:277, G:523, J:25	34-307, 312- 385	72, 289
gbs1103	ABC transporter (ATP-binding protein)	4-10,17-38,50-85,93-99,109-116,128- 185,189-197,199-210,223-256,263-287,289- 312,327-337,371-386,389-394,406-419,424- 432,438-450,458-463,475-502,507-513,519- 526,535-542,550-567	I:5	361-376	73, 290
gbs1116	xanthine permease (pbuX)	10-39,42-93,100-144,155-176,178-224,230- 244,246-255,273-282,292-301,308-325,332- 351,356-361,368-379,386-393,400-421	I:48	138-155	74, 291
gbs1126	similar to plasmid unknown protein	5-11,17-34,40-45,50-55,72-80,101-123,145- 151,164-172,182-187,189-195,208-218,220- 241,243-252,255-270,325-331,365-371,391- 398,402-418,422-428,430-435,443-452,463- 469,476-484,486-494,503-509,529-553,560- 565,570-590,608-614,619-627,654-661,744- 750,772-780,784-790,806-816,836-853,876- 885,912-918,926-933,961-975,980-987,996- 1006,1016-1028,1043-1053,1057-1062	R:2, K:3	994-1003, 1033-1056	75, 292
gbs1143	putative peptidoglycan linked protein (LPXTG)	17-45,64-71,73-81,99-109,186-192,223- 238,262-275,283-295,336-346,350-363,375- 385,410-421,425-431,441-448,454-463,468- 474,476-512,523-537,539-552,568-583,599-	C:3, D:2, F:15, J:3	274-350, 443-513	76, 293

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
		608,612-620,628-641,644-654,656-662,670- 681,685-695,702-708,716-723,725-735,757- 764,769-798,800-806,808-816,826-840,846- 854,856-862,874-881,885-902,907-928			
gbs1145	surface exclusion protein Sec10	4-22,29-41,45-51,53-61,70-76,85-92,99- 104,111-122,134-140,142-154,163-174,224- 232,255-265,273-279,283-297,330-335,337- 348,356-367,373-385,391-396,421-431,442- 455,475-485,493-505,526-538,544-561,587- 599,605-620,622-651,662-670,675-681,687- 692,697-712,714-735	C:2	252-262	77, 294
gbs1158	Similar to oxidoreductase	4-12,15-35,40-46,50-59,67-94,110-128,143- 169,182-188,207-215,218-228,238-250	K:2	74-90	78, 295
gbs1165	cysteine desulphurase (iscS-1)	9-18,42-58,78-85,88-95,97-106,115-122,128- 134,140-145,154-181,186-202,204-223,261- 267,269-278,284-293,300-336,358-368	F:5	12-29	79, 296
gbs1195	staphylokinase and streptokinase	7-34,46-53,62-72,82-88,100-105,111- 117,132-137,144-160,166-180,183-189,209- 221,231-236,246-253,268-282,286-293,323- 336,364-372,378-392,422-433	B:3, C:2, D:2, G:3, H:8	388-405	80, 297
gbs1209	ATP-dependent DNA helicase PcrA	21-27,34-50,72-77,80-95,164-177,192- 198,202-220,226-236,239-247,270-279,285- 292,315-320,327-334,348-355,364-371,388- 397,453-476,488-497,534-545,556-576,582- 588,601-607,609-616,642-662,674-681,687- 697,709-715,721-727,741-755	C:3, L:5	621-739	81, 298
gbs1214	conserved hypothetical protein	4-14,16-77,79-109	B:2	25-99	82, 299
gbs1242	CpsG, beta-1,4- galactosyltransferase	4-9,17-23,30-37,44-55,65-72,77-93,102- 121,123-132,146-153	L:24	17-29	83, 300
gbs1260	ABC transporter, ATP-binding protein	4-18,25-41,52-60,83-92,104-112,117- 123,149-155,159-167,170-192,201-210,220- 227,245-250	I:17	124-137	84, 301
gbs1270	gbs1270 hyaluronate lyase	8-25,50-55,89-95,138-143,148-153,159- 169,173-179,223-238,262-268,288-295,297- 308,325-335,403-409,411-417,432-446,463- 475,492-501,524-530,542-548,561-574,576- 593,604-609,612-622,637-654,665-672,678- 685,720-725,731-739,762-767,777-783,820-	C:19, D:5, L:19	1-128, 252- 341, 771- 793, 1043- 1058	85, 302

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge- nic region (aa)	Seq. ID (DNA, Prot.)
		838,851-865,901-908,913-920,958- 970,1000-1006,1009-1015,1020-1026,1043- 1052,1055-1061			
gbs1305	hypothetical protein	16-26,33-46	I:2	64-76	86, 303
gbs1306	Laminin binding protein	4-27,69-77,79-101,117-123,126-142,155- 161,171-186,200-206,213-231,233-244,267- 273,313-329,335-344,347-370,374-379,399- 408,422-443,445-453,461-468,476-482,518- 534,544-553,556-567,578-595,601-620,626- 636,646-658,666-681,715-721,762-768,778- 785,789-803,809-819	A:6, B:7, C:17, D:72, E:8, F:91, G:2, H:4, I:26, J:3, K:14	22-108, 153- 318, 391- 527, 638-757	87, 304
gbs1307	Lmb, laminin- binding surface protein	6-21,32-43,62-92,104-123,135-141,145- 152,199-216,218-226,237-247,260-269,274- 283,297-303	A:2, D:3	1-72, 127- 211	88, 305
gbs1308	C5a peptidase, authentic frameshift	6-26,50-56,83-89,108-114,123-131,172- 181,194-200,221-238,241-247,251-259,263- 271,284-292,304-319,321-335,353-358,384- 391,408-417,424-430,442-448,459-466,487- 500,514-528,541-556,572-578,595-601,605- 613,620-631,635-648,660-670,673-679,686- 693,702-708,716-725,730-735,749-755,770- 777,805-811,831-837,843-851,854-860,863- 869,895-901,904-914,922-929,933-938,947- 952,956-963,1000-1005,1008-1014,1021- 1030,1097-1103,1120-1130,1132-1140	B:4, C:15, D:70, E:18, F:26, G:5, H:4, J:2, K:40	1-213, 269- 592, 992- 1120	89, 306
gbs1309	hypothetical protein	9-16,33-39,47-59,65-79,81-95,103-108,115- 123,138-148,163-171,176-185,191-196,205- 211,213-221,224-256,261-276,294-302,357- 363,384-390	E:2, F:4, H:2, J:2	95-111, 161- 189	90, 307
gbs1311	transposase, C- terminal part	21-27,35-45,70-76,92-105,129-143,145- 155,161-166,170-191,204-211,214-231,234- 246,249-255,259-275	F:3	1-18	91, 308
gbs1321	hypothetical protein	21-35,45-53,56-64,69-97	F:7	1-16	92, 309
gbs1352	putative helicase and methylase	25-33,41-47,61-68,86-101,106-114,116- 129,134-142,144-156,163-176,181-190,228- 251,255-261,276-292,295-305,334-357,368- 380,395-410,424-429,454-460,469-482,510- 516,518-527,531-546,558-570,579-606,628- 636,638-645,651-656,668-674,691-698,717-	E:3, H:2, M:4	748-847, 1381-1391	93, 310

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
		734,742-754,765-770,792-797,827-835,847- 859,874-881,903-909,926-933,942-961,964- 977,989-1004,1010-1028,1031-1047,1057- 1075,1081-1095,1108-1117,1138-1144,1182- 1189,1193-1206,1220-1229,1239-1246,1257- 1267,1271-1279,1284-1301,1312-1320,1329- 1335,1341-1347,1358-1371,1399-1404,1417- 1426,1458-1463,1468-1476,1478-1485,1493- 1506,1535-1541,1559-1574,1583-1590,1595- 1601,1603-1611,1622-1628,1634-1644,1671- 1685,1689-1696,1715-1720,1734-1746,1766- 1775,1801-1806,1838-1844,1858-1871,1910- 1917,1948-1955,1960-1974,2000-2015,2019- 2036,2041-2063			
gbs1356	Putative peptidoglycan linked protein (LPXTG motif) - Agglutinin receptor	5-12,18-24,27-53,56-63,96-113,119-124,131- 136,157-163,203-209,215-223,233-246,264- 273,311-316,380-389,393-399,425-433,445- 450,457-462,464-470,475-482,507-513,527- 535,542-548,550-565,591-602,607-613,627- 642,644-664,673-712,714-732,739-764,769- 782,812-818,826-838,848-854,860-871,892- 906,930-938,940-954,957-973,990- 998,1002-1021,1024-1033,1037-1042,1050- 1060,1077-1083,1085-1092,1100-1129,1144- 1161,1169-1175,1178-1189,1192-1198,1201- 1207,1211-1221,1229-1239,1250-1270,1278- 1292,1294-1300,1314-1335,1344-1352,1360- 1374,1394-1405,1407-1414,1416-1424,1432- 1452,1456-1462,1474-1497,1500-1510,1516- 1522,1534-1542,1550-1559,1584-1603,1608- 1627	C:5, D:62, L:22	187-273, 306-441	94, 311
gbs1376	similar to ATP- dependent Clp proteinase (ATP- binding subunit), ClpL	70-80,90-97,118-125,128-140,142-148,154- 162,189-202,214-222,224-232,254-260,275- 313,317-332,355-360,392-398,425-432,448- 456,464-470,476-482,491-505,521-528,533- 546,560-567,592-597,605-614,618-626,637- 644,646-653,660-666,677-691	K:4	207-227	95, 312
gbs1377	similar to homocysteine S-	5-19,26-34,37-55,57-66,69-83,86-102,115- 134,138-143,154-172,178-195,209-246,251-	M:2	256-266	96, 313

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge- nic region (aa)	Seq. ID (DNA, Prot.)
	methyltransferase	257,290-302,306-311			
gbs1386	hydroxy-3- methylglutaryl- coenzyme A synthase	10-20,22-28,35-57,72-79,87-103,108- 128,130-144,158-171,190-198,225-242,274- 291,301-315,317-324,374-385	G:2	353-365	97, 314
gbs1390	hypothetical protein	4-9,17-30,34-54,59-66,73-94,118-130,135- 150,158-171,189-198,219-239,269-275,283- 301	E:3, K:4	89-106, 176- 193	98, 315
gbs1391	hypothetical protein	14-20,22-74,77-86,89-99,104-109,126- 135,154-165,181-195,197-212,216-224,264- 275	E:3	107-118	99, 316
gbs1403	similar to 5'- nucleotidase, putative peptidoglycan bound protein (LPXTN)	4-18,21-38,63-72,101-109,156-162,165- 179,183-192,195-210,212-218,230-239,241- 256,278-290,299-311,313-322,332-341,348- 366,386-401,420-426,435-450,455-460,468- 479,491-498,510-518,532-538,545-552,557- 563,567-573,586-595,599-609,620-626,628- 636,652-657,665-681	A:3, C:12, D:4, J:2	1-198	100, 317
gbs1408	Similar to ABC transporter (ATP- binding protein)	4-10,16-38,51-68,73-79,94-115,120-125,132- 178,201-208,216-223,238-266,269-295,297- 304,337-342,347-356,374-401,403-422,440- 447,478-504,510-516,519-530,537-544	D:2, K:4	191-206	101, 318
gbs1420	similar to cell wall proteins, putative peptidoglycan linked protein (LPXTG motif)	12-40,42-48,66-71,77-86,95-102,113- 120,129-137,141-148,155-174,208-214,218- 225,234-240,256-267,275-283,300-306,313- 321,343-350,359-367,370-383,398-405,432- 439,443-461,492-508,516-526,528-535	C:3, D:4	370-478	102, 319
gbs1429	hypothetical protein	6-14,20-37,56-62,90-95,97-113,118-125,140- 145,161-170,183-202,237-244,275-284,286- 305,309-316,333-359,373-401,405-412	B:2, C:2	176-187	103, 320
gbs1442	hypothetical thiamine biosynthesis protein, ThiI	33-44,50-55,59-80,86-101,129-139,147- 153,157-163,171-176,189-201,203-224,239- 245,257-262,281-287,290-297,304-320,322- 331,334-350,372-390,396-401	L:28	71-88, 353- 372	104, 321
gbs1452	rplT 50S ribosomal protein L20	5-11,15-24,26-33,40-47,75-88,95-103,105- 112	E:2	17-30	105, 322
gbs1464	ferrichrome ABC transporter (permease)	5-11,16-39,46-54,62-82,100-107,111- 124,126-150,154-165,167-183,204-238,245- 295,301-313,316-335	F:4	8-16	106, 323

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge- nic region (aa)	Seq. ID (DNA, Prot.)
gbs1470	conserved hypothetical protein	4-19,34-48,69-74,79-107,115-127,129- 135,143-153,160-169,171-182	L:4	142-153	107, 324
gbs1528	conserved hypothetical protein	4-30,65-74,82-106,110-120,124-132,135- 140,146-175,179-184,190-196,217-223,228- 233,250-267,275-292,303-315,322-332	L:7	174-186	108, 325
gbs1529	Putative peptidoglycan bound protein (LPXTG motif)	9-16,29-41,47-57,68-84,87-109,113-119,162- 180,186-193,195-201,203-208,218-230,234- 243,265-271,281-292,305-312,323-332,341- 347,349-363,368-374,383-390,396-410,434- 440,446-452,455-464,466-473,515-522,529- 542,565-570,589-600,602-613,618-623,637- 644,1019-1027,1238-1244,1258-1264,1268- 1276,1281-1292,1296-1302	C:2	883-936	109, 326
gbs1531	UvrB excinuclease ABC chain B	10-17,23-32,39-44,54-72,75-81,88-111,138- 154,160-167,178-185,201-210,236-252,327- 334,336-342,366-376,388-400,410-430,472- 482,493-526,552-558,586-592,598-603,612- 621,630-635,641-660	M:2	384-393	110, 327
gbs1533	glutamine ABC transporter, glutamine-binding protein	4-22,24-39,50-59,73-84,100-105,111- 117,130-138,155-161,173-178,182-189,205- 215,266-284,308-313,321-328,330-337,346- 363,368-374,388-395,397-405,426-434,453- 459,482-492,501-507,509-515,518-523,527- 544,559-590,598-612,614-629,646-659,663- 684,686-694,698-721	L:4	445-461	111, 328
gbs1536	hypothetical protein	14-22,27-33	E:10	3-17	112, 329
gbs1542	oxidoreductase, aldo/keto reductase family	29-41,66-73,81-87,90-108,140-146,150- 159,165-184,186-196,216-226,230-238,247- 253,261-269	L:13	126-140	113, 330
gbs1547	small protein, SmpB	5-12,16-25,27-33,36-45,60-68,83-88,103-126	L:11	86-101	114, 331
gbs1565	hypothetical protein	14-23,36-47,56-66,84-89,94-105,111- 127,140-153,160-174,176-183,189-203,219- 225,231-237,250-257	F:2, J:2, K:8, L:21	194-227	115, 332
gbs1586	peptidyl-prolyl cis- trans isomerase, cyclophilin-type	4-25,54-60,64-71,73-82,89-106,117-124,157- 169,183-188,199-210,221-232,236-244,255- 264	E:3	58-98	116, 333
gbs1591	S- methylthioadenosine nucleosidase/S- adenosylhomocystein e	13-19,26-36,41-53,55-71,77-84,86-108,114- 135,157-172,177-183,187-194,208-213,218- 226	E:18, L:2	110-125, 156-170	117, 334

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
	nucleosidase (pfs)				
gbs1632	similar to branched- chain amino acid ABC transporter, amino acid-binding protein	5-24,63-69,77-85,94-112,120-137,140- 146,152-159,166-172,179-187,193-199,206- 212,222-228,234-240,244-252,257-264,270- 289,298-309,316-328,337-348,363-375	B:2, E:4, I:3	1-56, 340- 352	118, 335
gbs1638	amino acid permease	18-39,42-71,78-120,124-144,152-173,179- 189,199-209,213-222,228-258,269-304,329- 361,364-372,374-389,396-441	E:8, G:9, H:9	313-327	119, 336
gbs1662	conserved hypothetical protein	19-25,91-98,108-120,156-162,168-174,191- 204,211-216,232-266,272-278,286-308,316- 321,327-333,344-355,358-364,384-391,395- 428,464-476,487-495,497-511,544-561,563- 573,575-582,588-594	E:3, H:2	10-25, 322- 338	120, 337
gbs1666	SWI/SNF family helicase	14-26,32-49,51-57,59-72,80-91,102-112,119- 125,147-161,164-173,175-183,188-213,217- 222,246-254,260-276,282-303,308-318,321- 328,333-350,352-359,371-378,392-401,407- 414,416-443,448-463,471-484,490-497,501- 514,519-527,539-551,557-570,578-590,592- 598,600-610,618-629,633-647,654-667,676- 689,702-709,718-726,728-737,741-760,764- 780,786-795,808-826,836-842,845-852,865- 874,881-887,931-945,949-957,968-974,979- 986,1003-1009,1023-1029	F:4	90-103	121, 338
gbs1673	conserved hypothetical protein	11-16,37-56,60-66,69-77,80-88,93-106,117- 139,166-171	E:2	72-90	122, 339
gbs1695	dihydroxyacetone kinase family protein	59-84,123-133,145-150,161-167,178-189	I:8	115-128	123, 340
gbs1754	excinuclease ABC, A subunit (uvrA)	15-33,39-46,52-64,74-87,108-124,127- 144,150-156,173-179,184-194,201-208,219- 236,243-269,272-295,302-309,343-349,356- 361,370-379,405-411,414-423,430-451,457- 464,466-475,477-483,496-502,507-522,541- 548,557-563,571-577,579-585,590-605,626- 642,650-662,671-691,704-710,751-769,775- 781,786-791,794-829,851-858,868-878,884- 904,913-919,931-939	I:2	132-142	124, 341
gbs1760	Similar to A/G-	33-58,64-71,74-80,83-88,96-120,122-	K:8	97-115, 199-	125, 342

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
	specific adenine glycosylase	139,146-157,167-177,207-213,220-225,236- 242,264-279,300-305,326-336,340-347,350- 360		211	
gbs1777	glycerol uptake facilitator protein, putative	4-26,43-57,70-99,102-117,121-133,142- 148,151-168,170-183,192-220,235-249,258- 279	E:4	30-41	126, 343
gbs1783	polyprenyl synthetase family protein	34-42,48-58,70-94,110-130,154-160,164- 172,178-183,195-203,211-222,229-250,256- 261,274-284,286-292,312-323	E:3	222-233	127, 344
gbs1784	ABC transporter, ATP-binding protein CydC	4-9,15-36,38-45,49-74,78-88,100-112,136- 191,211-220,226-233,239-246,254-274,287- 307,316-322,342-353,356-366,373-378,384- 393,405-431,449-457,459-468,487-511,515- 524,529-541,544-552,562-568,571-576	C:2, D:2	208-280	128, 345
gbs1790	hypothetical protein	10-27,31-37,39-54,71-108,124-143	A:23, C:6	2-107	129, 346
gbs1805	Similar to secreted unknown protein	16-27,38-57,64-70,90-102,104-113,116- 137,160-166	A:197, C:2	1-80	130, 347
gbs1816	HD domain protein	13-21,31-36,56-67,127-136,153-171,173- 180,184-200,214-222,225-231,239-263,267- 273	F:8	135-159	131, 348
gbs1821	Similar to 23S ribosomal RNA methyltransferase	12-27,31-51,68-74,77-87,94-101,108- 114,117-123,127-134,138-168,173-196,201- 207,212-217,227-237,247-257,264-280	K:5	205-223	132, 349
gbs1823	triad family protein	17-22,25-54,70-76,92-100	G:6, H:3	98-110	133, 350
gbs1834	two-component sensor histidine kinase	7-29,40-50,60-67,87-96,105-111,119- 164,172-199,206-212,220-227,237-259,272- 279,282-293,295-309,313-319,321-328,345- 363,376-386	E:3, F:6	159-176	134, 351
gbs1842	transcriptional antiterminator, BglG family	4-19,24-30,36-43,50-68,71-89,93-106,141- 152,154-172,179-197,199-215,229-239,246- 252,255-263,281-298,319-325,329-356,358- 368,374-390,397-409,420-429,432-444,450- 456,459-475,483-494,496-502,520-528,532- 556	I:19	362-377	135, 352
gbs1850	hypothetical transaldolase	18-25,40-62,77-85,91-97,105-116,123- 133,139-184,189-197	G:2	122-140	136, 353
gbs1869	phosphoglycerate kinase	4-49,52-58,62-70,79-105,109-133,142- 150,163-168,206-214,220-228,233-240,243-	L:9	643-658	137, 354

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge- nic region (aa)	Seq. ID (DNA, Prot.)
		254,274-281,303-311,327-338,357-373,378- 396,403-413,420-436,441-453,461-467,475- 481,484-498,506-512,514-521,523-529,562- 579,589-595,598-603,615-648,714-722,728- 742,749-758,777-792,795-807			
gbs1875	alkyl hydroperoxide reductase (large subunit) and NADH dehydrogenase	8-27,37-48,51-56,72-79,87-106,120-138,140- 147,167-176,187-197,205-216,222-229,234- 239,243-249,277-288,292-315,334-343,347- 353,363-391,398-404,430-447,461-467,478- 492,498-507	F:3	456-470	138, 355
gbs1879	endopeptidase O (pepO)	5-12,18-24,59-69,80-93,95-109,119-125,130- 137,139-147,158-163,168-176,182-202,206- 215,222-239,241-249,267-277,291-298,311- 318,321-327,338-344,348-355,373-386,393- 406,411-417,434-443,446-465,473-484,514- 521,532-553,584-594	L:26	221-237	139, 356
gbs1893	2-keto-3- deoxygluconate kinase	4-14,27-34,50-58,63-72,79-106,109-114,121- 142,146-154,161-167,169-175,178-201,223- 238,249-254,259-264,278-292,294-312,319- 330	F:8, K:9	167-191	140, 357
gbs1899	N-acetylmuramoyl- L-alanine amidase, family 4 protein	7-28,36-42,50-61,63-80,122-152,161- 174,176-191	B:2, C:2, E:3	140-190	141, 358
gbs1907	citrate carrier protein, CCS family	20-57,59-65,70-78,86-102,119-133,142- 161,163-173,177-188,192-202,204-220,222- 236,240-253,279-319,326-331,337-383,390- 399,406-412,420-427,431-438	L:2	381-395	142, 359
gbs1924	similar to pneumococcal histidine triad protein B precursor (C-terminal part)	13-18,28-34,37-43,50-59,75-81,83-97,105- 121,139-147,200-206,209-227,231-247,260- 271,318-327,366-381,388-394,399-406	K:3	182-201	143, 360
gbs1925	similar to pneumococcal histidine triad protein B precursor (N-terminal part)	6-29,37-43,51-56,70-77,82-102,110-119,127- 143,178-190,201-209,216-243,261-269,281- 292,305-313,327-339,341-354,356-373,391- 397,423-429,438-445,450-478	A:2, B:5, C:12, D:57	21-314	144, 361
gbs1962	conserved hypothetical protein	4-12,15-21,32-41,59-76,80-89,96-104	E:3	90-103	145, 362

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
gbs2008	similar to C5A peptidase, putative peptidoglycan linked protein (LPXTG motif)	9-28,30-41,44-54,69-74,77-82,90-97,104- 123,125-135,149-155,164-173,177-184,217- 226,230-235,238-244,258-272,282-297,300- 305,309-315,317-322,327-336,348-362,368- 374,380-387,400-411,414-424,451-458,460- 466,483-494,497-503,506-511,521-528,540- 553,569-587,598-606,628-642,661-681,688- 700,718-733,740-749,752-764,769-783,823- 834,848-854,862-872,878-884,886-898,915- 920,938-951,954-961,963-972,982-989,996- 1003,1010-1016,1021-1032,1038-1044,1047- 1057,1060-1070,1079-1088,1094-1102,1117- 1127,1129-1135,1142-1153,1158-1204,1212- 1229,1234-1263,1269-1277,1308-1313,1327- 1338,1344-1376,1400-1415,1436-1443,1448- 1458,1497-1504,1511-1522,1544-1566	A:253, B:2, C:3, D:6, H:2	3-82, 509- 576	146, 363
gbs2018	putative peptidoglycan linked protein (LPXTG motif)	8-36,40-64,71-79,88-94,102-109,118- 127,138-148,151-159,163-174,192-198,200- 206,220-233,268-273,290-301,304-309,316- 323,331-349,378-391,414-420,427-437,455- 475,494-510,541-547,549-555,616-640	A:132, B:6, C:13, D:63, E:15, H:2, J:9, K:13	1-60, 55-139, 212-308, 386-458, 458-624	147, 364
gbs2029	hypothetical protein	16-31,35-42,70-77,91-101,120-130,132- 140,143-153,185-190,195-202,215-222,228- 238,241-251,257-264,268-277,288-302,312- 324,326-333,341-348,364-382,415-429,438- 454,458-466,491-499,501-521	G:8	273-281	148, 365
gbs2042	hypothetical protein	8-14,32-57,74-149,155-177,179-212,221- 266,271-296,304-324,329-346,349-359,368- 401,413-419,426-454,465-478,493-510	L:11	466-490	149, 366
gbs2054	DNA mismatch repair protein HexA	22-28,33-51,64-89,96-119,126-132,138- 146,152-159,161-169,172-179,193-198,205- 211,221-231,235-254,273-280,297-303,312- 320,328-346,351-373,378-384,391-398,448- 454,460-468,470-481,516-558,574-593,597- 602,613-623,626-646,649-656,668-673,675- 683,696-708,715-722,724-739,745-751,759- 777,780-804,816-822	E:8	102-113	150, 367
gbs2058	hypothetical protein	12-28,41-91,98-107,112-120,125-131,151- 193,215-221,240-250,263-280	L:3	128-138	151, 368

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
gbs2060	aspartyl-tRNA synthetase (aspS)	16-24,32-38,46-62,68-81,90-105,127- 133,144-150,160-166,178-184,186-202,210- 219,232-240,252-258,264-273,293-324,337- 344,349-357,360-369,385-398,410-416,419- 427,441-449,458-476,508-515,523-539,544- 549,562-569,571-579	L:3, L:12	96-109, 127- 139	152, 369
gbs2075	hypothetical protein	19-25,28-34,56-61,85-97,110-116	M:2	39-53	153, 370
gbs2106	protein of unknown function/lipoprotein, putative	4-37,41-50,62-72,91-97,99-109,114-125,136- 141,149-158,160-166,201-215	A:5, B:6, C:4, D:14, E:11, I:8, K:23	27-225	154, 371
gbs2118	similar to inosine monophosphate dehydrogenase	15-31,44-51,96-105,122-130,149-157,162- 168,178-183,185-192,198-204,206-213,221- 234,239-245,248-255,257-266,289-335,349- 357,415-422,425-441,448-454,462-468	K:17	463-481	155, 372
gbs2131	ABC transporter, permease protein, putative	5-31,39-55,63-72,76-99,106-155,160- 177,179-199,207-217,223-240,245-255,261- 267,294-316,321-343,354-378,382-452,477- 488,529-536,555-569,584-591,593-612,620- 627,632-640,647-654,671-680,698-704,723- 730,732-750,769-775,781-788,822-852	I:2	505-525	156, 373
ARF0112	Hypothetical protein	none	F:6	3-18	157, 374
ARF0147	Hypothetical protein	4-14	E:3, I:3	12-24	158, 375
ARF0532	Hypothetical protein	4-11,22-30	F:10	12-25	159, 376
ARF0534	Hypothetical protein	5-12	E:2, G:2	4-18	160, 377
ARF0557	Hypothetical protein	4-28	E:2, G:6, H:4	7-14	161, 378
ARF0862	Hypothetical protein	6-16	G:7, H:4	8-16	162, 379
ARF0891	Hypothetical protein	4-15,18-33	K:6	24-36	163, 380
ARF0895	Hypothetical protein	4-10,16-21	I:21	20-31	164, 381
ARF0943	Hypothetical protein	none	C:2, K:9	6-19	165, 382
ARF0973	Hypothetical protein	11-18	D:2, G:3, H:8, I:2, K:2	3-10	166, 383
ARF0999	Hypothetical protein	13-24	B:4, K:3	3-15	167, 384
ARF1010	Hypothetical protein	15-27	K:2	7-16	168, 385
ARF1230	Hypothetical protein	11-16	K:11	1-15	169, 386
ARF1503	Hypothetical protein	4-16	E:13	9-21	170, 387
ARF1556	Hypothetical protein	4-24,40-48,54-67	F:2	22-39	171, 388

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
ARF1585	Hypothetical protein	6-30,34-55,62-68,78-106	I:5, J:4	68-74	172, 389
ARF1588	Hypothetical protein	none	I:2	3-14	173, 390
ARF1735	Hypothetical protein	9-19	I:13	6-21	174, 391
ARF1809	Hypothetical protein	4-17	H:2, L:17	1-9	175, 392
ARF1826	Hypothetical protein	5-30	I:6	1-8	176, 393
ARF1882	Hypothetical protein	4-16,23-46,51-56	K:23	45-55	177, 394
ARF1996	Hypothetical protein	none	F:3	7-16	178, 395
CRF0123	Hypothetical protein	none	F:32	2-14	179, 396
CRF0180	Hypothetical protein	4-36,43-65	E:6, G:6, H:12	50-62	180, 397
CRF0208	Hypothetical protein	10-30	I:2	14-21	181, 398
CRF0258	Hypothetical protein	9-17	I:2	1-10	182, 399
CRF0285	Hypothetical protein	4-12	F:2	3-16	183, 400
CRF0311	Hypothetical protein	4-15	H:4	5-23	184, 401
CRF0446	Hypothetical protein	none	L:20	10-21	185, 402
CRF0455	Hypothetical protein	none	F:5	6-16	186, 403
CRF0491	Hypothetical protein	4-29,31-38	G:4	2-14	187, 404
CRF0520	Hypothetical protein	4-35	H:4	33-42	188, 405
CRF0530	Hypothetical protein	none	G:13, H:8, K:3	2-17	189, 406
CRF0570	Hypothetical protein	9-18,30-35	I:2	15-33	190, 407
CRF0649	Hypothetical protein	4-9	G:8, H:6	6-12	191, 408
CRF0853	Hypothetical protein	none	I:6	3-17	192, 409
CRF0955	Hypothetical protein	12-21,37-44,52-61,72-80	E:7, L:44	38-48	193, 410
CRF0983.1	Hypothetical protein	4-10,29-44,54-61,69-78	K:59	13-27	194, 411
CRF0983.2	Hypothetical protein	13-23,36-53	L:33	2-15	195, 412
CRF1083	Hypothetical protein	4-25,28-46,56-72,81-99,120-132,134- 142,154-160	F:18	129-141	196, 413
CRF1095	Hypothetical protein	4-15,24-33,35-41,64-86	L:15	21-33	197, 414
CRF1212.1	Hypothetical protein	9-15	I:5	4-13	198, 415
CRF1212.2	Hypothetical protein	4-11,13-19,34-48	L:30	15-32	199, 416
CRF1290	Hypothetical protein	4-21	I:7	11-31	200, 417
CRF1383	Hypothetical protein	23-57	K:13	38-50	201, 418
CRF1416	Hypothetical protein	4-32	E:16, J:7	3-13	202, 419
CRF1500	Hypothetical protein	4-10,13-25,32-42,56-68,72-84	E:16	26-38	203, 420
CRF1513	Hypothetical protein	4-20,31-48,52-58,65-71,80-93,99-108,114- 123	I:2	37-49	204, 421

<i>S. agalactiae</i> antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunoge nic region (aa)	Seq. ID (DNA, Prot.)
CRF1518	Hypothetical protein	6-12,14-20	F:28	3-25	205, 422
CRF1663	Hypothetical protein	14-25,27-38	F:10	5-14	206, 423
CRF1667	Hypothetical protein	4-41,57-105,109-118,123-136,144-152	G:4	36-99	207, 424
CRF1832	Hypothetical protein	None	E:5, L:8	6-19	208, 425
CRF1866	Hypothetical protein	none	G:3, H: 18	2-19	209, 426
CRF1892	Hypothetical protein	14-47	L:11	1-14	210, 427
CRF1942	Hypothetical protein	4-21,29-44	F:14	2-18	211, 428
CRF1992	Hypothetical protein	23-29	K:10	10-28	212, 429
CRF2047	Hypothetical protein	6-16,22-36	K:9	11-22	213, 430
CRF2050	Hypothetical protein	4-19,30-44	L:2	18-27	214, 431
CRF2096	Hypothetical protein	5-15,37-45,58-65	G:2	38-47	215, 432
CRF2113	Hypothetical protein	4-15,23-34	L:5	4-15	216, 433
NRF1311	transposase, C- terminal part	30-36,44-54,79-85,101-114,138-152,154- 164,170-175,179-200,213-220,223-240,243- 255,258-264,268-284	F:3	10-28	217, 434

Table 1B: Immunogenic proteins identified by amino acid sequence identity with peptides identified by bacterial surface display. Antigenic peptides, which have been identified by bacterial surface display possess identical counterparts in the listed proteins from *S. agalactiae*. The peptides have been shown to react with multiple human sera (see table 2). Sera directed against these peptides can therefore recognize multiple proteins.

<i>S. agalactiae</i> antigenic protein (new)	Identical region	Peptide sequence	Peptide name	Protein identified by BSD	Immunoge nic region (aa)	Sequenc e ID (DNA, protein)
gbs0384	210 - 226 738 - 753	MEYKGNFSQKTINRFKS QTQRSGKINTDFMRQL	SGO0995.1 SGO0995.2	gbs0995 gbs0995	210 - 226 738 - 753	435, 449
gbs0393	326 - 344 326 - 348 338 - 354 371 - 392 801 - 809 877 - 901	VKTIGYGKLTGKVNHHYVA VKTIGYGKLTGKVNHHYVANKDG VNHHYVANKDGSVTAFFV AAVNQNIVFRVLTGDGRPIFEK TVKKGTNL VTHITTEKSKPVEPQKATPKAPAKGL	SGO0986.2 SGO1143.1 SGO0986.3 SGO1143.2 SGO0986.4 SGO0986.5	gbs0986 gbs1143 gbs0986 gbs1143 gbs0986 gbs0986	326 - 344 327 - 349 338 - 354 372 - 393 801 - 809 877 - 901	436, 450
gbs0396	893 - 906	RQELLTPTQLSKLQ	SGO0983.1	gbs0983	893 - 906	437, 451
gbs0407	51 - 69	VRYDKLEALVAYHGAKSAS	SGO0972.1	gbs0972	51 - 69	438, 452
gbs0408	110 - 125	HQPNRIYLTDKLVPYI	SGO0971.1	gbs0971	110 - 125	439, 453
gbs0410	291 - 305	QSIKQHDKEKLRTVL	SGO0969.1	gbs0969	291 - 305	440, 454
gbs0714	210 - 226 738 - 753	MEYKGNFSQKTINRFKS QTQRSGKINTDFMRQL	SGO0995.1 SGO0995.2	gbs0995 gbs0995	210 - 226 738 - 753	441, 455
gbs0723	326 - 344 326 - 348 338 - 354 371 - 392	VKTIGYGKLTGKVNHHYVA VKTIGYGKLTGKVNHHYVANKDG VNHHYVANKDGSVTAFFV AAVNQNIVFRVLTGDGRPIFEK	SGO0986.2 SGO1143.1 SGO0986.3 SGO1143.2	gbs0986 gbs1143 gbs0986 gbs1143	326 - 344 327 - 349 338 - 354 372 - 393	442, 456

	801-809	TVIKKGTNL	SGO0986.4	gbs0986	801-809	
	877-901	VTHHTEKSKPVEFQKATPKAPAKGL	SGO0986.5	gbs0986	877-901	
gbs0726	893-906	RQELLTPQLSKLQ	SGO0983.1	gbs0983	893-906	443, 457
gbs0737	551-69	VRYDKLEALVAYHGAKSAS	SGO0972.1	gbs0972	51-69	444, 458
gbs0738	110-125	HQPNRIYLTDKLVPI	SGO0971.1	gbs0971	110-125	445, 459
gbs0740	291-305	OSIKQHDKLRTVL	SGO0969.1	gbs0969	291-305	446, 460
gbs0897	32-44	EGDVLLHMSDKT	SGO0898.1	gbs0898	32-44	447, 461
gbs0966	399-410	PGLTVEEKFTF	SGO0144.1	gbs0144	420-431	448, 462

Table 2. Epitope serology with human sera

Peptides	positivity	aa from	aa to	Seq ID
gbs0012.1	++	120	143	218
gbs0012.2	+	138	161	218
gbs0012.3	+	156	179	218
gbs0016.2	+++	110	129	219
gbs0016.3	+	168	184	219
gbs0048.1	+	74	90	222
gbs0053.1	+++	759	773	223
gbs0061.1	+++	237	260	224
gbs0084.1	+	265	284	225
gbs0107.1	++	65	74	226
gbs0108.1	++	41	50	227
gbs0123.1	+	163	174	229
gbs0127.1	++	26	37	230
gbs0183.1	+	174	189	232
gbs0235.1	++	240	258	234
gbs0260.1	+	285	297	236
gbs0286.1	+	238	247	238
gbs0288.1	+	491	519	239
gbs0437.1	++	114	140	243
gbs0539.1	+	267	284	250
gbs0579.1	+	439	453	252
gbs0580.1	++	162	178	253
gbs0628.1	++	347	364	254
gbs0632.1	+++	699	715	255
gbs0634.1	+	60	71	256
gbs0667.1	++	244	257	257
gbs0672.1	+	44	63	258
gbs0672.2	+	57	76	258
gbs0785.1	+	185	196	260
gbs0851.1	+	119	129	263
gbs0896.1	++	182	195	266
gbs0898.1	++	32	44	267
gbs0898.2	+	424	442	267
gbs0904.1	+	247	256	268
gbs0918.1	++	678	694	269
gbs0918.2	+	785	805	269
gbs0918.4	+	55	77	269
gbs0918.5	+++	72	94	269
gbs0995.1	+	210	226	281
gbs1087.3	+	37	59	289
gbs1165.1	+	13	29	296
gbs1816.1	+	136	159	348
gbs1821.1	+	205	222	349
gbs1823.1	+	99	110	350
gbs1834.1	+	160	176	351
gbs1875.1	+	457	470	355
gbs1879.1	+	221	237	356
gbs1893.1	+	167	190	357
gbs1925.1	+	96	120	361
gbs2018.3	+++	399	417	364
gbs2018.4	+++	503	519	364
gbs2018.5	+++	544	563	364
gbs2106.2	+	46	68	371
gbs2106.7	+	159	183	371
gbs2106.8	+	184	198	371
gbs2118.1	++	463	481	372

Table 3: Gene distribution in *S. agalactiae* strains.

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype IA strain)*	Seq. ID (DNA, Prot.)
gbs0012	weakly similar to beta-lactamase	44/44	n.d.	1, 218
gbs0016	glucan-binding protein B (<i>S.mutans</i>)	40/44	0/224	2, 219
gbs0024	Phosphoribosylformylglycinamide	46/46	10/228	3, 220
gbs0031	surface immunogenic protein	46/46	1/225	4, 221
gbs0048	Unknown	30/46	0/61	5, 222
gbs0053	aldehyde-alcohol dehydrogenase (<i>adhB</i>)	45/45	0/224	6, 223
gbs0061	rplB ribosomal protein L2	46/46	0/218	7, 224
gbs0084	DNA-directed RNA polymerase, alpha subunit (<i>rpoA</i>)	45/45	0/207	8, 225
gbs0107	conserved hypothetical protein	46/46	0/235	9, 226
gbs0108	deoxyuridine 5'-triphosphate nucleotidohydrolase	44/44	0/125	10, 227
gbs0113	ribose ABC transporter	44/45	0/227	11, 228
gbs0123	similar to argininosuccinate synthase	44/44	0/184	12, 229
gbs0127	rpmV 50S ribosomal protein L28	46/46	0/40	13, 230
gbs0144	oligopeptide ABC transporter, substrate- binding	45/45	0/282	14, 231
gbs0183	membrane protein, putative	44/44	0/223	15, 232
gbs0184	oligopeptide ABC transporter, oligopeptide-binding	46/46	1/203	16, 233
gbs0235	glycine betaine/carnitine/choline ABC transporter	46/46	0/219	17, 234
gbs0255	conserved hypothetical protein	46/46	0/180	18, 235
gbs0260	glycyl-tRNA synthetase (beta subunit	46/46	0/209	19, 236
gbs0268	transketolase (<i>tkt</i>)	46/46	0/208	20, 237
gbs0286	NH ₃ -dependent NAD ⁺ synthetase	45/45	0/191	21, 238
gbs0288	similar to penicillin-binding protein 1A	45/45	0/212	22, 239
gbs0343	seryl-tRNA synthetase (<i>serS</i>)	46/46	0/228	23, 240
gbs0428	similar to fibrinogen binding protein, putative peptidoglycan linked protein (LPXTG motif)	45/46	1/126	25, 242
gbs0437	glucose-6-phosphate isomerase (<i>pgi</i>)	45/45	0/232	26, 243
gbs0460	decarboxylase	46/46	1/81	27, 244
gbs0465	oxydoreductase	46/46	0/126	28, 245
gbs0489	acetyltransferase, GNAT family	45/45	3/144	30, 247
gbs0492	gbs0492 valyl-tRNA synthetase	44/44	3/125	31, 248
gbs0538	amino acid ABC transporter (ATP-binding protein)	46/46	0/214	32, 249

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype IA strain)*	Seq. ID (DNA, Prot.)
gbs0539	similar to phosphomannomutase	46/46	0/244	33, 250
gbs0555	beta-lactam resistance factor (fibA)	46/46	0/218	34, 251
gbs0579	dipeptidase	46/46	0/218	35, 252
gbs0580	zinc ABC transporter, zinc-binding adhesion liprot	45/45	2/235	36, 253
gbs0628	cell wall surface anchor family protein - (IPxTG)	42/44	0/219	37, 254
gbs0632	cell wall surface anchor family protein, putative (FPKGTG motive)	44/45	0/238	38, 255
gbs0667	regulatory protein, putative, truncation	44/44	0/229	40, 257
gbs0672	transcriptional regulator (GntR family)	43/43	0/203	41, 258
gbs0687	unknown proteins	45/45	0/149	42, 259
gbs0785	Similar to penicillin binding protein 2B	45/45	0/218	43, 260
gbs0828	unknown proteins	46/46	1/120	45, 262
gbs0851	hypothetical protein	46/46	0/140	46, 263
gbs0865	gbs0865 Unknown	44/44	0/241	47, 264
gbs0890	exonuclease RxB (rxB)	46/46	0/232	48, 265
gbs0896	similar to acetoin dehydrogenase	46/46	0/239	49, 266
gbs0898	acetoin dehydrogenase, thymine PPi dependent	45/45	0/180	50, 267
gbs0904	phosphoglucosyltransferase/phosphomannomuta se family prote	46/46	0/169	51, 268
gbs0918	weakly similar to histidine triad protein, putative lipoprotein	45/45	1/209	52, 269
gbs0931	pyruvate kinase	46/46	0/185	53, 270
gbs0947	similar to L-Lactate Dehydrogenase	46/46	0/233	54, 271
gbs0948	DNA gyrase, A subunit (gyrA)	44/44	0/172	55, 272
gbs1035	conserved hypothetical protein	46/46	0/210	69, 286
gbs1066	gbs1066 Unknown	17/46	2/92	71, 288
gbs1087	highly repetitive peptidoglycan bound protein (LPXTG motif)	42/45	n.d.	72, 289
gbs1103	ABC transporter (ATP-binding protein)	46/46	1/165	73, 290
gbs1116	xanthine permease (pbuX)	45/45	1/170	74, 291
gbs1158	Similar to oxidoreductase	44/44	1/170	78, 295
gbs1165	cysteine desulphurase (iscS-1)	43/43	0/148#	79, 296
gbs1195	staphylokinase and streptokinase	45/45	60/142	80, 297
gbs1209	ATP-dependent DNA helicase PcrA	43/44	1/94#	81, 298
gbs1214	conserved hypothetical protein	43/46	0/97	82, 299
gbs1260	ABC transporter, ATP-binding protein	44/46	1/198	84, 301

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype IA strain)*	Seq. ID (DNA, Prot.)
gbs1306	Laminin binding protein (Spellerberg, B et al 1999)	45/46	0/215	87, 304
gbs1307	lmb laminin-binding surface protein	45/45	n.d.	88, 305
gbs1308	C5a peptidase, authentic frameshift	46/46	0/205	89, 306
gbs1309	hypothetical protein	44/46	0/214	90, 307
gbs1356	Putative peptidoglycan linked protein (LPXTG motif) - Agglutinin receptor	20/46	50/211#	94, 311
gbs1376	similar to ATP-dependent Clp proteinase (ATP-binding subunit), ClpL	45/45	0/197	95, 312
gbs1377	similar to homocysteine S- methyltransferase	45/45	0/55	96, 313
gbs1386	-hydroxy-3-methylglutaryl-coenzyme A synthase	44/44	0/219	97, 314
gbs1390	gbs1390 Unknown	43/43	0/198	98, 315
gbs1391	gbs1391 Unknown	44/44	0/214	99, 316
gbs1403	similar to 5'-nucleotidase, putative peptidoglycan bound protein (LPXTN)	45/45	3/189	100, 317
gbs1408	Similar to ABC transporter (ATP-binding protein)	45/45	0/205	101, 318
gbs1429	unknown proteins	46/46	1/193	103, 320
gbs1452	rplT 50S ribosomal protein L20	46/46	0/101	105, 322
gbs1464	ferrichrome ABC transporter (permease	44/44	2/232	106, 323
gbs1470	conserved hypothetical protein	46/46	2/164	107, 324
gbs1528	conserved hypothetical protein	45/45	0/213	108, 325
gbs1531	UvrB excinuclease ABC chain B	45/45	0/108	110, 327
gbs1533	glutamine ABC transporter, glutamine- binding prote	44/44	0/166	111, 328
gbs1542	oxidoreductase, aldo/keto reductase family	45/45	1/219	113, 330
gbs1565	hypothetical protein	43/43	1/218	115, 332
gbs1586	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	45/45	1/227	116, 333
gbs1591	5-methylthioadenosine nucleosidase/S- adenosylhomoc	45/45	0/203	117, 334
gbs1632	similar to branched-chain amino acid ABC transporter, amino acid-binding protein	45/45	0/223	118, 335
gbs1638	amino acid permease	45/45	0/100	119, 336
gbs1662	conserved hypothetical protein	45/45	0/213	120, 337
gbs1666	SWI/SNF family helicase	45/45	0/200	121, 338
gbs1673	conserved hypothetical protein	45/45	0/147	122, 339
gbs1695	dihydroxyacetone kinase family protein	43/43	1/165	123, 340

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype IA strain)*	Seq. ID (DNA, Prot.)
gbs1754	excinuclease ABC, A subunit (uvrA)	43/43	0/224	124, 341
gbs1760	Similar to A/G-specific adenine glycosylase	46/46	0/181	125, 342
gbs1777	glycerol uptake facilitator protein, putative	43/43	0/199	126, 343
gbs1783	polyprenyl synthetase family protein	45/45	0/217	127, 344
gbs1784	ABC transporter, ATP-binding protein CydC	45/45	1/220	128, 345
gbs1790	unknown proteins	41/43	3/75#	129, 346
gbs1805	Similar to secreted unknown proteins	45/45	0/66	130, 347
gbs1816	HD domain protein	43/43	1/176	131, 348
gbs1821	Similar to 23S ribosomal RNA methyltransferase	43/43	2/155#	132, 349
gbs1834	two-component sensor histidine kinase	44/44	0/213	134, 351
gbs1842	transcriptional antiterminator, BglG family	43/43	0/208	135, 352
gbs1850	hypothetical transaldolase	44/44	0/194	136, 353
gbs1875	alkyl hydroperoxide reductase (large subunit) and NADH dehydrogenase	46/46	0/192	138, 355
gbs1879	endopeptidase O (pepO)	43/43	0/135	139, 356
gbs1893	2-keto-3-deoxygluconate kinase	36/46	0/228	140, 357
gbs1899	N-acetylmuramoyl-L-alanine amidase, family 4 prote	43/43	0/149	141, 358
gbs1907	citrate carrier protein, CCS family	43/43	0/219	142, 359
gbs1925	similar to pneumococcal histidine triad protein B precursor (N-terminal part)	43/43	0/103	144, 361
gbs1962	conserved hypothetical protein	28/46	0/136	145, 362
gbs2008	similar to C5A peptidase, putative peptidoglycan linked protein (LPXTG motif)	43/43	n.d.	146, 363
gbs2018	putative peptidoglycan linked protein (LPXTG motif)	43/45	0/104	147, 364
gbs2029	unknown proteins	44/44	1/238	148, 365
gbs2054	DNA mismatch repair protein HexA	46/46	0/206	150, 367
gbs2060	aspartyl-tRNA synthetase (aspS)	46/46	2/211	152, 369
gbs2106	protein of unknown function/lipoprotein, putative	44/44	0/160	154, 371
gbs2118	similar to inosine monophosphate dehydrogenase	43/43	0/113	155, 372
gbs2131	ABC transporter, permease protein, putative	45/45	0/237	156, 373

Table 4. Immunogenicity of epitopes in mice

ORF	aa from	aa to	IB	Peptide ELISA	Seq ID
gbs0016	110	129	+		219
	168	184	+		
gbs0986	877	901	+		277
	333	354	+		
	326	344	+		
	801	809	+		
gbs1805	1	54		+++++	347
gbs2018	544	563	++	+++++	364
	31	51	+	+++	
	107	119	+		
	399	417	++	++++	
	503	519	+	++++	
gbs0012	120	198	++	+	218
gbs0016	20	35	+	++	219
gbs0031	118	201		++++	221
gbs0428	48	132	+	+++++	242
gbs0538	118	136	+	++++	249
gbs0580	162	178	+	+	253
gbs0628	347	364	+	+++++	254
gbs0632	699	715	+	+++++	255
gbs0672	50	76		+	258
gbs0918	785	819	+	+++++	269
	44	128	++		
gbs0971	90	128		+++++	274
gbs1087	314	384	+		289
gbs1143	327	349		+++	293
gbs1306	242	314	++	++++	304
	405	478	++		
	23	100	+		
gbs1307	129	210	++		305
gbs1309	162	188		++	307
gbs1352	750	772	++	+++++	310
gbs1632	1	56		++	335
gbs1662	322	337	+	+++++	337
gbs1673	72	90	+	+++++	339
gbs1784	374	395		+	345
gbs1816	136	159	+	++++	348
gbs1899	141	164	+		358
gbs1925	96	157	++	+	361
gbs2008	1	82		+	363
gbs2018	489	556	+	+++++	364
gbs2106	159	183		++	371
	49	133	+	+++++	

References

- Altschul, S., et al. (1990). Journal of Molecular Biology 215: 403-10.
- Balter, S. et al. In Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, 154-160.
- Bennett, D., et al. (1995). J Mol Recognit 8: 52-8.
- Brodeur, B., et al. (2000). Infect Immun 68: 5610-8.
- Burnie, J., et al. (1998). J Antimicrob Chemother 41: 319-22.
- Campbell, J., et al. (2000). Obstet Gynecol 96: 498-503.
- Cheng, Q., et al. (2002). Infect Immun 70: 6409-15.
- Clackson, T., et al. (1991). Nature 352: 624-8.
- Devereux, J., et al. (1984). Nucleic acids research 12: 387-95.
- Doherty, E., et al. (2001). Annu Rev Biophys Biomol Struct 30: 457-475.
- Eisenbraun, M., et al. (1993). DNA Cell Biol 12: 791-7.
- Etz, H., et al. (2001). J Bacteriol 183: 6924-35.
- Farley, M. (2001). Clin Infect Dis 33: 556-61.
- Ganz, T. (1999). Science 286: 420-421.
- Georgiou, G. (1997). Nature Biotechnology 15: 29-34.
- Glaser, P., et al. (2002). Mol Microbiol 45: 1499-513.
- Hashemzadeh-Bonehi, L., et al. (1998). Mol Microbiol 30: 676-678.
- Heinje, von G (1987) e.g. Sequence Analysis in Molecular Biology, Academic Press.
- Hemmer, B., et al. (1999). Nat Med 5: 1375-82.
- Hoe, N., et al. (2001). J Infect Dis 183: 633-9.
- Hornef, M., et al. (2002). Nat Immunol 3: 1033-40.
- Jackson, L., et al. (1995). Ann Intern Med 123: 415-20.
- Johanson, K., et al. (1995). J Biol Chem 270: 9459-71.
- Jones, P., et al. (1986). Nature 321: 522-5.
- Kajava, A., et al. (2000). J Bacteriol 182: 2163-9.
- Kohler, G., et al. (1975). Nature 256: 495-7.
- Larsson, C., et al. (1999). Vaccine 17: 454-8.
- Lewin, A., et al. (2001). Trends Mol Med 7: 221-8.
- Marks, J., et al. (1992). Biotechnology (N Y) 10: 779-83.
- McCafferty, J., et al. (1990). Nature 348: 552-4.
- Michel, J., et al. (1991). Infect Immun 59: 2023-8.
- Navarre, W., et al. (1999). Microbiol Mol Biol Rev 63: 174-229.
- Nizet, V. & Rubens, C.E. in Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 125-136.
- Okano, H., et al. (1991). J Neurochem 56: 560-7.
- Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression ; CRC Press, Boca Ration, FL (1988).
- Paoletti, L., et al. (2002). Semin Neonatol 7: 315-23.
- Paoletti, L.C. et al. In Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 137-153.
- Phillips-Quagliata, J., et al. (2000). J Immunol 165: 2544-55.
- Rammensee, H., et al. (1999). Immunogenetics 50: 213-9.
- Seeger, C., et al. (1984). Proc Natl Acad Sci U S A 81: 5849-52.
- Shibuya, A., et al. (2000). Nature Immunology 1: 441-6.
- Skerra, A. (1994). Gene 151: 131-5.
- Tang, D., et al. (1992). Nature 356: 152-4.
- Tempest, P., et al. (1991). Biotechnology (N Y) 9: 266-71.
- Tettelin, H., et al. (2002). Proc Natl Acad Sci U S A 99: 12391-6.
- Tourdot, S., et al. (2000). Eur J Immunol 30: 3411-21.
- Wiley, J., et al. (1987) Current Protocols in Molecular Biology.

Claims:

1. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:
 - a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from Seq ID No 14, 90, 157-216,
 - b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
 - c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
 - d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
 - e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).
2. The isolated nucleic acid molecule according to claim 1, wherein the sequence identity is at least 80%, preferably at least 95%, especially 100%.
3. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of
 - a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from Seq ID No 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448,
 - b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
 - c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
 - d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
 - e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).
4. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of
 - a) a nucleic acid molecule selected from Seq ID No 32, 86, 91, 101, 127,
 - b) a nucleic acid molecule which is complementary to the nucleic acid of a),
 - c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).
5. The nucleic acid molecule according to any one of the claims 1, 2, 3 or 4, wherein the nucleic acid is DNA.
6. The nucleic acid molecule according to any one of the claims 1, 2, 3, 4, or 5 wherein the nucleic acid is RNA.
7. An isolated nucleic acid molecule according to any one of claims 1 to 5, wherein the nucleic acid molecule is isolated from a genomic DNA, especially from a *S. agalactiae* genomic DNA.
8. A vector comprising a nucleic acid molecule according to any one of claims 1 to 7.
9. A vector according to claim 8, wherein the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragment thereof encoded by the nucleic acid molecule according to any one of claims 1 to 7.

10. A host cell comprising the vector according to claim 8 or 9.
11. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 1, 2, 5, 6 or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of Seq ID No 231, 307, 374-433.
12. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 3, 5, 6, or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of Seq ID No 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462.
13. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 4, 5, 6, or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of Seq ID No 249, 303, 308, 318, 344.
14. Fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1A, especially peptides comprising amino acid 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of Seq ID No 218; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of Seq ID No 219; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of Seq ID No 220; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of Seq ID No 221; 29-38, 44-64, 70-76, 78-87, 94-100, 102-112, 119-134, 140-149, 163-173, 178-186, 188-194, 207-234, 247-262, 269-290 and 73-92 of Seq ID No 222; 10-28, 36-63, 77-87, 103-119, 127-136, 141-169, 171-183, 195-200, 207-232, 236-246, 251-265, 268-283, 287-297, 314-322, 335-343, 354-363, 384-390, 405-411, 419-436, 443-455, 467-473, 480-513, 518-529, 550-557, 565-585, 602-608, 616-625, 632-660, 665-677, 685-701, 726-736, 738-747, 752-761, 785-796, 801-813, 838-853, 866-871 and 757-774 of Seq ID No 223; 31-38, 61-66, 74-81, 90-115, 123-145, 154-167, 169-179, 182-193, 200-206, 238-244, 267-272 and 235-251 of Seq ID No 224; 19-25, 38-54, 56-64, 66-72, 74-92, 94-100, 116-129, 143-149, 156-183, 204-232, 253-266, 269-275, 294-307 and 241-313 of Seq ID No 225; 5-34, 50-56, 60-65, 74-85, 89-97, 108-119, 159-165, 181-199, 209-225, 230-240, 245-251, 257-262, 274-282, 300-305 and 64-75 of Seq ID No 226; 5-13, 16-21, 27-42, 45-52, 58-66, 74-87, 108-114, 119-131 and 39-51 of Seq ID No 227; 6-23, 46-54, 59-65, 78-84, 100-120, 128-133, 140-146, 159-165, 171-183, 190-204, 224-232, 240-248, 250-259, 274-280, 288-296, 306-315 and 267-274 of Seq ID No 228; 5-12, 15-24, 26-36, 42-65, 68-80, 82-104, 111-116, 125-144, 159-167, 184-189, 209-218, 235-243, 254-265, 269-283, 287-300, 306-316, 318-336, 338-352, 374-392 and 162-174 of Seq ID No 229; 30-42, 45-54 and 25-37 of Seq ID No 230; 10-30, 53-59, 86-95, 116-130, 132-147, 169-189, 195-201, 212-221, 247-256, 258-265, 278-283, 291-298, 310-316, 329-339, 341-352, 360-367, 388-396, 398-411, 416-432, 443-452, 460-466, 506-512, 515-521, 542-548 and 419-431 of Seq ID No 231; 4-27, 30-53, 60-67, 70-90, 92-151, 159-185, 189-195, 198-210, 215-239 and 173-189 of Seq ID No 232; 4-26, 41-54, 71-78, 116-127, 140-149, 151-158, 161-175, 190-196, 201-208, 220-226, 240-252, 266-281, 298-305, 308-318, 321-329, 344-353, 372-378, 384-405, 418-426, 429-442, 457-463, 494-505, 514-522 and 174-188

of Seq ID No 233; 17-25, 27-39, 61-67, 81-89, 99-110, 120-131, 133-139, 147-161, 167-172, 179-185, 192-198, 203-213, 226-238, 243-258, 261-267, 284-290, 296-307, 311-328, 340-352, 356-371 and 239-256 of Seq ID No 234; 8-30, 40-49, 67-80, 114-123, 126-142, 152-162, 188-194 and 57-70 of Seq ID No 235; 4-23, 28-34, 36-47, 50-61, 76-81, 89-94, 96-104, 112-119, 126-146, 155-181, 195-200, 208-214, 220-229, 244-260, 263-276, 282-288, 292-300, 317-323, 336-351, 353-359, 363-375, 382-399, 415-432, 444-455, 458-471, 476-481, 484-492, 499-517, 522-529, 535-541, 543-568, 572-584, 586-600, 607-617, 626-637, 656-675 and 282-297 of Seq ID No 236; 6-24, 30-35, 38-45, 63-91, 134-140, 146-160, 167-188, 214-220, 226-234, 244-250, 260-270, 286-301, 316-329, 340-371, 429-446, 448-459, 474-481, 485-491, 512-526, 537-544, 550-565, 573-583, 596-613, 621-630, 652-658 and 87-97 of Seq ID No 237; 8-20, 26-48, 56-67, 76-86, 94-109, 115-121, 123-129, 143-160, 178-186, 191-198, 201-208, 221-236, 238-244, 260-268 and 237-247 of Seq ID No 238; 4-40, 42-57, 73-87, 98-117, 126-135, 150-156, 166-174, 196-217, 231-236, 248-258, 276-284, 293-301, 307-313, 339-347, 359-365, 375-387, 395-402, 428-440, 445-456, 485-490, 497-505, 535-541, 547-555, 610-625, 648-656, 665-671 and 448-528 of Seq ID No 239; 10-18, 39-45, 51-61, 80-96, 98-106, 110-115, 158-172, 174-183, 191-200, 220-237, 249-255, 274-289, 308-324, 331-341, 372-381, 384-397, 405-414 and 322-338 of Seq ID No 240; 30-36, 38-56, 85-108, 134-147, 149-160, 163-183, 188-201, 206-211, 219-238, 247-254 and 5-13 of Seq ID No 241; 11-40, 98-103, 110-115, 133-145, 151-159, 172-179, 192-201, 204-212, 222-228, 235-245, 258-268, 283-296, 298-309, 322-329, 342-351, 354-362, 372-378, 385-393, 407-418, 495-516 and 1-148 of Seq ID No 242; 5-19, 21-36, 73-94, 112-119, 122-137, 139-145, 152-167, 184-190, 198-204, 208-224, 249-265, 267-281, 299-304, 309-317, 326-333, 356-364, 368-374, 381-389, 391-414, 419-425, 430-435 and 113-140 of Seq ID No 243; 45-54, 59-67, 78-91 and 15-23 of Seq ID No 244; 11-22, 33-47, 52-80, 88-112, 124-129 and 6-25 of Seq ID No 245; 26-41, 51-63, 80-89, 93-115, 150-163, 187-193, 220-237, 240-249, 286-294, 296-306, 316-329, 345-353, 361-370, 407-425, 428-437, 474-482, 484-494, 504-517, 533-541, 549-558, 595-613, 616-625, 660-668, 673-685, 711-726, 736-744, 749-761, 787-802, 812-820, 825-837, 863-878, 888-896, 901-913, 939-954, 964-972, 977-989, 1003-1008, 1016-1022, 1028-1034, 1041-1053, 1059-1074, 1101-1122, 420-511 and 581-704 of Seq ID No 246; 18-25, 27-55, 71-83, 89-95, 102-113, 120-146, 150-156, 174-185 and 159-175 of Seq ID No 247; 24-30, 38-56, 63-68, 87-93, 136-142, 153-164, 183-199, 213-219, 226-234, 244-261, 269-278, 283-289, 291-297, 320-328, 330-336, 340-346, 348-356, 358-366, 382-387, 401-408, 414-419, 449-455, 468-491, 504-512, 531-537, 554-560, 597-608, 621-627, 632-643, 650-662, 667-692, 703-716, 724-737, 743-758, 783-794, 800-818, 846-856 and 806-884 of Seq ID No 248; 4-14, 21-39, 86-92, 99-107, 121-131, 136-144, 147-154, 158-166, 176-185, 193-199, 207-222, 224-230 and 117-136 of Seq ID No 249; 65-76, 85-97, 103-109, 115-121, 125-146, 163-169, 196-205, 212-219, 228-237, 241-247, 254-262, 269-288, 294-303, 305-313, 328-367, 395-401, 405-412, 418-429, 437-447, 481-488, 506-513, 519-524, 530-541, 546-557 and 266-284 of Seq ID No 250; 5-14, 37-42, 49-71, 78-92, 97-112, 127-136, 147-154, 156-163, 186-198, 216-225, 233-243, 248-253, 295-307, 323-332, 359-366, 368-374, 380-398 and 194-223 of Seq ID No 251; 4-11, 33-39, 45-72, 100-113, 119-129, 136-144, 169-175, 177-185, 200-208, 210-219, 262-276, 278-297, 320-326, 336-344, 347-362, 381-394, 443-453 and 438-454 of Seq ID No 252; 4-29, 31-52, 55-61, 95-110, 138-158, 162-171, 179-187, 202-229, 239-248, 251-256, 262-267, 269-285, 304-310, 351-360, 362-368, 381-388, 415-428, 435-440, 448-458 and 161-178 of Seq ID No 253; 4-17, 19-28, 32-43, 47-59, 89-110, 112-126, 128-134, 140-148, 152-161, 169-184, 191-204, 230-235, 255-264, 328-338, 341-347, 401-409, 413-419, 433-441, 449-458, 463-468, 476-482, 486-492, 500-506, 529-545 and 305-381 of Seq ID No 254; 10-29, 38-45, 53-61, 134-145, 152-160, 163-170, 202-208, 219-229, 248-258, 266-275, 282-288, 315-320, 328-334, 377-385, 392-402, 418-424, 447-453, 460-471, 479-487, 491-497, 500-507, 531-537, 581-594, 615-623, 629-635, 644-652, 659-666, 668-678, 710-717, 719-728, 736-741, 747-760, 766-773, 784-789, 794-800, 805-817, 855-861, 866-887 and 698-715 of Seq ID No 255; 16-26, 29-37, 44-58, 62-68, 74-80, 88-95, 97-120, 125-144, 165-196 and 58-72 of Seq ID No 256; 14-21, 23-46, 49-60, 63-74, 78-92, 96-103, 117-129, 134-161, 169-211, 217-231, 239-248, 252-281, 292-299, 313-343 and 243-257 of Seq ID No 257; 11-27, 46-52, 67-72, 76-84, 91-112, 116-153, 160-175, 187-196, 202-211, 213-220 and 43-76 of Seq ID No 258; 5-29, 37-56, 78-86, 108-118, 152-161 and 120-130 of Seq ID No 259; 8-14, 19-41, 52-66, 75-82, 87-92, 106-121, 127-133, 136-143, 158-175, 180-187, 196-204, 221-228, 239-245, 259-265, 291-306, 318-323, 328-340, 352-358, 361-368, 375-381, 391-399, 411-418, 431-442, 446-455, 484-496, 498-510, 527-533, 541-549, 558-565, 575-585, 587-594, 644-655, 661-668, 671-677 and 184-196 of Seq ID No 260; 4-22, 29-38, 55-62, 75-81,

102-107, 110-134, 143-150, 161-167, 172-179, 191-215, 223-233, 241-247, 251-264, 266-272, 288-309, 340-352, 354-366, 394-402, 414-438 and 198-218 of Seq ID No 261; 24-44, 49-70, 80-91, 105-118, 128-136, 140-154 and 77-92 of Seq ID No 262; 5-22, 31-36, 41-47, 67-74, 83-90, 105-122, 135-143, 160-167 and 118-129 of Seq ID No 263; 4-25, 33-73, 81-93, 96-106, 114-120, 122-128, 130-172, 179-208, 210-241, 251-283, 296-301 and 92-100 of Seq ID No 264; 14-24, 29-38, 43-50, 52-72, 86-97, 101-107, 110-125, 127-141, 145-157, 168-175, 177-184, 186-195, 205-226, 238-250, 255-261, 284-290, 293-304, 307-314, 316-323, 325-356, 363-371, 383-390, 405-415, 423-432, 442-454, 466-485, 502-511, 519-527, 535-556, 558-565, 569-574, 612-634, 641-655, 672-686, 698-709, 715-722, 724-732, 743-753, 760-769, 783-792, 818-825, 830-839, 842-849, 884-896, 905-918, 926-940, 957-969, 979-1007, 1015-1021, 1049-1057 and 336-349 of Seq ID No 265; 6-16, 26-31, 33-39, 62-73, 75-85, 87-100, 113-123, 127-152, 157-164, 168-181, 191-198, 208-214, 219-226, 233-254, 259-266, 286-329 and 181-195 of Seq ID No 266; 4-13, 32-39, 53-76, 99-108, 110-116, 124-135, 137-146, 149-157, 162-174, 182-190, 207-231, 242-253, 255-264, 274-283, 291-323, 334-345, 351-360, 375-388, 418-425, 456-474, 486-492, 508-517, 520-536, 547-560, 562-577, 31-45 and 419-443 of Seq ID No 267; 15-26, 30-37, 42-49, 58-90, 93-99, 128-134, 147-154, 174-179, 190-197, 199-205, 221-230, 262-274, 277-287, 300-314, 327-333, 343-351, 359-377, 388-396, 408-413, 416-425, 431-446 and 246-256 of Seq ID No 268; 5-26, 34-42, 47-54, 61-67, 71-104, 107-115, 131-138, 144-153, 157-189, 196-202, 204-210, 228-245, 288-309, 316-329, 332-341, 379-386, 393-399, 404-412, 414-421, 457-468, 483-489, 500-506, 508-517, 523-534, 543-557, 565-580, 587-605, 609-617, 619-627, 631-636, 640-646, 662-668, 675-682, 705-710, 716-723, 727-732, 750-758, 784-789, 795-809, 869-874, 14-138, 166-286, 372-503, 674-696 and 754-859 of Seq ID No 269; 5-17, 32-38, 40-47, 80-89, 113-119, 125-137, 140-154, 157-163, 170-177, 185-199, 213-225, 228-236, 242-248, 277-290, 292-305, 323-333, 347-353, 364-370, 385-394, 399-406, 423-433, 441-451, 462-474, 477-487 and 116-124 of Seq ID No 270; 7-16, 18-30, 32-49, 53-61, 63-85, 95-101, 105-115, 119-134, 143-150, 159-178, 185-202, 212-229, 236-250, 254-265, 268-294 and 63-72 of Seq ID No 271; 4-12, 19-47, 73-81, 97-103, 153-169, 188-198, 207-213, 217-223, 236-242, 255-265, 270-278, 298-305, 309-317, 335-347, 354-363, 373-394, 419-424, 442-465, 486-492, 500-507, 542-549, 551-558, 560-572, 580-589, 607-614, 617-623, 647-653, 666-676, 694-704, 706-714, 748-754, 765-772, 786-792, 795-806 and 358-370 of Seq ID No 272; 18-28, 30-38, 40-46, 49-55, 69-78, 82-98, 104-134, 147-153, 180-190, 196-202, 218-236, 244-261, 266-273, 275-286, 290-295, 301-314, 378-387, 390-395, 427-434 and 290-305 of Seq ID No 273; 4-13, 20-31, 39-51, 54-61, 69-84, 87-105, 117-124 and 108-125 of Seq ID No 274; 24-34, 43-54, 56-66, 68-79 and 50-69 of Seq ID No 275; 5-43, 71-77, 102-131, 141-148, 150-156, 159-186, 191-207, 209-234, 255-268, 280-286, 293-299, 317-323, 350-357, 363-372, 391-397, 406-418, 428-435, 455-465, 484-497, 499-505, 525-531, 575-582, 593-607, 621-633, 638-649, 655-673, 684-698, 711-725, 736-741, 743-752, 759-769, 781-793, 813-831, 843-853, 894-905, 908-916, 929-946, 953-963, 970-978, 1001-1007, 1011-1033, 165-178 and 818-974 of Seq ID No 276; 16-44, 63-86, 98-108, 185-191, 222-237, 261-274, 282-294, 335-345, 349-362, 374-384, 409-420, 424-430, 440-447, 453-460, 465-473, 475-504, 522-534, 538-551, 554-560, 567-582, 598-607, 611-619, 627-640, 643-653, 655-661, 669-680, 684-690, 701-707, 715-731, 744-750, 756-763, 768-804, 829-837, 845-853, 855-879, 884-890, 910-928, 77-90, 144-212, 279-355, 434-536, 782-810 and 875-902 of Seq ID No 277; 4-22, 29-41, 45-51, 53-66, 70-77, 86-95, 98-104, 106-124, 129-135, 142-151, 153-161, 169-176, 228-251, 284-299, 331-337, 339-370, 380-387, 393-398, 406-411, 423-433, 440-452, 461-469, 488-498, 501-516, 523-530, 532-559, 562-567, 570-602, 612-628, 630-645, 649-659, 666-672, 677-696, 714-723, 727-747 and 212-227 of Seq ID No 278; 4-9, 17-31, 35-41, 56-61, 66-75, 81-87, 90-124, 133-138, 149-163, 173-192, 213-219, 221-262, 265-275, 277-282, 292-298, 301-307, 333-346, 353-363, 371-378, 419-430, 435-448, 456-469, 551-570, 583-599, 603-612 and 275-291 of Seq ID No 279; 28-34, 53-58, 72-81, 100-128, 145-154, 159-168, 172-189, 217-225, 227-249, 256-263, 299-309, 322-330, 361-379, 381-388, 392-401, 404-417, 425-436, 440-446, 451-464, 469-487, 502-511, 543-551, 559-564, 595-601, 606-612, 615-626, 633-642, 644-650, 664-670, 674-684, 692-701, 715-723, 726-734, 749-756, 763-771, 781-787, 810-843, 860-869, 882-889, 907-917, 931-936, 941-948, 951-958, 964-971, 976-993, 1039-1049, 1051-1065, 1092-1121, 1126-1132, 1145-1151, 1158-1173, 1181-1192, 1194-1208, 1218-1223, 1229-1243, 1249-1254, 1265-1279, 1287-1297, 1303-1320, 1334-1341, 1343-1358, 1372-1382, 1406-1417, 1419-1425, 1428-1434, 1441-1448, 1460-1473, 1494-1504, 1509-1514, 1529-1550, 654-669 and 1400-1483 of Seq ID No 280; 10-16, 20-25, 58-65, 97-109, 118-132, 134-146, 148-155, 186-195, 226-233, 244-262, 275-284, 295-310, 317-322, 330-339, 345-351, 366-375,

392-403, 408-415, 423-430, 435-444, 446-457, 467-479, 486-499, 503-510, 525-537, 540-585, 602-612, 614-623, 625-634, 639-645, 650-669, 700-707, 717-724, 727-739, 205-230 and 733-754 of Seq ID No 281; 5-22, 37-43, 72-81, 105-113, 128-133, 148-160, 188-194, 204-230, 238-245, 251-257 and 194-213 of Seq ID No 282; 16-21, 35-41, 56-72, 74-92, 103-109 and 62-68 of Seq ID No 283; 4-15, 17-82, 90-104, 107-159, 163-170, 188-221, 234-245, 252-265 and 220-235 of Seq ID No 284; 16-22, 36-46, 61-75, 92-107, 113-121, 139-145, 148-160 and 30-42 of Seq ID No 285; 4-12, 20-26, 43-49, 55-62, 66-78, 121-127, 135-141, 146-161, 164-170, 178-189, 196-205, 233-238, 269-279, 288-318, 325-332, 381-386, 400-407 and 328-346 of Seq ID No 286; 5-12, 31-49, 57-63, 69-79, 89-97, 99-114, 116-127, 134-142, 147-154, 160-173, 185-193, 199-204, 211-222, 229-236, 243-249, 256-274 and 58-68 of Seq ID No 287; 10-20, 28-34, 39-53, 68-79, 84-90, 99-106 and 73-79 of Seq ID No 288; 14-37, 45-50, 61-66, 77-82, 93-98, 109-114, 125-130, 141-146, 157-162, 173-178, 189-194, 205-210, 221-226, 237-242, 253-258, 269-274, 285-290, 301-306, 316-332, 349-359, 371-378, 385-406, 34-307 and 312-385 of Seq ID No 289; 4-10, 17-38, 50-85, 93-99, 109-116, 128-185, 189-197, 199-210, 223-256, 263-287, 289-312, 327-337, 371-386, 389-394, 406-419, 424-432, 438-450, 458-463, 475-502, 507-513, 519-526, 535-542, 550-567 and 361-376 of Seq ID No 290; 10-39, 42-93, 100-144, 155-176, 178-224, 230-244, 246-255, 273-282, 292-301, 308-325, 332-351, 356-361, 368-379, 386-393, 400-421 and 138-155 of Seq ID No 291; 5-11, 17-34, 40-45, 50-55, 72-80, 101-123, 145-151, 164-172, 182-187, 189-195, 208-218, 220-241, 243-252, 255-270, 325-331, 365-371, 391-398, 402-418, 422-428, 430-435, 443-452, 463-469, 476-484, 486-494, 503-509, 529-553, 560-565, 570-590, 608-614, 619-627, 654-661, 744-750, 772-780, 784-790, 806-816, 836-853, 876-885, 912-918, 926-933, 961-975, 980-987, 996-1006, 1016-1028, 1043-1053, 1057-1062, 994-1003 and 1033-1056 of Seq ID No 292; 17-45, 64-71, 73-81, 99-109, 186-192, 223-238, 262-275, 283-295, 336-346, 350-363, 375-385, 410-421, 425-431, 441-448, 454-463, 468-474, 476-512, 523-537, 539-552, 568-583, 599-608, 612-620, 628-641, 644-654, 656-662, 670-681, 685-695, 702-708, 716-723, 725-735, 757-764, 769-798, 800-806, 808-816, 826-840, 846-854, 856-862, 874-881, 885-902, 907-928, 274-350 and 443-513 of Seq ID No 293; 4-22, 29-41, 45-51, 53-61, 70-76, 85-92, 99-104, 111-122, 134-140, 142-154, 163-174, 224-232, 255-265, 273-279, 283-297, 330-335, 337-348, 356-367, 373-385, 391-396, 421-431, 442-455, 475-485, 493-505, 526-538, 544-561, 587-599, 605-620, 622-651, 662-670, 675-681, 687-692, 697-712, 714-735 and 252-262 of Seq ID No 294; 4-12, 15-35, 40-46, 50-59, 67-94, 110-128, 143-169, 182-188, 207-215, 218-228, 238-250 and 74-90 of Seq ID No 295; 9-18, 42-58, 78-85, 88-95, 97-106, 115-122, 128-134, 140-145, 154-181, 186-202, 204-223, 261-267, 269-278, 284-293, 300-336, 358-368 and 12-29 of Seq ID No 296; 7-34, 46-53, 62-72, 82-88, 100-105, 111-117, 132-137, 144-160, 166-180, 183-189, 209-221, 231-236, 246-253, 268-282, 286-293, 323-336, 364-372, 378-392, 422-433 and 388-405 of Seq ID No 297; 21-27, 34-50, 72-77, 80-95, 164-177, 192-198, 202-220, 226-236, 239-247, 270-279, 285-292, 315-320, 327-334, 348-355, 364-371, 388-397, 453-476, 488-497, 534-545, 556-576, 582-588, 601-607, 609-616, 642-662, 674-681, 687-697, 709-715, 721-727, 741-755 and 621-739 of Seq ID No 298; 4-14, 16-77, 79-109 and 25-99 of Seq ID No 299; 4-9, 17-23, 30-37, 44-55, 65-72, 77-93, 102-121, 123-132, 146-153 and 17-29 of Seq ID No 300; 4-18, 25-41, 52-60, 83-92, 104-112, 117-123, 149-155, 159-167, 170-192, 201-210, 220-227, 245-250 and 124-137 of Seq ID No 301; 8-25, 50-55, 89-95, 138-143, 148-153, 159-169, 173-179, 223-238, 262-268, 288-295, 297-308, 325-335, 403-409, 411-417, 432-446, 463-475, 492-501, 524-530, 542-548, 561-574, 576-593, 604-609, 612-622, 637-654, 665-672, 678-685, 720-725, 731-739, 762-767, 777-783, 820-838, 851-865, 901-908, 913-920, 958-970, 1000-1006, 1009-1015, 1020-1026, 1043-1052, 1055-1061, 1-128, 252-341, 771-793 and 1043-1058 of Seq ID No 302; 16-26, 33-46 and 64-76 of Seq ID No 303; 4-27, 69-77, 79-101, 117-123, 126-142, 155-161, 171-186, 200-206, 213-231, 233-244, 267-273, 313-329, 335-344, 347-370, 374-379, 399-408, 422-443, 445-453, 461-468, 476-482, 518-534, 544-553, 556-567, 578-595, 601-620, 626-636, 646-658, 666-681, 715-721, 762-768, 778-785, 789-803, 809-819, 22-108, 153-318, 391-527 and 638-757 of Seq ID No 304; 6-21, 32-43, 62-92, 104-123, 135-141, 145-152, 199-216, 218-226, 237-247, 260-269, 274-283, 297-303, 1-72 and 127-211 of Seq ID No 305; 6-26, 50-56, 83-89, 108-114, 123-131, 172-181, 194-200, 221-238, 241-247, 251-259, 263-271, 284-292, 304-319, 321-335, 353-358, 384-391, 408-417, 424-430, 442-448, 459-466, 487-500, 514-528, 541-556, 572-578, 595-601, 605-613, 620-631, 635-648, 660-670, 673-679, 686-693, 702-708, 716-725, 730-735, 749-755, 770-777, 805-811, 831-837, 843-851, 854-860, 863-869, 895-901, 904-914, 922-929, 933-938, 947-952, 956-963, 1000-1005, 1008-1014, 1021-1030, 1097-1103, 1120-1130, 1132-1140, 1-213, 269-592 and 992-1120 of Seq ID No

306; 9-16, 33-39, 47-59, 65-79, 81-95, 103-108, 115-123, 138-148, 163-171, 176-185, 191-196, 205-211, 213-221, 224-256, 261-276, 294-302, 357-363, 384-390, 95-111 and 161-189 of Seq ID No 307; 21-27, 35-45, 70-76, 92-105, 129-143, 145-155, 161-166, 170-191, 204-211, 214-231, 234-246, 249-255, 259-275 and 1-18 of Seq ID No 308; 21-35, 45-53, 56-64, 69-97 and 1-16 of Seq ID No 309; 25-33, 41-47, 61-68, 86-101, 106-114, 116-129, 134-142, 144-156, 163-176, 181-190, 228-251, 255-261, 276-292, 295-305, 334-357, 368-380, 395-410, 424-429, 454-460, 469-482, 510-516, 518-527, 531-546, 558-570, 579-606, 628-636, 638-645, 651-656, 668-674, 691-698, 717-734, 742-754, 765-770, 792-797, 827-835, 847-859, 874-881, 903-909, 926-933, 942-961, 964-977, 989-1004, 1010-1028, 1031-1047, 1057-1075, 1081-1095, 1108-1117, 1138-1144, 1182-1189, 1193-1206, 1220-1229, 1239-1246, 1257-1267, 1271-1279, 1284-1301, 1312-1320, 1329-1335, 1341-1347, 1358-1371, 1399-1404, 1417-1426, 1458-1463, 1468-1476, 1478-1485, 1493-1506, 1535-1541, 1559-1574, 1583-1590, 1595-1601, 1603-1611, 1622-1628, 1634-1644, 1671-1685, 1689-1696, 1715-1720, 1734-1746, 1766-1775, 1801-1806, 1838-1844, 1858-1871, 1910-1917, 1948-1955, 1960-1974, 2000-2015, 2019-2036, 2041-2063, 748-847 and 1381-1391 of Seq ID No 310; 5-12, 18-24, 27-53, 56-63, 96-113, 119-124, 131-136, 157-163, 203-209, 215-223, 233-246, 264-273, 311-316, 380-389, 393-399, 425-433, 445-450, 457-462, 464-470, 475-482, 507-513, 527-535, 542-548, 550-565, 591-602, 607-613, 627-642, 644-664, 673-712, 714-732, 739-764, 769-782, 812-818, 826-838, 848-854, 860-871, 892-906, 930-938, 940-954, 957-973, 990-998, 1002-1021, 1024-1033, 1037-1042, 1050-1060, 1077-1083, 1085-1092, 1100-1129, 1144-1161, 1169-1175, 1178-1189, 1192-1198, 1201-1207, 1211-1221, 1229-1239, 1250-1270, 1278-1292, 1294-1300, 1314-1335, 1344-1352, 1360-1374, 1394-1405, 1407-1414, 1416-1424, 1432-1452, 1456-1462, 1474-1497, 1500-1510, 1516-1522, 1534-1542, 1550-1559, 1584-1603, 1608-1627, 187-273 and 306-441 of Seq ID No 311; 70-80, 90-97, 118-125, 128-140, 142-148, 154-162, 189-202, 214-222, 224-232, 254-260, 275-313, 317-332, 355-360, 392-398, 425-432, 448-456, 464-470, 476-482, 491-505, 521-528, 533-546, 560-567, 592-597, 605-614, 618-626, 637-644, 646-653, 660-666, 677-691 and 207-227 of Seq ID No 312; 5-19, 26-34, 37-55, 57-66, 69-83, 86-102, 115-134, 138-143, 154-172, 178-195, 209-246, 251-257, 290-302, 306-311 and 256-266 of Seq ID No 313; 10-20, 22-28, 35-57, 72-79, 87-103, 108-128, 130-144, 158-171, 190-198, 225-242, 274-291, 301-315, 317-324, 374-385 and 353-365 of Seq ID No 314; 4-9, 17-30, 34-54, 59-66, 73-94, 118-130, 135-150, 158-171, 189-198, 219-239, 269-275, 283-301, 89-106 and 176-193 of Seq ID No 315; 14-20, 22-74, 77-86, 89-99, 104-109, 126-135, 154-165, 181-195, 197-212, 216-224, 264-275 and 107-118 of Seq ID No 316; 4-18, 21-38, 63-72, 101-109, 156-162, 165-179, 183-192, 195-210, 212-218, 230-239, 241-256, 278-290, 299-311, 313-322, 332-341, 348-366, 386-401, 420-426, 435-450, 455-460, 468-479, 491-498, 510-518, 532-538, 545-552, 557-563, 567-573, 586-595, 599-609, 620-626, 628-636, 652-657, 665-681 and 1-198 of Seq ID No 317; 4-10, 16-38, 51-68, 73-79, 94-115, 120-125, 132-178, 201-208, 216-223, 238-266, 269-295, 297-304, 337-342, 347-356, 374-401, 403-422, 440-447, 478-504, 510-516, 519-530, 537-544 and 191-206 of Seq ID No 318; 12-40, 42-48, 66-71, 77-86, 95-102, 113-120, 129-137, 141-148, 155-174, 208-214, 218-225, 234-240, 256-267, 275-283, 300-306, 313-321, 343-350, 359-367, 370-383, 398-405, 432-439, 443-461, 492-508, 516-526, 528-535 and 370-478 of Seq ID No 319; 6-14, 20-37, 56-62, 90-95, 97-113, 118-125, 140-145, 161-170, 183-202, 237-244, 275-284, 286-305, 309-316, 333-359, 373-401, 405-412 and 176-187 of Seq ID No 320; 33-44, 50-55, 59-80, 86-101, 129-139, 147-153, 157-163, 171-176, 189-201, 203-224, 239-245, 257-262, 281-287, 290-297, 304-320, 322-331, 334-350, 372-390, 396-401, 71-88 and 353-372 of Seq ID No 321; 5-11, 15-24, 26-33, 40-47, 75-88, 95-103, 105-112 and 17-30 of Seq ID No 322; 5-11, 16-39, 46-54, 62-82, 100-107, 111-124, 126-150, 154-165, 167-183, 204-238, 245-295, 301-313, 316-335 and 8-16 of Seq ID No 323; 4-19, 34-48, 69-74, 79-107, 115-127, 129-135, 143-153, 160-169, 171-182 and 142-153 of Seq ID No 324; 4-30, 65-74, 82-106, 110-120, 124-132, 135-140, 146-175, 179-184, 190-196, 217-223, 228-233, 250-267, 275-292, 303-315, 322-332 and 174-186 of Seq ID No 325; 9-16, 29-41, 47-57, 68-84, 87-109, 113-119, 162-180, 186-193, 195-201, 203-208, 218-230, 234-243, 265-271, 281-292, 305-312, 323-332, 341-347, 349-363, 368-374, 383-390, 396-410, 434-440, 446-452, 455-464, 466-473, 515-522, 529-542, 565-570, 589-600, 602-613, 618-623, 637-644, 1019-1027, 1238-1244, 1258-1264, 1268-1276, 1281-1292, 1296-1302 and 883-936 of Seq ID No 326; 10-17, 23-32, 39-44, 54-72, 75-81, 88-111, 138-154, 160-167, 178-185, 201-210, 236-252, 327-334, 336-342, 366-376, 388-400, 410-430, 472-482, 493-526, 552-558, 586-592, 598-603, 612-621, 630-635, 641-660 and 384-393 of Seq ID No 327; 4-22, 24-39, 50-59, 73-84, 100-105, 111-117, 130-138, 155-161, 173-178, 182-189, 205-215, 266-284, 308-313, 321-328, 330-337, 346-363, 368-374, 388-395,

397-405, 426-434, 453-459, 482-492, 501-507, 509-515, 518-523, 527-544, 559-590, 598-612, 614-629, 646-659, 663-684, 686-694, 698-721 and 445-461 of Seq ID No 328; 14-22, 27-33 and 3-17 of Seq ID No 329; 29-41, 66-73, 81-87, 90-108, 140-146, 150-159, 165-184, 186-196, 216-226, 230-238, 247-253, 261-269 and 126-140 of Seq ID No 330; 5-12, 16-25, 27-33, 36-45, 60-68, 83-88, 103-126 and 86-101 of Seq ID No 331; 14-23, 36-47, 56-66, 84-89, 94-105, 111-127, 140-153, 160-174, 176-183, 189-203, 219-225, 231-237, 250-257 and 194-227 of Seq ID No 332; 4-25, 54-60, 64-71, 73-82, 89-106, 117-124, 157-169, 183-188, 199-210, 221-232, 236-244, 255-264 and 58-98 of Seq ID No 333; 13-19, 26-36, 41-53, 55-71, 77-84, 86-108, 114-135, 157-172, 177-183, 187-194, 208-213, 218-226, 110-125 and 156-170 of Seq ID No 334; 5-24, 63-69, 77-85, 94-112, 120-137, 140-146, 152-159, 166-172, 179-187, 193-199, 206-212, 222-228, 234-240, 244-252, 257-264, 270-289, 298-309, 316-328, 337-348, 363-375, 1-56 and 340-352 of Seq ID No 335; 18-39, 42-71, 78-120, 124-144, 152-173, 179-189, 199-209, 213-222, 228-258, 269-304, 329-361, 364-372, 374-389, 396-441 and 313-327 of Seq ID No 336; 19-25, 91-98, 108-120, 156-162, 168-174, 191-204, 211-216, 232-266, 272-278, 286-308, 316-321, 327-333, 344-355, 358-364, 384-391, 395-428, 464-476, 487-495, 497-511, 544-561, 563-573, 575-582, 588-594, 10-25 and 322-338 of Seq ID No 337; 14-26, 32-49, 51-57, 59-72, 80-91, 102-112, 119-125, 147-161, 164-173, 175-183, 188-213, 217-222, 246-254, 260-276, 282-303, 308-318, 321-328, 333-350, 352-359, 371-378, 392-401, 407-414, 416-443, 448-463, 471-484, 490-497, 501-514, 519-527, 539-551, 557-570, 578-590, 592-598, 600-610, 618-629, 633-647, 654-667, 676-689, 702-709, 718-726, 728-737, 741-760, 764-780, 786-795, 808-826, 836-842, 845-852, 865-874, 881-887, 931-945, 949-957, 968-974, 979-986, 1003-1009, 1023-1029 and 90-103 of Seq ID No 338; 11-16, 37-56, 60-66, 69-77, 80-88, 93-106, 117-139, 166-171 and 72-90 of Seq ID No 339; 59-84, 123-133, 145-150, 161-167, 178-189 and 115-128 of Seq ID No 340; 15-33, 39-46, 52-64, 74-87, 108-124, 127-144, 150-156, 173-179, 184-194, 201-208, 219-236, 243-269, 272-295, 302-309, 343-349, 356-361, 370-379, 405-411, 414-423, 430-451, 457-464, 466-475, 477-483, 496-502, 507-522, 541-548, 557-563, 571-577, 579-585, 590-605, 626-642, 650-662, 671-691, 704-710, 751-769, 775-781, 786-791, 794-829, 851-858, 868-878, 884-904, 913-919, 931-939 and 132-142 of Seq ID No 341; 33-58, 64-71, 74-80, 83-88, 96-120, 122-139, 146-157, 167-177, 207-213, 220-225, 236-242, 264-279, 300-305, 326-336, 340-347, 350-360, 97-115 and 199-211 of Seq ID No 342; 4-26, 43-57, 70-99, 102-117, 121-133, 142-148, 151-168, 170-183, 192-220, 235-249, 258-279 and 30-41 of Seq ID No 343; 34-42, 48-58, 70-94, 110-130, 154-160, 164-172, 178-183, 195-203, 211-222, 229-250, 256-261, 274-284, 286-292, 312-323 and 222-233 of Seq ID No 344; 4-9, 15-36, 38-45, 49-74, 78-88, 100-112, 136-191, 211-220, 226-233, 239-246, 254-274, 287-307, 316-322, 342-353, 356-366, 373-378, 384-393, 405-431, 449-457, 459-468, 487-511, 515-524, 529-541, 544-552, 562-568, 571-576 and 208-280 of Seq ID No 345; 10-27, 31-37, 39-54, 71-108, 124-143 and 2-107 of Seq ID No 346; 16-27, 38-57, 64-70, 90-102, 104-113, 116-137, 160-166 and 1-80 of Seq ID No 347; 13-21, 31-36, 56-67, 127-136, 153-171, 173-180, 184-200, 214-222, 225-231, 239-263, 267-273 and 135-159 of Seq ID No 348; 12-27, 31-51, 68-74, 77-87, 94-101, 108-114, 117-123, 127-134, 138-168, 173-196, 201-207, 212-217, 227-237, 247-257, 264-280 and 205-223 of Seq ID No 349; 17-22, 25-54, 70-76, 92-100 and 98-110 of Seq ID No 350; 7-29, 40-50, 60-67, 87-96, 105-111, 119-164, 172-199, 206-212, 220-227, 237-259, 272-279, 282-293, 295-309, 313-319, 321-328, 345-363, 376-386 and 159-176 of Seq ID No 351; 4-19, 24-30, 36-43, 50-68, 71-89, 93-106, 141-152, 154-172, 179-197, 199-215, 229-239, 246-252, 255-263, 281-298, 319-325, 329-356, 358-368, 374-390, 397-409, 420-429, 432-444, 450-456, 459-475, 483-494, 496-502, 520-528, 532-556 and 362-377 of Seq ID No 352; 18-25, 40-62, 77-85, 91-97, 105-116, 123-133, 139-184, 189-197 and 122-140 of Seq ID No 353; 4-49, 52-58, 62-70, 79-105, 109-133, 142-150, 163-168, 206-214, 220-228, 233-240, 243-254, 274-281, 303-311, 327-338, 357-373, 378-396, 403-413, 420-436, 441-453, 461-467, 475-481, 484-498, 506-512, 514-521, 523-529, 562-579, 589-595, 598-603, 615-648, 714-722, 728-742, 749-758, 777-792, 795-807 and 643-658 of Seq ID No 354; 8-27, 37-48, 51-56, 72-79, 87-106, 120-138, 140-147, 167-176, 187-197, 205-216, 222-229, 234-239, 243-249, 277-288, 292-315, 334-343, 347-353, 363-391, 398-404, 430-447, 461-467, 478-492, 498-507 and 456-470 of Seq ID No 355; 5-12, 18-24, 59-69, 80-93, 95-109, 119-125, 130-137, 139-147, 158-163, 168-176, 182-202, 206-215, 222-239, 241-249, 267-277, 291-298, 311-318, 321-327, 338-344, 348-355, 373-386, 393-406, 411-417, 434-443, 446-465, 473-484, 514-521, 532-553, 584-594 and 221-237 of Seq ID No 356; 4-14, 27-34, 50-58, 63-72, 79-106, 109-114, 121-142, 146-154, 161-167, 169-175, 178-201, 223-238, 249-254, 259-264, 278-292, 294-312, 319-330 and 167-191 of Seq ID No 357; 7-28, 36-42, 50-61, 63-80, 122-

152, 161-174, 176-191 and 140-190 of Seq ID No 358; 20-57, 59-65, 70-78, 86-102, 119-133, 142-161, 163-173, 177-188, 192-202, 204-220, 222-236, 240-253, 279-319, 326-331, 337-383, 390-399, 406-412, 420-427, 431-438 and 381-395 of Seq ID No 359; 13-18, 28-34, 37-43, 50-59, 75-81, 83-97, 105-121, 139-147, 200-206, 209-227, 231-247, 260-271, 318-327, 366-381, 388-394, 399-406 and 182-201 of Seq ID No 360; 6-29, 37-43, 51-56, 70-77, 82-102, 110-119, 127-143, 178-190, 201-209, 216-243, 261-269, 281-292, 305-313, 327-339, 341-354, 356-373, 391-397, 423-429, 438-445, 450-478 and 21-314 of Seq ID No 361; 4-12, 15-21, 32-41, 59-76, 80-89, 96-104 and 90-103 of Seq ID No 362; 9-28, 30-41, 44-54, 69-74, 77-82, 90-97, 104-123, 125-135, 149-155, 164-173, 177-184, 217-226, 230-235, 238-244, 258-272, 282-297, 300-305, 309-315, 317-322, 327-336, 348-362, 368-374, 380-387, 400-411, 414-424, 451-458, 460-466, 483-494, 497-503, 506-511, 521-528, 540-553, 569-587, 598-606, 628-642, 661-681, 688-700, 718-733, 740-749, 752-764, 769-783, 823-834, 848-854, 862-872, 878-884, 886-898, 915-920, 938-951, 954-961, 963-972, 982-989, 996-1003, 1010-1016, 1021-1032, 1038-1044, 1047-1057, 1060-1070, 1079-1088, 1094-1102, 1117-1127, 1129-1135, 1142-1153, 1158-1204, 1212-1229, 1234-1263, 1269-1277, 1308-1313, 1327-1338, 1344-1376, 1400-1415, 1436-1443, 1448-1458, 1497-1504, 1511-1522, 1544-1566, 3-82 and 509-576 of Seq ID No 363; 8-36, 40-64, 71-79, 88-94, 102-109, 118-127, 138-148, 151-159, 163-174, 192-198, 200-206, 220-233, 268-273, 290-301, 304-309, 316-323, 331-349, 378-391, 414-420, 427-437, 455-475, 494-510, 541-547, 549-555, 616-640, 1-60, 55-139, 212-308, 386-458 and 458-624 of Seq ID No 364; 16-31, 35-42, 70-77, 91-101, 120-130, 132-140, 143-153, 185-190, 195-202, 215-222, 228-238, 241-251, 257-264, 268-277, 288-302, 312-324, 326-333, 341-348, 364-382, 415-429, 438-454, 458-466, 491-499, 501-521 and 273-281 of Seq ID No 365; 8-14, 32-57, 74-149, 155-177, 179-212, 221-266, 271-296, 304-324, 329-346, 349-359, 368-401, 413-419, 426-454, 465-478, 493-510 and 466-490 of Seq ID No 366; 22-28, 33-51, 64-89, 96-119, 126-132, 138-146, 152-159, 161-169, 172-179, 193-198, 205-211, 221-231, 235-254, 273-280, 297-303, 312-320, 328-346, 351-373, 378-384, 391-398, 448-454, 460-468, 470-481, 516-558, 574-593, 597-602, 613-623, 626-646, 649-656, 668-673, 675-683, 696-708, 715-722, 724-739, 745-751, 759-777, 780-804, 816-822 and 102-113 of Seq ID No 367; 12-28, 41-91, 98-107, 112-120, 125-131, 151-193, 215-221, 240-250, 263-280 and 128-138 of Seq ID No 368; 16-24, 32-38, 46-62, 68-81, 90-105, 127-133, 144-150, 160-166, 178-184, 186-202, 210-219, 232-240, 252-258, 264-273, 293-324, 337-344, 349-357, 360-369, 385-398, 410-416, 419-427, 441-449, 458-476, 508-515, 523-539, 544-549, 562-569, 571-579, 96-109 and 127-139 of Seq ID No 369; 19-25, 28-34, 56-61, 85-97, 110-116 and 39-53 of Seq ID No 370; 4-37, 41-50, 62-72, 91-97, 99-109, 114-125, 136-141, 149-158, 160-166, 201-215 and 27-225 of Seq ID No 371; 15-31, 44-51, 96-105, 122-130, 149-157, 162-168, 178-183, 185-192, 198-204, 206-213, 221-234, 239-245, 248-255, 257-266, 289-335, 349-357, 415-422, 425-441, 448-454, 462-468 and 463-481 of Seq ID No 372; 5-31, 39-55, 63-72, 76-99, 106-155, 160-177, 179-199, 207-217, 223-240, 245-255, 261-267, 294-316, 321-343, 354-378, 382-452, 477-488, 529-536, 555-569, 584-591, 593-612, 620-627, 632-640, 647-654, 671-680, 698-704, 723-730, 732-750, 769-775, 781-788, 822-852 and 505-525 of Seq ID No 373; 3-18 of Seq ID No 374; 4-14 and 12-24 of Seq ID No 375; 4-11, 22-30 and 12-25 of Seq ID No 376; 5-12 and 4-18 of Seq ID No 377; 4-28 and 7-14 of Seq ID No 378; 6-16 and 8-16 of Seq ID No 379; 4-15, 18-33 and 24-36 of Seq ID No 380; 4-10, 16-21 and 20-31 of Seq ID No 381; 6-19 of Seq ID No 382; 11-18 and 3-10 of Seq ID No 383; 13-24 and 3-15 of Seq ID No 384; 15-27 and 7-16 of Seq ID No 385; 11-16 and 1-15 of Seq ID No 386; 4-16 and 9-21 of Seq ID No 387; 4-24, 40-48, 54-67 and 22-39 of Seq ID No 388; 6-30, 34-55, 62-68, 78-106 and 68-74 of Seq ID No 389; 3-14 of Seq ID No 390; 9-19 and 6-21 of Seq ID No 391; 4-17 and 1-9 of Seq ID No 392; 5-30 and 1-8 of Seq ID No 393; 4-16, 23-46, 51-56 and 45-55 of Seq ID No 394; 7-16 of Seq ID No 395; 2-14 of Seq ID No 396; 4-36, 43-65 and 50-62 of Seq ID No 397; 10-30 and 14-21 of Seq ID No 398; 9-17 and 1-10 of Seq ID No 399; 4-12 and 3-16 of Seq ID No 400; 4-15 and 5-23 of Seq ID No 401; 10-21 of Seq ID No 402; 6-16 of Seq ID No 403; 4-29, 31-38 and 2-14 of Seq ID No 404; 4-35 and 33-42 of Seq ID No 405; 2-17 of Seq ID No 406; 9-18, 30-35 and 15-33 of Seq ID No 407; 4-9 and 6-12 of Seq ID No 408; 3-17 of Seq ID No 409; 12-21, 37-44, 52-61, 72-80 and 38-48 of Seq ID No 410; 4-10, 29-44, 54-61, 69-78 and 13-27 of Seq ID No 411; 13-23, 36-53 and 2-15 of Seq ID No 412; 4-25, 28-46, 56-72, 81-99, 120-132, 134-142, 154-160 and 129-141 of Seq ID No 413; 4-15, 24-33, 35-41, 64-86 and 21-33 of Seq ID No 414; 9-15 and 4-13 of Seq ID No 415; 4-11, 13-19, 34-48 and 15-32 of Seq ID No 416; 4-21 and 11-31 of Seq ID No 417; 23-57 and 38-50 of Seq ID No 418; 4-32 and 3-13 of Seq ID No 419; 4-10, 13-25, 32-42, 56-68, 72-84 and 26-38 of

Seq ID No 420; 4-20, 31-48, 52-58, 65-71, 80-93, 99-108, 114-123 and 37-49 of Seq ID No 421; 6-12, 14-20 and 3-25 of Seq ID No 422; 14-25, 27-38 and 5-14 of Seq ID No 423; 4-41, 57-105, 109-118, 123-136, 144-152 and 86-99 of Seq ID No 424; 6-19 of Seq ID No 425; 2-19 of Seq ID No 426; 14-47 and 1-14 of Seq ID No 427; 4-21, 29-44 and 2-18 of Seq ID No 428; 23-29 and 10-28 of Seq ID No 429; 6-16, 22-36 and 11-22 of Seq ID No 430; 4-19, 30-44 and 18-27 of Seq ID No 431; 5-15, 37-45, 58-65 and 38-47 of Seq ID No 432; 4-15, 23-34 and 4-15 of Seq ID No 433; 30-36, 44-54, 79-85, 101-114, 138-152, 154-164, 170-175, 179-200, 213-220, 223-240, 243-255, 258-264, 268-284 and 10-28 of Seq ID No 434; the peptides comprising amino acid sequences of column "Identical region" of the Table 1B, especially peptides comprising amino acid 210-226 and 738-753 of Seq ID No 449; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 450; 893-906 of Seq ID No 451; 51-69 of Seq ID No 452; 110-125 of Seq ID No 453; 291-305 of Seq ID No 454; 210-226 and 738-753 of Seq ID No 455; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 456; 893-906 of Seq ID No 457; 51-69 of Seq ID No 458; 110-125 of Seq ID No 459; 291-305 of Seq ID No 460; 32-44 of Seq ID No 461; 399-410 of Seq ID No 462; the serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 2, especially peptides comprising amino acid 120-143, 138-161 and 156-179 of Seq ID No 218; 110-129 and 168-184 of Seq ID No 219; 74-90 of Seq ID No 222; 759-773 of Seq ID No 223; 237-260 of Seq ID No 224; 265-284 of Seq ID No 225; 65-74 of Seq ID No 226; 41-50 of Seq ID No 227; 163-174 of Seq ID No 229; 26-37 of Seq ID No 230; 174-189 of Seq ID No 232; 240-256 of Seq ID No 234; 285-297 of Seq ID No 236; 238-247 of Seq ID No 238; 491-519 of Seq ID No 239; 114-140 of Seq ID No 243; 267-284 of Seq ID No 250; 439-453 of Seq ID No 252; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 60-71 of Seq ID No 256; 244-257 of Seq ID No 257; 44-63 and 57-76 of Seq ID No 258; 185-196 of Seq ID No 260; 119-129 of Seq ID No 263; 182-195 of Seq ID No 266; 32-44 and 424-442 of Seq ID No 267; 247-256 of Seq ID No 268; 678-694, 785-805, 55-77 and 72-94 of Seq ID No 269; 210-226 of Seq ID No 281; 37-59 of Seq ID No 289; 13-29 of Seq ID No 296; 136-159 of Seq ID No 348; 205-222 of Seq ID No 349; 99-110 of Seq ID No 350; 160-176 of Seq ID No 351; 457-470 of Seq ID No 355; 221-237 of Seq ID No 356; 167-190 of Seq ID No 357; 96-120 of Seq ID No 361; 399-417, 503-519 and 544-563 of Seq ID No 364; 46-68, 159-183 and 184-198 of Seq ID No 371; 463-481 of Seq ID No 372; the immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 4; especially peptides comprising amino acid 110-129 and 168-184 of Seq ID No 219; 877-901, 333-354, 326-344 and 801-809 of Seq ID No 277; 1-54 of Seq ID No 347; 544-563, 31-51, 107-119, 399-417 and 503-519 of Seq ID No 364; 120-198 of Seq ID No 218; 20-35 of Seq ID No 219; 118-201 of Seq ID No 221; 48-132 of Seq ID No 242; 118-136 of Seq ID No 249; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 50-76 of Seq ID No 258; 785-819 and 44-128 of Seq ID No 269; 90-128 of Seq ID No 274; 314-384 of Seq ID No 289; 327-349 of Seq ID No 293; 242-314, 405-478 and 23-100 of Seq ID No 304; 129-210 of Seq ID No 305; 162-188 of Seq ID No 307; 750-772 of Seq ID No 310; 1-56 of Seq ID No 335; 322-337 of Seq ID No 337; 72-90 of Seq ID No 339; 374-395 of Seq ID No 345; 136-159 of Seq ID No 348; 141-164 of Seq ID No 358; 96-157 of Seq ID No 361; 1-82 of Seq ID No 363; 489-556 of Seq ID No 364; 159-183 and 49-133 of Seq ID No 371.

15. A process for producing a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising expressing the nucleic acid molecule according to any one of claims 1 to 7.
16. A process for producing a cell, which expresses a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising transforming or transfecting a suitable host cell with the vector according to claim 8 or claim 9.
17. A pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of claims 11 to 14 or a nucleic acid molecule according to any one of claims 1 to 7.

18. A pharmaceutical composition, especially a vaccine, according to claim 17, characterized in that it further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, neuroactive compounds, especially human growth hormone, albumin, Freund's complete or incomplete adjuvants or combinations thereof.
19. Use of a nucleic acid molecule according to any one of claims 1 to 7 or a hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *S. agalactiae* infection.
20. An antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.
21. An antibody according to claim 20, wherein the antibody is a monoclonal antibody.
22. An antibody according to claim 20 or 21, wherein said effective part comprises Fab fragments.
23. An antibody according to any one of claims 20 to 22, wherein the antibody is a chimeric antibody.
24. An antibody according to any one of claims 20 to 23, wherein the antibody is a humanized antibody.
25. A hybridoma cell line, which produces an antibody according to any one of claims 20 to 24.
26. A method for producing an antibody according to claim 20, characterized by the following steps:
 - initiating an immune response in a non-human animal by administering an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 11 to 14, to said animal,
 - removing an antibody containing body fluid from said animal, and
 - producing the antibody by subjecting said antibody containing body fluid to further purification steps.
27. Method for producing an antibody according to claim 21, characterized by the following steps:
 - initiating an immune response in a non-human animal by administering an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 12 to 15, to said animal,
 - removing the spleen or spleen cells from said animal,
 - producing hybridoma cells of said spleen or spleen cells,
 - selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
 - producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.
28. Use of the antibodies according to any one of claims 20 to 24 for the preparation of a medicament for treating or preventing *S. agalactiae* infections.
29. An antagonist, which binds to the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

30. A method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 comprising:
 - a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
 - b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.
31. A method for identifying an antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 to its interaction partner comprising:
 - a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to any one of claims 11-14,
 - b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to any one of the claims 20 to 24,
 - c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form an interaction complex,
 - d) providing a candidate antagonist,
 - e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
 - f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.
32. Use of any of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.
33. A process for *in vitro* diagnosing a disease related to expression of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11-14.
34. A process for *in vitro* diagnosis of a bacterial infection, especially a *S. agalactiae* infection, comprising analysing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14.
35. Use of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is selected from the group comprising anticalines.
36. Use of the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and Spiegelmers.
37. Use of a nucleic acid molecule according to any one of claims 11 to 14 for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

Summary:

The present invention discloses isolated nucleic acid molecules encoding a hyperimmune serum reactive antigen or a fragment thereof as well as hyperimmune serum reactive antigens or fragments thereof from *S. agalactiae*, methods for isolating such antigens and specific uses thereof.

[no Fig. on front page]

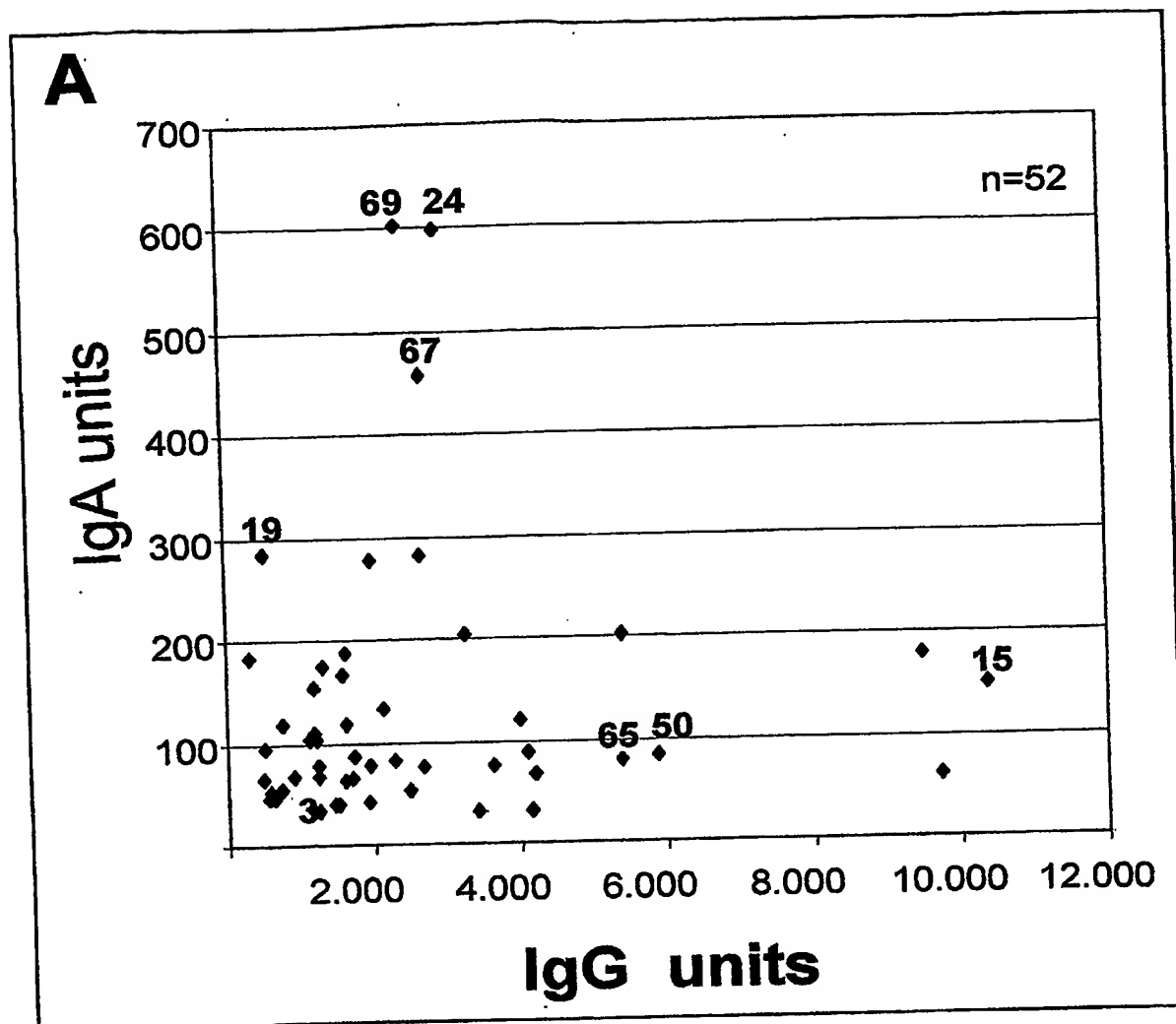


Fig. 1

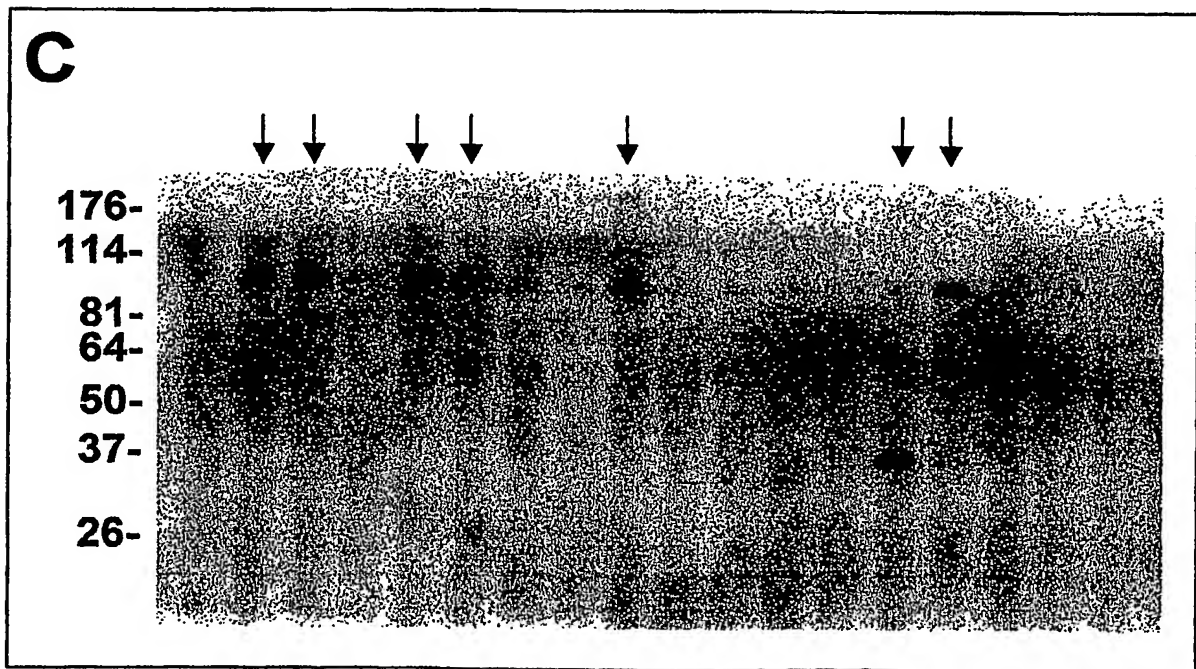
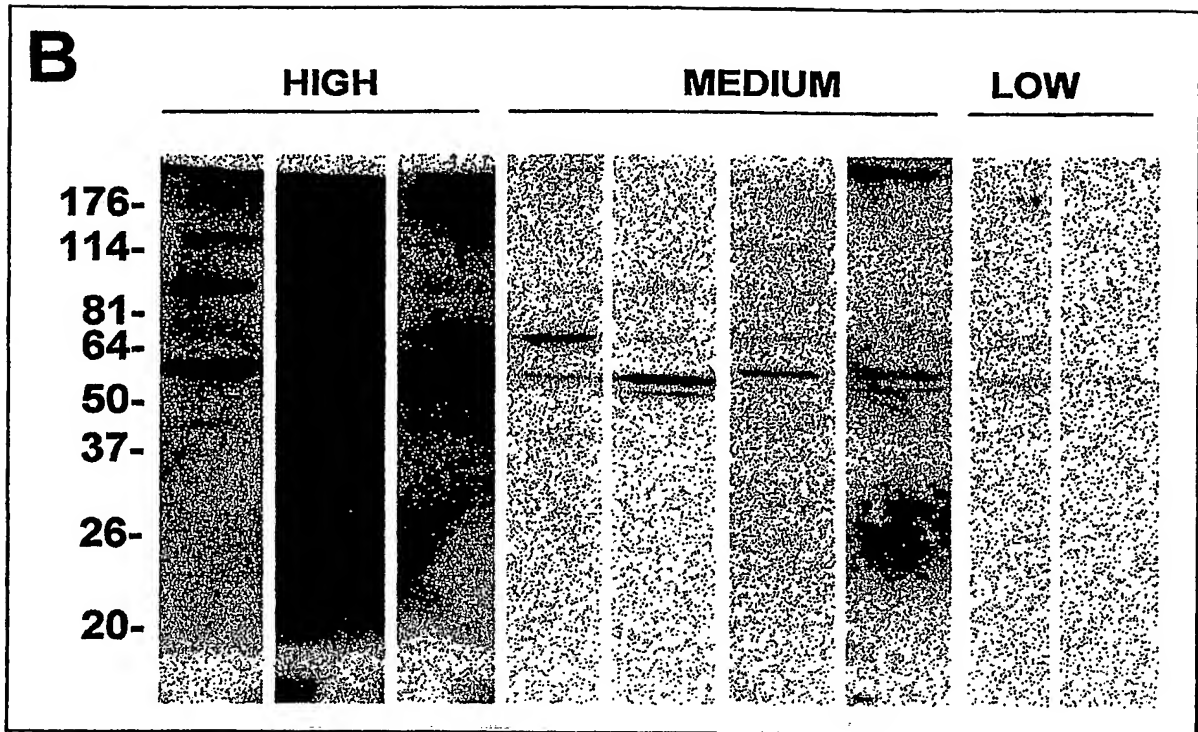


Fig. 1

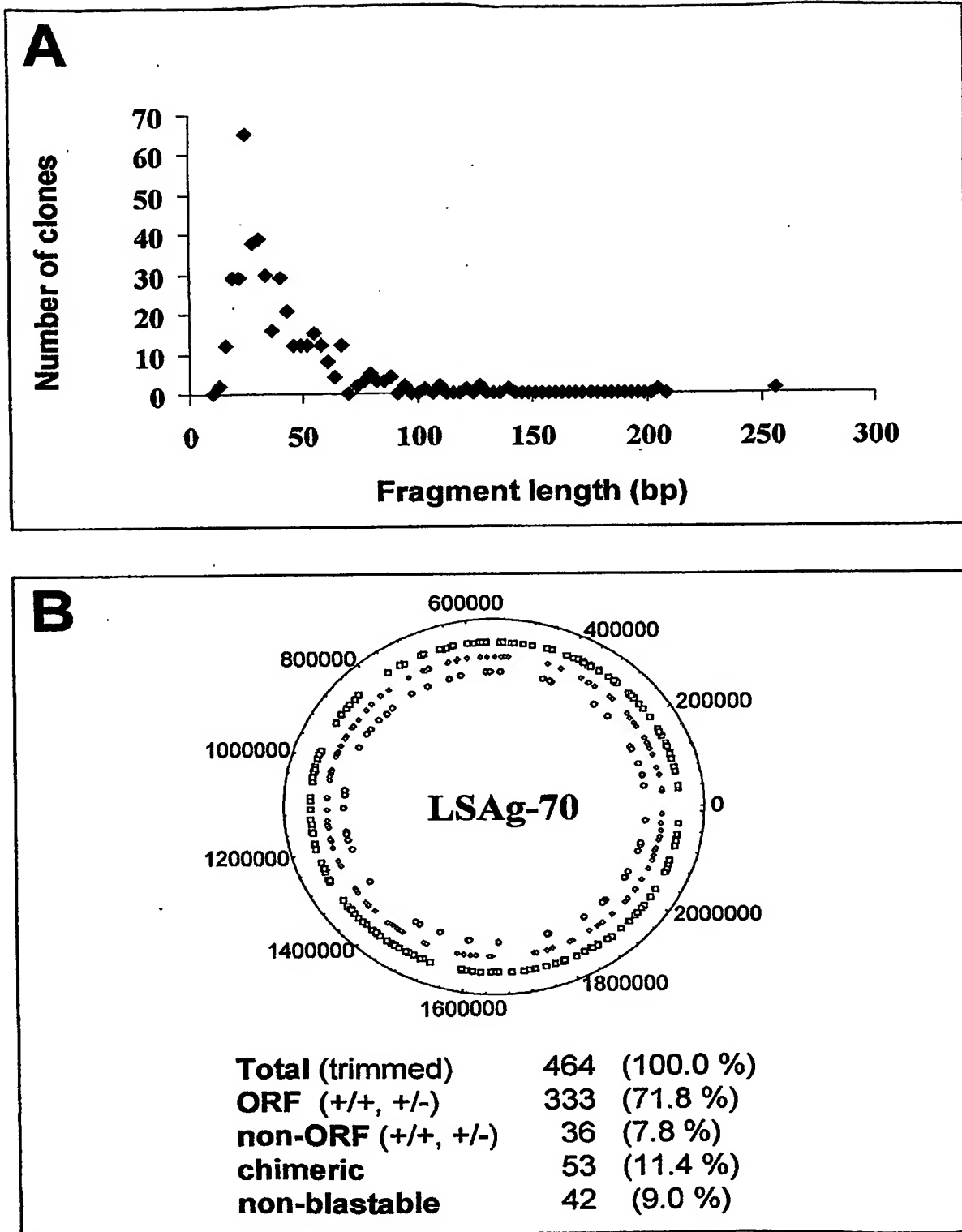


Fig. 2

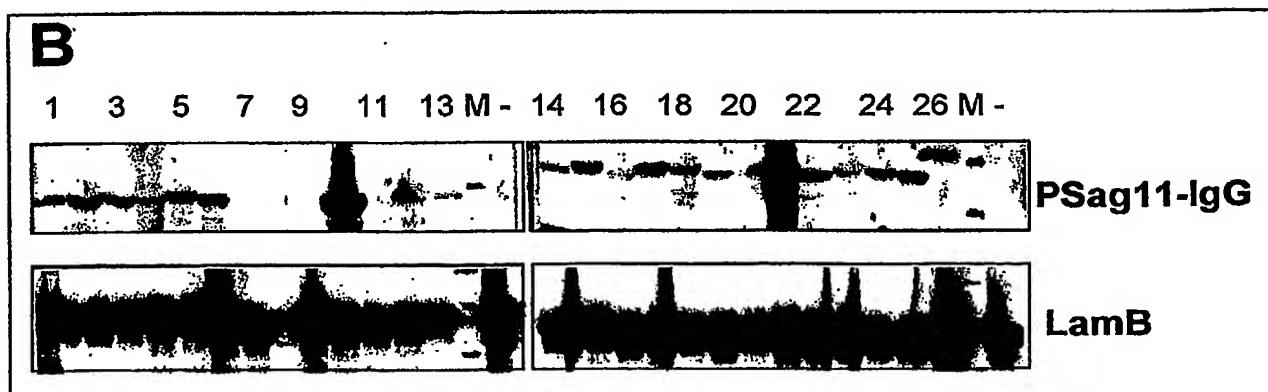
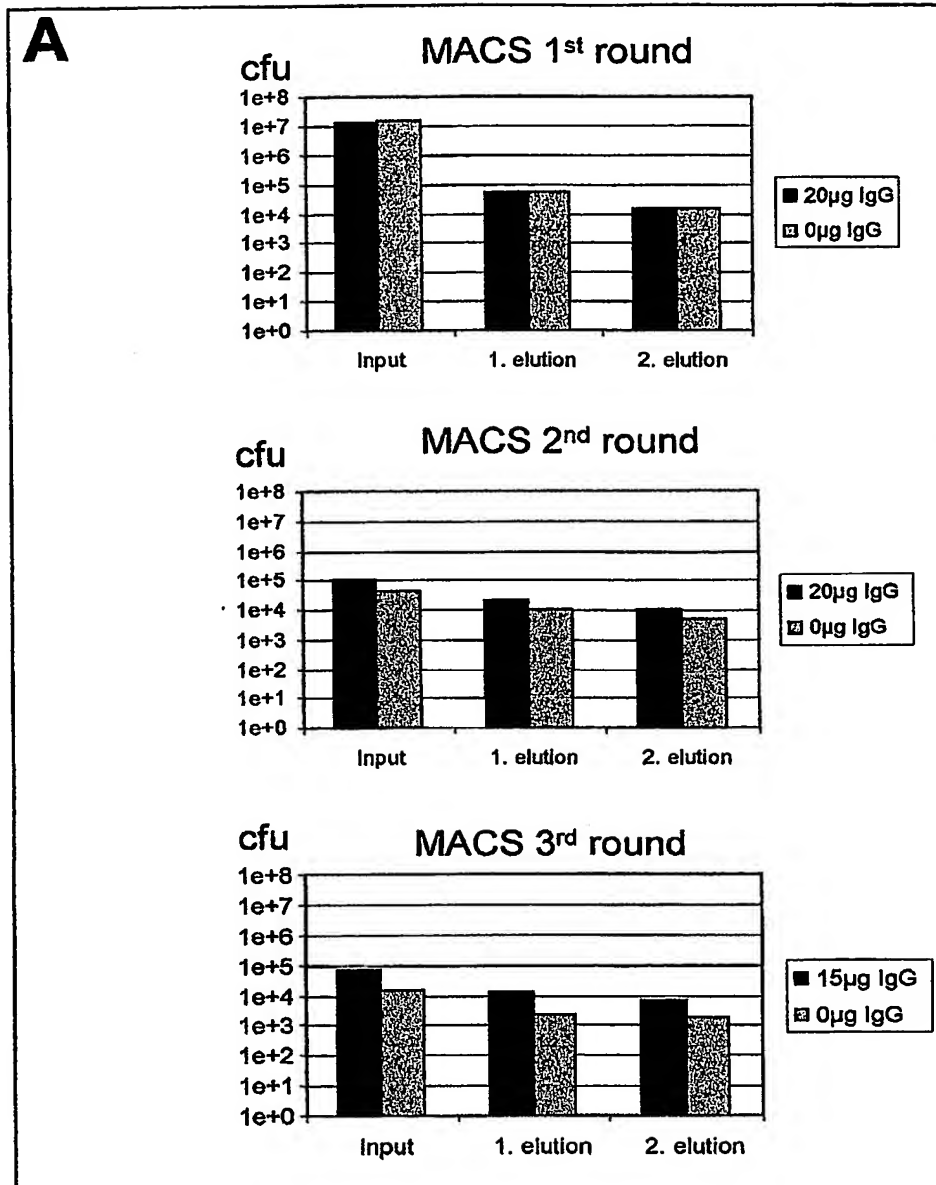


Fig. 3

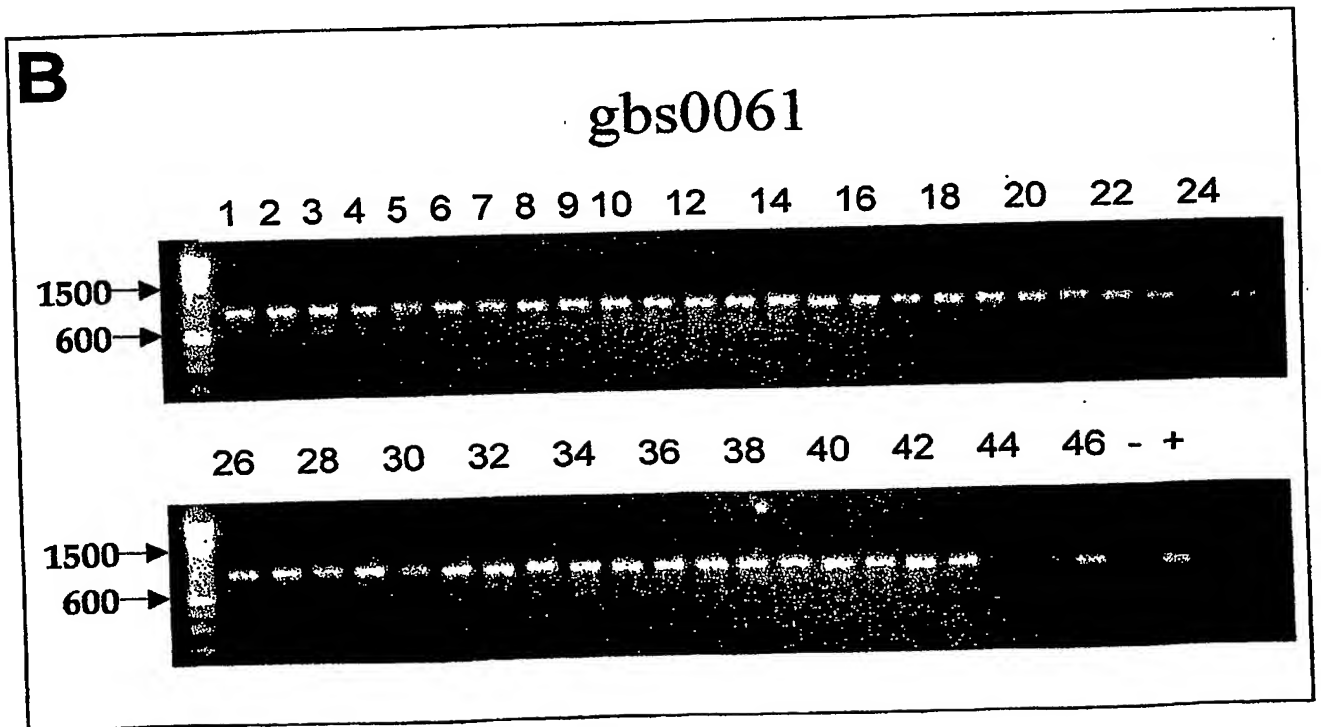
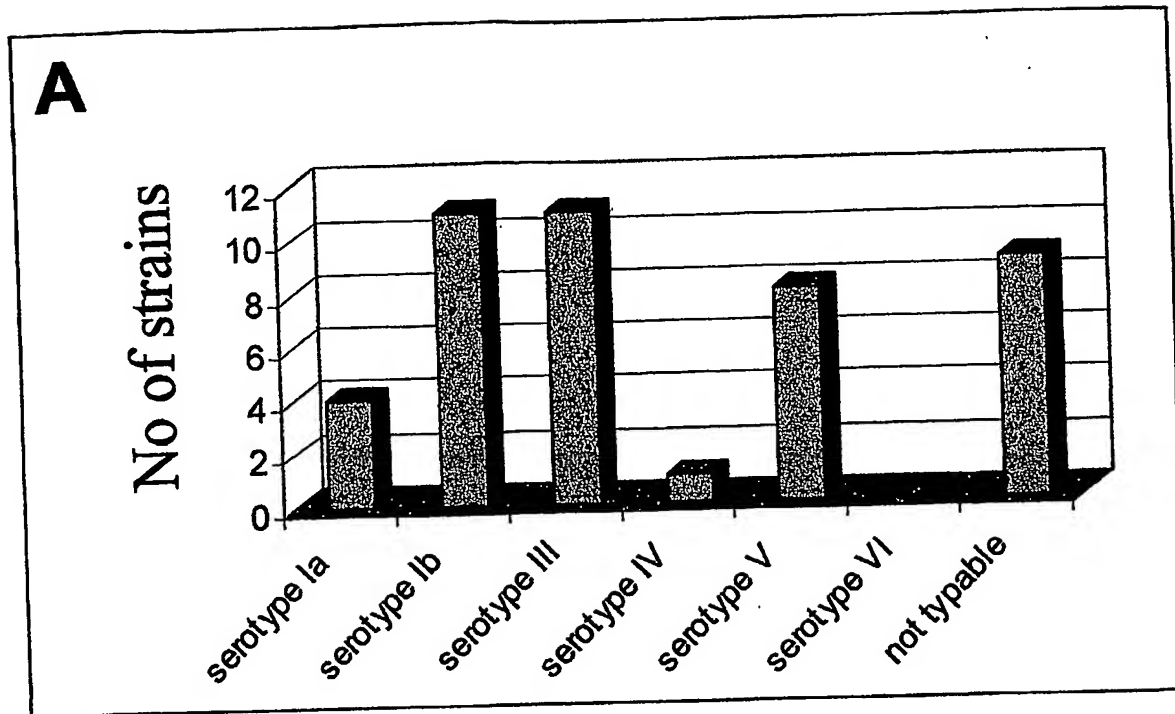


Fig. 4

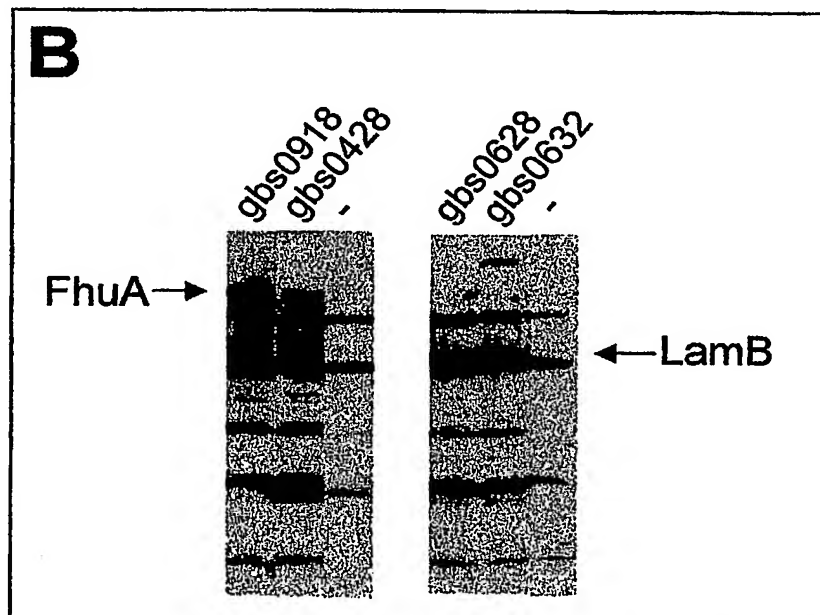
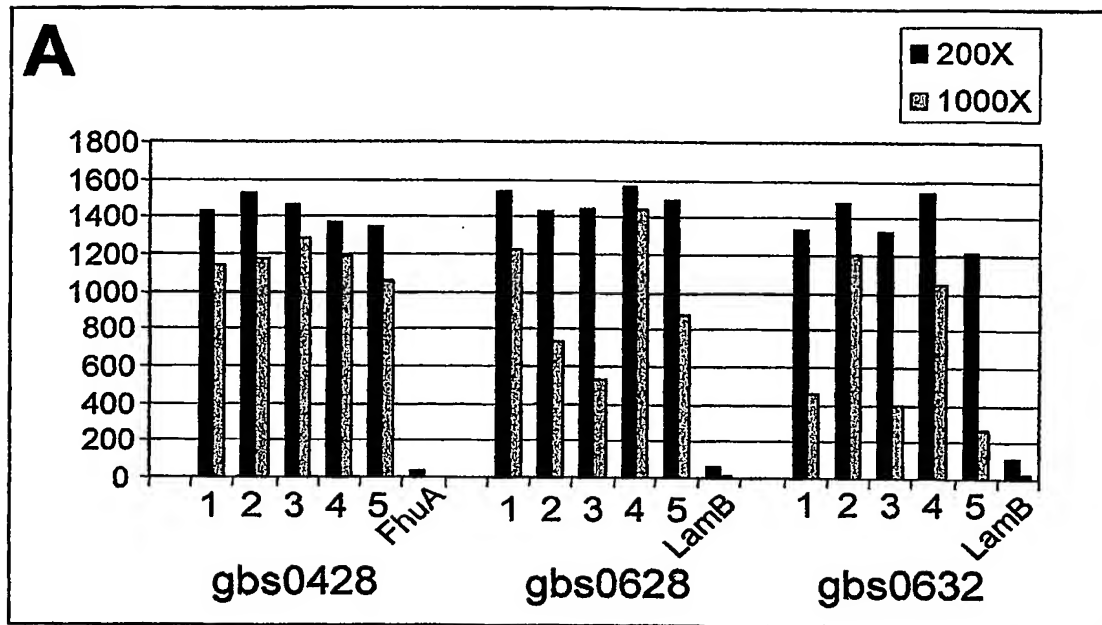


Fig. 5

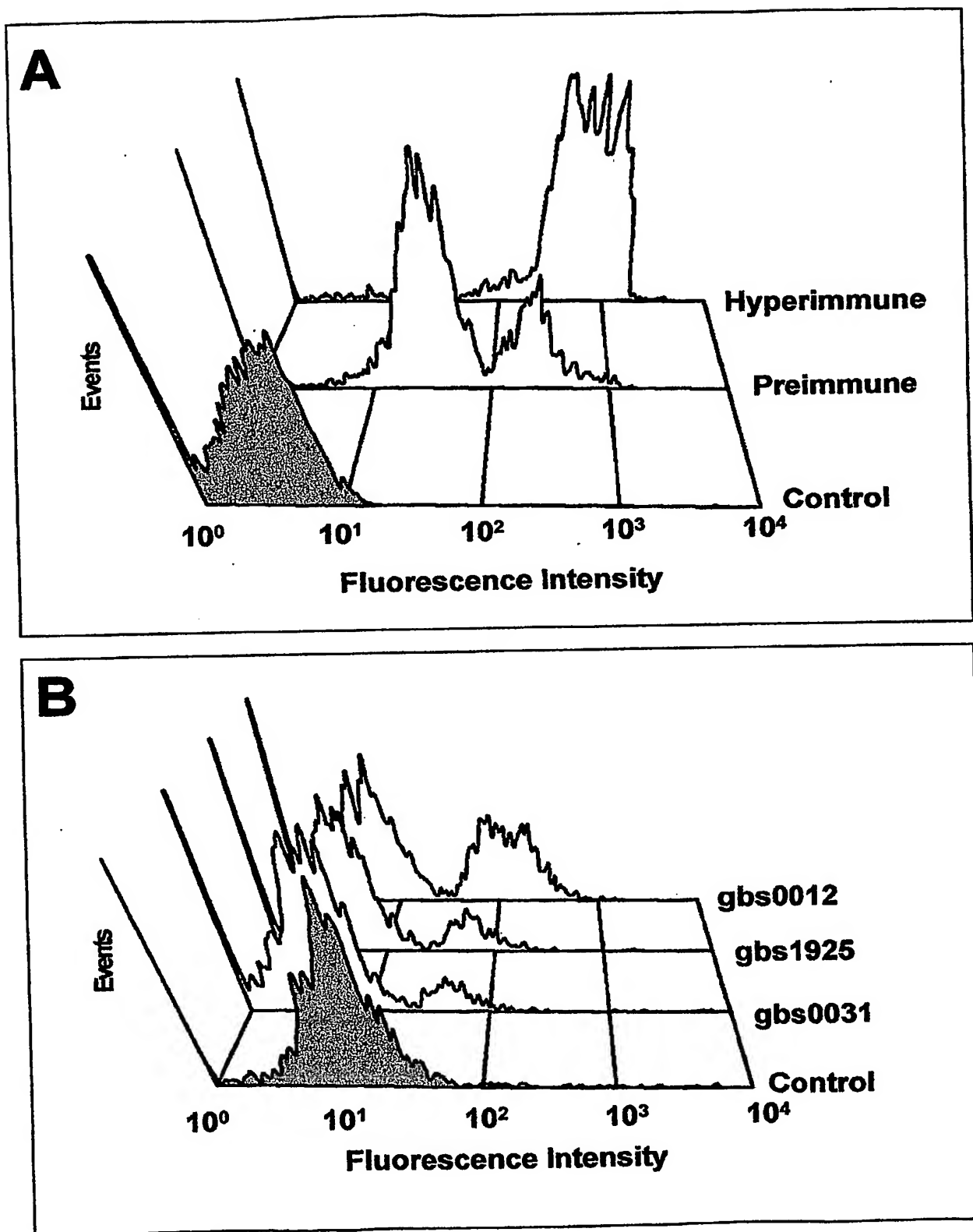


Fig. 6

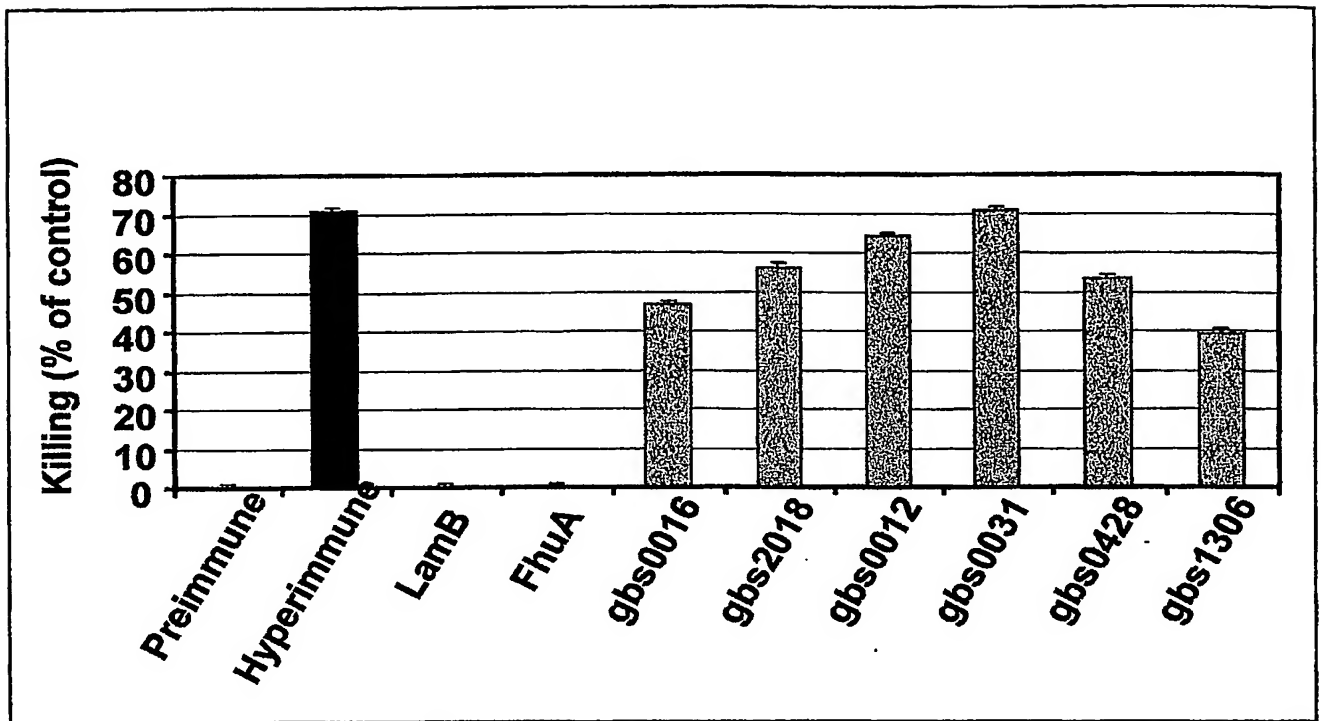


Fig. 7

GBS patentin.ST25
SEQUENCE LISTING

<110> Interce11 AG

<120> GBS antigens

<130> GBS-50

<160> 462

<170> PatentIn version 3.1

<210> 1

<211> 1287

<212> DNA

<213> Streptococcus agalactiae

```

<400> 1
atgaagaaag ttttaacctt cttattatgt agcttatatt ttgtatcaat cccagctata      60
agtaccgagg agccattaac gctttctcaa aatagacgat acgccttaac tcagacagtt      120
gtggataagg aaatgtatgt tgatgctatt ccagagagac caactacaaa aattgaaata      180
agcagttttc aagatgaagc ttttaaccata acaggagaga ctttagttcc aaatacttta      240
ttgtcgattg tttctcttac aattaattca aatggaattc cagtatttac ttgtccaat      300
ggacagttca taaaggctag tcgtgaagct atttttaatg atttagtttc taagcagcaa      360
tctgtctcat tggattattg gttaaaacct tcttttgtga cttatgaagc accttacaca      420
aatggtgtta gtgaagttaa aaataattta aaaccttatt ccagagtgc a tttagtagaa      480
caagcagaaa cagaacatgg tatattattat aaaacggaca gtgggttttg gatatcagta      540
gaagatctat cggttgctga taatcgtatg gctaagggtc aagaagtatt attggaaaaa      600
tataataaag ataaatatgg tatatacatc aaacaattaa atacacagac agtagctggt      660
attaatatgg ataggtcaat gtactctgca agtattgcaa aattagcaac actttatgct      720
agccaagagc aagtaaaatt aggaaaactg tcattggaca gcaaatttga atacaaagat      780
aatgttaatc aatttcctaa tagctatgat ccaagtggta gtgggaaatt agagaaaaaa      840
gctgatcata aattatatac cgttaaggag ttacttgaag caactgccaa ggaatcagat      900
aatgttgcaa caaatatgct aggttattat gtcaataatc aatatgattc aatgtttcaa      960
acacaagtag acacaatttc tggtatgcac tgggatatga aaaaacgcca gatttctcca     1020

```


GBS patentin.ST25

caagctgcgg gtaaaatgat ggaagcaatt tattatcaaa atggagatat tgттаattac	1080
ctatcaaaga ctgattttga taatacaaga atccctaaaa atataccagt taaagtagca	1140
cataaaattg gagatgctta tgactacaaa catgatgcgg ctattgttta tgcagaacaa	1200
ccttttatta tgattatctt tacggataaa tcatcttacg atgatatcac taagattgct	1260
gacgacgttt accaggtttt aaaataa	1287

<210> 2

<211> 1344

<212> DNA

<213> Streptococcus agalactiae

<400> 2	
atgaaaaaaa gaatattatc agcagtcctt gtgagtggag taactcttgg aactgctgcc	60
gtaacagtaa acgctgatga ctttgactcg aaaattgctg ctactgattc agtaatcaat	120
actttatcag ggcaacaagc agcagcacia aaccagggtga ctgctattaa aggacaagtt	180
ggtgcttttag agtctcaaca atcagaatta gaagcgcaaa atgctcaact tgaggctgta	240
tctcagcagt taggtcaaga gattcaaaact ctttctaata aaattgttgc acgtaacgaa	300
tctttgaaaa agcaagttcg tagtgctcaa aagggtaact tgactaacta tattaatact	360
attttaaatt cgaaatcagt atctgatgct gttaatcgtg ttgttgctat tcgtgagggt	420
gtttcagcta atgaaaagat gtttagcacia caagaggctg acaaagcggc cttagaagct	480
aaacaaattg aaaatcaaaa tgctataaat actgtagcag ctaacaagca agctatcgaa	540
aataataaag cagccttagc aacacaaaga gcacaattag aagcagctca attagagtta	600
tctgctcaat tgactacagt ccaaaatgaa aaagcatctt taattcaggc aaaagcacia	660
gctgaggaag ctgcgcgtaa ggcagctgaa gcacaagcag cagctgaagc gaaagcacia	720
gctgaagcga aagcacaagc tgagtctgta gcaaaagcac aggagcagc acaagttgag	780
tctgccacag ctctactga aacagttcaa acacaaccga gaactgaaat aaagccttct	840
aatcttacgg ctacttcttc ggcaactact gttgctacia ctacagctac agctactaat	900
gagccaaaag ttactcaacc ttctgtagta actaaagcag ttgaagcacc taaagcagtt	960
gtttcttcaa cacctagagc ggtatcaaaa cctgttgtca gaagttatga ttcaagtaac	1020
acatacccaa tgggacaatg tacttgggga gctaagtcaa tggcttcttg ggttggtaac	1080
tattggggaa atgctaataca gtgggggtgct agtgcacgtg cagctggtta ttctgtagga	1140
actaccctc gtgttggtgc agtagctgtt tggccatatg atgggtggtg ttacgggcac	1200
gttgtagtag taacgtcagt ggctaacaat tcatctatcc aagttatgga atcaactat	1260
gctggaaata tgagtattgg caattaccgt ggttcattta accctagtgc ttctggctct	1320
gtttactata ttaccctaaa ttaa	1344

GBS patentin.ST25

<210> 3

<211> 3726

<212> DNA

<213> Streptococcus agalactiae

<400> 3

atgaataaac gtatTTTTgt tgagaaaaag gctgactttg acattaaatc ggctagtctt	60
gtgaaagagt tgacgcataa tctacaactg acttctttga aggatttgcg tattgtgcag	120
gtctatgatg tcttcaattt ggctgaggat ttgctggcgc gtgctgagaa gcatatTTTc	180
tctgagcagg tgacagactg tcttttgacg gaaactgaaa tctactgcgga gcttgataag	240
gttgccTTtct ttgccattga ggcgcttCct ggtcaatttg accaacgtgc tgctagtTcg	300
caagaatctt tgctattgct tgggaagtgc agtcaggTta aggtcaatac agcccagctt	360
tacttggtca ataaggatat tgcagaagca gagcttgaag ccgttaagaa ctatctTTtg	420
aatcctgttg attcacgttt caaggacatt accttgccgc ttgaagagca ggctttctct	480
gtgtctgata agacaatccc tagtcttgat ttctttgaaa cttataaggc tgacgatttt	540
gcggcctata aggcagagca gggcttggct atggaggTcg atgatcttct cttcatccaa	600
gattatttca aatcaatcgg gcgtgtgccca actgagactg agttgaaagt tttggatact	660
tactggTcag accactgccg tcacacaacc tttgaaactg agttgaaaaa catcgacttt	720
tcagcttcta aattccaaaa acaattgcag gcgacttatg acaaatatat cgccatgcgt	780
gatgaacttg gtcgttctga aaagccgcag acacttatgg atatggcgac tatctttggt	840
cgttatgaac gtgccaatgg acgactggat gatatggaag tctcagatga aatcaatgcc	900
tgctcagttg aaattgaagt agatgttgat ggtgtaaaag agccttggct cctcatgttt	960
aagaatgaga ctcacaatca cccaacagaa attgagccat ttggtggcgc agcaacttgt	1020
atcggtggtg ccattcgtga cccgttgtca ggacgttcat acgtttatca ggctatgcgt	1080
atttcaggcg caggcgatat tacgactccg attgcggaaa cacgtgctgg taaattgccg	1140
caacaggTta tttctaaaac tgcggcgcac ggctattctt catatggtaa ccagattggg	1200
cttgcgacaa cttatgtgcg tgagtacttt caccctggct ttgtagccaa acgcatggag	1260
cttggagctg tggttggtgc tgcacctaag gaaaatgtgg ttcgtgaaaa accagaagca	1320
ggcgatgtgg tcatcttgct cggtggtaaa acaggTcgtg acggtgtcgg cggtgcgaca	1380
ggttcatcta aggttcaaac ggttgaatct gtggaaacag ctggcgcaga ggtacaaaaa	1440
gggaatgcc a tcgaagaacg taagattcaa cgccttttcc gtaatggtaa tgtcactcgc	1500
ctaatcaaga aatcaaatga cttcgggtgca ggtggtgtct gtgttgccat cggtgaattg	1560
gctgacggtc ttgaaatcga tttggacaag gtaccgctta aataccaagg tcttaatggt	1620
actgaaattg caatctcaga atcacaagag cgtatgtcag tcgttgttcg tcctagtgc	1680

GBS patentin.ST25

gtggatacct	tcacgcagc	ctgcaacaag	gaaaatatcg	atgccgttgt	ggttgctact	1740
attactgcaa	aaccaaacct	tgtcatgact	tgggatgggt	aaacaattgt	tgacttgga	1800
cgccgtttcc	ttgataccaa	cggtgtccgt	gtcgttggtg	atgctaaagt	cggtgacaaa	1860
gacttgacag	ttccagaggt	acgcacaaca	tcagcagaga	cacttgaagc	ggatacgctt	1920
aaggctctgt	ctgacctcaa	ccacgctagt	caaaaaggct	tccaaactat	ctttgactca	1980
tctgttggtc	gctcaaccgt	taaccaccca	atcggtggcc	gttaccaaat	cacaccaaca	2040
gaaagctctg	ttcaaaaatt	gccagttcaa	cacggtgtca	caacaactgc	atctgttatg	2100
gctcaagggt	acaatcctta	tattgcagaa	tggtcacctt	accacgggtc	tgcctatgct	2160
gtcattgaag	cgacagctcg	cttggttagca	acgggtgctg	actgggtctc	tgacggtttc	2220
tcttaccaag	agtatttcga	gcgtatggat	aaacaggcag	agcgttttgg	tcagccagta	2280
tcagctcttc	ttggttctat	tgaggctcag	attcaacttg	gattgccatc	aatcggcgggt	2340
aaggactcta	tgtctggtag	tttcgaagaa	ttgacagtac	cgccaacctt	ggtagctttc	2400
gggtgtgaaa	cagcggacag	ccgcaagggt	ctctctcctg	agtttaaagc	ggctgggtgag	2460
aatatctact	acattccagg	tcaagctatt	tcagaagata	ttgattttga	ccttatcaag	2520
gctaacttta	gccagttcga	gactattcaa	gctcaacata	agattactgc	tgcttcagct	2580
gttaaatacg	gtgggtgctc	agaaagtctt	gctctcatga	cttttggtaa	ccgtatcggg	2640
gcctctgttg	aaattgcaga	gcttgacagt	agcttgacag	ctcaactcgg	aggctttgtc	2700
tttacatcag	ctgaggaaat	tgctgactcg	gtgaaaatcg	gtcaaaactca	ggcagccttt	2760
acacttactg	tcaatggaaa	tgaccttgct	ggggcaagcc	ttctatcagt	cttcgaaggc	2820
aaattggaag	aggtttacc	aacagagttt	gaacaggcag	acgctcttga	agaagttcct	2880
gctgtggtat	cagatactgt	tatcaaggct	aaggaaacaa	ttgaaaaacc	agtgggtttac	2940
attccagtct	tccctggtag	caactcagaa	tatgattcag	ctaaggcctt	tgaacagggt	3000
ggagctagtg	tcaacttggg	agcatttgta	accttgaatg	aggctgctat	tgctgactca	3060
gttgacacaa	tggtcgctaa	tattgctaag	gcaaatatca	tcttctttgc	tggaggattc	3120
tcagcagcgg	atgaaccaga	tgggtctgct	aagtttatcg	tcaatatctt	gcttaacaag	3180
aaggttcgcg	cagctattga	cagcttcac	gaaaaagggt	gccttatcat	cggtatctgt	3240
aatgggtttcc	aagcccttgt	taaatcagg	cttcttccat	acggaaactt	cgaggaagct	3300
ggtgagacaa	gtccaacctt	cttctataac	gatgccaaacc	agcacgttgc	caagatgggt	3360
gagactcgta	tcgcaaatat	caactcacct	tgggttgtag	gagttgaggt	cggcgatatt	3420
catgccatcc	cagtttcaca	cggtgaagg	aaatttggtg	tcagcgcttc	tgaatttgca	3480
gagctaagag	acaatgggtca	aatctggagc	caatatgtgg	actttgacgg	acaacctctt	3540
atggattcta	aatacaatcc	aaatggctct	gtcaatgcc	tcgaagggat	taccagcaag	3600
aatgggtcaaa	tcacggttaa	gatggggcac	tcagaacgct	gggaagacgg	cctcttccaa	3660
aatatccctg	gtaacaaaga	ccaagccttg	tttgctagt	cagtaaaata	ttttacagga	3720

GBS patentin.ST25

aaataa

3726

<210> 4

<211> 1305

<212> DNA

<213> Streptococcus agalactiae

<400> 4

atgaaaatga ataaaaaggt actattgaca tcgacaatgg cagcttcgct attatcagtc	60
gcaagtgttc aagcacaaga aacagatacg acgtggacag cacgtactgt ttcagaggta	120
aaggctgatt tggtaaagca agacaataaa tcatcatata ctgtgaaata tggtgataca	180
ctaagcgtta tttcagaagc aatgtcaatt gatatgaatg tcttagcaaa aataaataac	240
attgcagata tcaatcttat ttatcctgag acaacactga cagtaactta cgatcagaag	300
agtcatactg ccacttcaat gaaaatagaa acaccagcaa caaatgctgc tgggtcaaaca	360
acagctactg tggatttgaa aaccaatcaa gtttctgttg cagacaaaa agtttctctc	420
aatacaattt cggaaggat gacaccagaa gcagcaacaa cgattgtttc gccaatgaag	480
acatattctt ctgcgccagc tttgaaatca aaagaagtat tagcacaaga gcaagctggt	540
agtcaagcag cagctaata acaggtatca ccagctcctg tgaagtcgat tacttcagaa	600
gttccagcag ctaaagagga agttaaacca actcagacgt cagtcagtca gtcaacaaca	660
gtatcaccag cttctgttgc cgctgaaaca ccagctccag tagctaaagt agcaccggta	720
agaactgtag cagcccctag agtggcaagt gttaaagtag tcactcctaa agtagaaact	780
ggtgcatcac cagagcatgt atcagctcca gcagttcctg tgactacgac ttcaccagct	840
acagacagta agttacaagc gactgaagtt aagagcgttc cggtagcaca aaaagctcca	900
acagcaacac cggtagcaca accagcttca acaacaaatg cagtagctgc acatcctgaa	960
aatgcagggc tccaacctca tgttgcagct tataaagaaa aagtagcgtc aacttatgga	1020
gttaatgaat tcagtacata ccgtgcggga gatccagggtg atcatggtaa aggttttagca	1080
gttgacttta ttgtaggtac taatcaagca cttggtaata aagttgcaca gtactctaca	1140
caaaatatgg cagcaaataa catttcatat gttatctggc aacaaaagtt ttactcaaat	1200
acaaacagta tttatggacc tgctaatact tggaatgcaa tgccagatcg tgggtggcgtt	1260
actgccaaacc actatgacca cgttcacgta tcatttaaca aataa	1305

<210> 5

<211> 903

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 5
 atgttaaaac attttggtag taaagtaaga aatttgagag taactagaaa tattactcgc 60
 gaagattttt gtggtgatga aactgagtta tctgtaagac aattagctag gattgaaagt 120
 ggacagtcaa ttccaaactt gactaaagct cactacatag ctaaacaatt gaatgtaaaa 180
 ttggatattt taacaggagg agagagctta gaattaccta aacggtataa agagttgaag 240
 tacaaattgt tgcgtacccc gacttacgga gatgctaata gacttgcagt tagagaagca 300
 tattttgatg aaatctatga agtattttat gaggagctcc cagaagatga aagactaatt 360
 attgattgta tgcaatcaaa attagatggt catttttctg ttaatgataa ttttggaatc 420
 actattttac atgactactt tgatcaaatt aagaaaaaaa aggaatatac cacaaatgat 480
 tttgttatga tagatttata tttactttgc ttttctatta actatggaat gaagagcttg 540
 tattcttttag agaactatca ttttattatg tcaaaattgt tagagcaaga taatttactt 600
 cctgaggata attttcaatt gaacaacgtt ttattaaatc atgtcgaatt agcttttcaa 660
 ttttaagcaga aaaaatatgt acagcaaatt attcatagaa gtaatgctat tatgacagaa 720
 atccatgatt ttcaaaaaag accaatacta agcttaatag agtggaataa tttattaatt 780
 attgaaaaag atagaacaaa agcagaaaca tgttttaaac aatcaattct atttgcagag 840
 ttaatagggtg atctatattt aaaaggaaaa ttaatagagg agtggaataa agatttaaca 900
 tga 903

<210> 6

<211> 2643

<212> DNA

<213> Streptococcus agalactiae

<400> 6
 atgactgaaa aaactaaagc ggtagaaact acagatgttg ctcttgcaat tgatacattg 60
 gttcaaaaacg gtttaaaagc acttgatgag atgctgcaac ttaatcaaga acaagttgat 120
 tatattgtag ctaaagcttc tgttgcagcc ttggatgccc atggagaact tgctcttcat 180
 gcagtagaag aaactgggtcg tgggtgtcttt gaagataaag cgacaaaaaa tttatttgca 240
 tgtgaacacg tcgttaacaa catgctcat acaaagacag tgggagttat tgaagaagac 300
 gatgtcacag gcttgacatt aattgctgaa ccagtgggag ttgtctgtgg tattacgcc 360
 acaaccaacc cgacttcaac tgctattttc aagtcattaa tctctcttaa aacacgtaat 420
 ccaattattt ttgccttcca cccatcagca caagaatcat cagcacatgc agcacgtatt 480
 gttcgtgatg ctgctattgc tgctggagct cctgaaaatt gtgtccaatg gattgaacaa 540
 ccatcgattg atgcaactaa tgctttgatg aaccatgatg gtattgccac tacccttgcg 600
 acaggtggta atgcatggt taaagctgcc tactcatgtg ggaaacctgc ccttggtgta 660

GBS patentin.ST25

ggtgctggga	atgttccagc	ttatgttgaa	aaatcagcta	atatccgaca	agccgctcac	720
gatattgtta	tgtctaaatc	atttgataac	ggtatggtat	gtgcatcaga	acaggctggt	780
attattgata	aagaaattta	taaagaattt	gttgaagaat	ttaaatctta	tcatacttat	840
ttcgттаата	agaaagaaaa	agctcttctt	gaagaattct	gttttggtgc	aaaagcaaат	900
agcaaaaact	gtgctggtgc	aaaattaaat	ccaaatattg	ttggaaaatc	agcagtttgg	960
attgctgaac	aagctggatt	tactgttcca	gaaggaacaa	atattcttgc	cgcagaatgt	1020
actgaagtta	gtgaaaaaga	acctttgaca	cgtgaaaaac	tatcacctgt	tattgccgta	1080
ttgaaagctg	aatctacaga	agatgggtgt	gaaaaagctc	gtcaaatggt	tgagtttaat	1140
ggtctaggac	actcagctgc	tattcataca	aaagatgcag	acttagctcg	tgaatttgga	1200
actagaattc	gtgctatccg	tgttattttg	aattctcctt	ctacttttgg	tggtattggg	1260
gatgtttaca	atgctttctt	gccatcattg	actcttggtt	gtggttcgta	tggacgtaac	1320
tcagttggtg	ataacgttag	tgctataaat	ctcttgaata	tcaaaaaagt	aggaagacgt	1380
agaaataata	tgcaatgggt	taaagtcctt	tcaaaaacat	acttcgaacg	tgattctatt	1440
caatattttg	aaaaatgtcg	cgatgttgaa	cgtgtcatga	ttgttacaga	tcacgccatg	1500
gttgagcttg	gtttcttggg	tcgtatcatt	gaacaacttg	atcttcgtcg	caataaagtt	1560
gtttatcaga	tttttgctga	agtagaacca	gatccagaca	ttacaacagt	aatgaaagga	1620
acagatttga	tgcgtaacct	caaaccagac	actattattg	cattaggtgg	tggttctcct	1680
atggatgctg	cgaaagttat	gtggctcttc	tatgaacaac	cagaagttga	tttccatgac	1740
ctcgttcaaa	aattcatgga	tatccgtaaa	cgtgcgttca	aattcccaga	acttggtgaag	1800
aaaacaaaat	ttgttgctat	tccaacaact	tctggaacag	gttctgaagt	gacaccattt	1860
gccgttatct	ctgacaaagc	aaataatcgt	aaatatccaa	tcgctgatta	ttcattaaca	1920
ccaactgtag	ctatcgttga	tccggccctt	gttatgactg	ttcctgggtt	tattgctggc	1980
gatacgggta	tggtatgtatt	gacacatgca	acagaggctt	atgtttcaca	gatggcaaат	2040
gattatacag	acggacttgc	ccttcaagca	attaaaattg	tgtttgacta	cttagaacgc	2100
tcagtaaaag	atgctgattt	tgaagcacgt	gaaaagatgc	acaatgcgtc	aactatggca	2160
ggtatggctt	tcgccaatgc	attcttaggt	atttctcact	caatggcgca	taaaattggc	2220
gcacaatttc	ataccgtaca	cggacgtaca	aatgcaattc	ttttgccgta	tgttatccgc	2280
tataatggaa	ctcgtccagc	taaaacagca	acatggccta	agtacaatta	ctatcgtgct	2340
gatgaaaaat	atcaagatat	cgctaaatta	ctcggcttac	cagcagcaac	accagaagaa	2400
gctgtcgaat	catatgcaaa	agctgtgtat	gaccttgga	cacgtttagg	tattaagatg	2460
aatttccgcg	accaaggcat	tgatgaaaaa	gaatggaaaг	aaaaatctcg	tgaactagct	2520
ttcttagcat	atgaagatca	atgttcacca	gcaaатccac	gccttccgat	ggtagatcac	2580
atgcaagaaa	tcатcgaaga	tgcttattat	ggttatgagg	aacgtccagg	acgtcgtaag	2640
taa						2643

GBS patentin.ST25

<210> 7
 <211> 834
 <212> DNA
 <213> Streptococcus agalactiae

<400> 7
 gtgggtatta aagtttataa accaacgaca aatggccgtc gtaatatgac ttctttggat 60
 tttgcagaaa tcactacaaa cactcctgag aaatcattgc ttgtttcact aaagaataaa 120
 gcaggacgta acaacaacgg acgtattact gttcgtcacc aagggtggtg acacaaacgt 180
 cattaccgtt tgattgactt caaacgtaat aaagatggtg ttgaagcagt tgttaaaaca 240
 attgaatacg atccaaatcg tactgcaaat attgctcttg tacactatac tgatggtggt 300
 aaagcttaca ttcttgcgcc taaaggcctt gaagtaggtc aacgcattat ttctggtcca 360
 gaagcagata tcaaagttgg taacgcactt ccacttgcta acattccagt cggtagcagt 420
 atccataata ttgaattgca accaggtaaa ggtgctgaat tgattcgtgc cgcgggtgct 480
 tctgctcaag tacttgggtca agaaggtaaa tatgttcttg ttcgcccttca atcaggtgaa 540
 gtacgtatga tccttgggtac ttgccgtgca acaattggtg ctgttggtgaa tgaacaacaa 600
 tcacttggtt acattgggtg agcaggacgt aatcgttggg aagggtgttcg ccctacagtt 660
 cgtggttctg taatgaaccc taatgatcac ccacacggtg gtggtgaagg taaagcacca 720
 gttggtcgta aagcaccatc tactccatgg ggtaaacctg cacttgggact taaaactcgt 780
 aataagaaag ctaaatacaga caaacttatt gttcgtcgtc gtaaccacaaa ataa 834

<210> 8
 <211> 939
 <212> DNA
 <213> Streptococcus agalactiae

<400> 8
 atgattgagt ttgaaaaacc aataataaca aaaattgatg aaaataaaga ttacggcaga 60
 tttgtcatcg aaccactaga acgtgggtac ggtacaactc taggaaactc tcttcgtcgt 120
 gtgcttctgt cttcacttcc aggtgcagca gtcacatcaa tcaaaattga tggagtatta 180
 cacgaatttg atactatccc aggtgtacgt gaagatgtga tgcaaatcat ccttaatgta 240
 aaaggacttg ctgtgaaatc ttacgtcgaa gacgaaaaga ttatcgaact agacgttgaa 300
 ggtcctgcag aaattactgc cggagatatt ttaacagata gtgatatcga aattgtaaac 360
 cctgaccatt atcttttcac aattgctgaa ggtcacagtt tgaaagcaac aatgacagtt 420
 gctaaaaacc gaggttatgt tccagcagaa ggaaataaaa aagatgatgc accagtggga 480

GBS patentin.ST25

acattggctg tagattcaat ctatacacca gtgaaaaaag ttaattatca agttgaacct	540
gctcgtgtag gtagtaacga tggctttgat aaattaacta ttgaaatcat gacaaatggc	600
acaatcattc ctgaggatgc tcttggtctt tcagctcgcg tcttaattga acacttaaac	660
ttgtttactg atttaacaga ggttgctaaa gcaactgaag taatgaagga aacagagaaa	720
gtgaacgatg agaaagtgtc tgaccgcaca attgaggaac ttgatttgtc agtgcgctca	780
tataactgtt taaaacgtgc tggaattaat acagtatttg atttaacaga aaaaactgag	840
cctgaaatga tgaaagtccg aaacttagga cgtaagagtc ttgaagaagt taaaatcaaa	900
cttgccgatc taggtcttgg attaaaaaac gataaataa	939

<210> 9

<211> 927

<212> DNA

<213> Streptococcus agalactiae

<400> 9

atgaaaaaga ttcgattatc aaagtttatt aaaatgattg ttgttatttt gtttttaatt	60
agtgtagcag ctagttttta tttttccac gttgccaag ttcgagatga taaatccttt	120
atttcaaatg gtcaacgtaa gcctggaaac tctttatatg cttatgataa atcctttgat	180
aagctattaa agcaaaaaat agaaatgaca aacccaaata taaagcaagt tgcttggtat	240
gttcctgctg ctaagaaaac tcataagaca gctgttgctg ttcattggtt tgccaatagc	300
aaagagaata tgaaggcata tggttggctg tttcataagt taggatacaa tgttcttatg	360
cctgacaata ttgcacatgg tgaaagtcac gggcagttga taggctatgg ctggaacgac	420
cgcgagaaca ttatcaaatg gacagaaatg atagttgata agaatccatc aagccaaatt	480
actttatttg gtgtttcaat ggggtggagca acagtcatga tggctagtgg tgaaaaatta	540
cctagtcagg ttgttaatat cattgaagat tgcggttatt ctagtgtttg ggatgaatta	600
aaatttcagg ctaaagagat gtatggttta ccagccttcc cactcttata tgaagtttca	660
acaatttcta aaatcagagc aggtttttcg tatggacaag caagtagtgt cgaacaattg	720
aaaaagaata atttaccagc cctctttatt catggtgata aggataattt tgttccaaca	780
agtatggttt atgacaacta taaagctaca gcaggtgaaga aagagcttta tattgtaaaa	840
ggggcaaac atgcgaaatc ttttgaaaca gagccagaaa aatatgagaa acgtatctct	900
agttttttga aaaaatatga aaaataa	927

<210> 10

<211> 447

<212> DNA

GBS patentin.ST25

<213> Streptococcus agalactiae

<400> 10

atgtcaaaag tacgtggctt tgaattagtt agccaattta gcaataaaga gttattacca	60
aaacgagaaa cagctcacgc agctggctat gatttataaag tagctaaaaa aacgggttatt	120
gaacctggtg aaattacatt ggtcccgacc ggtattaaag cacacatgca accaggggag	180
gtcctgtacc tttatgatcg ttcacgaat ccacgtaaaa aagggttgt cctaataaat	240
tcagttggtg ttattgatgg tgactactat aataaccaag tcaatgaagg acatattttt	300
gcacagatgc aaaatattac tgatcaggct gttatttttag aagaagggga acggattgtt	360
caggctgttt ttgccccatt cttattggca gatgacgatc aggctacagg aatgcgtaca	420
ggtggttttg gtagtactgg aaaataa	447

<210> 11

<211> 969

<212> DNA

<213> Streptococcus agalactiae

<400> 11

atgaaatttg gaaaaaaact tggctttcta gccttattga tgtctattgt cctcattcta	60
ggtgcatgtg gtaaaactgg acttggaat tctactggga attctacaaa aaatgtaacc	120
aaaaaatctg ctaaaaactt gaaactaggt gtatctattt caacaactaa caatccctac	180
tttgttgcga tgaaagacgg tattgacaaa tatgctagca ataaaaaat aagcattaag	240
gtagctgatg ctcaagatga cgccgcacgt caagcagatg atgtccaaaa ctttattagt	300
caaaacgtag atgctatttt gattaatccc gttgactcaa aagctattgt aacagctatt	360
aagtctgcaa acaacgctaa tattcctgtt attctaattg accgtggtag tgagggaggc	420
aaagtattaa ctactgtcgc ttcagataac gttgctgctg gtaagatggc tgcggattat	480
gctgttaaaa aactaggcaa aaaagcaaaa gcctttgaat tatctggagt accaggtgcc	540
tctgctactg tagaccgtgg taaaggattt cattcagttg caaaatctaa acttgacatt	600
ctttcaagcc aatctgcca ttttgaccgc gccaaagctt tgaatactac acaaaatattg	660
attcaaggac ataaagatgt ccaaattatt ttcgcacaaa atgatgaaat ggcacttggg	720
gctgcacagg ctgtcaaadc tgctggcttg caaaatgttc ttatcgtagg aattgatggt	780
cagccagatg cccatgatgc cattaataaa ggagatattt cagccactat tgcacaacaa	840
ccagctaaga tgggagaaat agcaattcaa gcagcaattg atcattataa aggcaaaaaa	900
gtagagaaag aaacaatttc tccaatttac cttgttacca aagacaatgt tgaaaaatac	960
aattggtaa	969

GBS patentin.ST25

<210> 12

<211> 1191

<212> DNA

<213> Streptococcus agalactiae

<400> 12

```

atgggaaaag aaaaattaat tttagcttat tctggtggtt tagatacctc tgttgctata   60
gcttggttaa aaaaagatta tgacgttatt gctgtctgta tggatgttgg cgaaggtaaa   120
gatcttgatt ttattcacga taaggcttta acaatagggtg ccatagaatc ttatatTTTA   180
gatgttaaag atgagttcgc tgagcatttt gtgttaccag ctttacaggc acatgcgatg   240
tatgaacaaa aatacccgct tgtttcagcg ctttagtcgtc caattattgc tcaaaaatta   300
gttgaaatgg cacatcaaac aggtgcgacc acaattgccc atggatgtac aggtaaagga   360
aatgaccaag tgcgttttga agttgcaatt gcagcactag atcctgaatt aaaagtaatt   420
gccctgttc gtgagtggaa gtggcatcgt gaagaggaaa ttacttttgc aaaagctaac   480
ggcgtaccta ttccagcaga tttagataac cttatttcta tagaccaaaa tttatggggga   540
cgtgccaatg aatgtggtgt gcttgagaat ctttggaaac aagcgccaga agaagctttt   600
ggtattacaa aatcaccaga agaagctcct gattgtgcag aatatattga tattacgttc   660
caaatggga agcctatagc tataaacaat caagaaatga cactagcaga tttgatttta   720
tcgctaaatg aaattgcagg aaaacatggt attggacgca ttgatcatgt tgaaaatcgt   780
ttagtcggta tcaaatacag tgaaatttat gaatgtcctg cggcaatggt actgttagct   840
gctcataaag aaattgaaga tttaacatta gtccgtgaag tgtctcattt taaacctatc   900
cttgaaaatg aactatcaa tcttatttat aatgctttat ggtttagtcc agctacaaaa   960
gctatcattg cctatgtcaa agaaacacaa aaagtgggta atgggtactac aaaagttaag  1020
ttatataaag gttctgccaa agtcgttgct cgccactcgt ctaattcatt atatgatgag  1080
aacttagcaa cttatacagc tgctgataac tttgatcaag atgcagcagt tggttttatc  1140
aaactctggg gacttccaac ccaagttaat gcacaagtaa acaaaggata a          1191

```

<210> 13

<211> 189

<212> DNA

<213> Streptococcus agalactiae

<400> 13

```

atggctaaag tatgttattt cacaggacgt aaaacagttt ctggtaacaa ccgttcacac   60
gcgatgaacc aaacaaaacg tactgttaaa ccaaacttc aaaaagttac tgttcttatc   120
gacggtaaac caaaaaaagt ttgggtttca gctcgtgcgc ttaaactctgg taaagtagaa  180

```

cgcgttttaa

189

<210> 14

<211> 1656

<212> DNA

<213> Streptococcus agalactiae

<400> 14

```

atggcaaaac agaaaaataa ctggcgccgt gttggagttg gtgtccttac acttgcttca    60
gttgcgactc ttgctgcatg tggaagtaaa tcagcttccc aggattctaa tggagcgatt    120
aattgggcta ttccaacaga aatcaataca ctagatttat ctaaagttac agacacttac    180
tcaaatctag ctattggtaa ctctagtagt aatttccttc gcttagataa ggatggaaag    240
acgagaccag atttggctac taaagttgat gtttcaaaag atgggttaac ttatacagct    300
acattacgta aaggcttgaa gtggtcagat ggcagtaaac ttactgcaaa ggattttggt    360
tattcatggc aacgtttagt tgatcctaag acagcttcac aatatgctta ccttgctggt    420
gaagggcatg tgcttaatgc cgataaaatc aacgaaggac aagagaaaga cttgaataag    480
ctagggttta aggcagaagg cgatgacaaa gttgttatta ctttatctag tccgtctcca    540
caattcatct actaccttgc attcactaat ttcatgccac aaaaacaaga agttgttgaa    600
aaatatggaa aagattacgc aactacttca aaaaatacag ttactcagg accatatact    660
gttgaagggtt ggaatgggtc aaatgggtact ttcaccctga agaaaaacaa aaattattgg    720
gacgctaaaa atgtaaaaac aaaagaagtt cgcattccaga ctgttaaaaa accagatacc    780
gccgttcaaa tgtataaacg tgggtgaatta gatgcagcta atatctcaaa tacttctgct    840
atztatcaag ctaataaaaa taataaagat gtcacagatg ttctagaagc gaccactgcc    900
tatatgcaat ataatactac tggttctgtg aaagggttg ataatgttaa gattcgtcgc    960
gccttaaaact tagcaactaa ccgtaaagga gttgttcaag cagccgttga tacaggctca   1020
aaaccggcaa ttgcttttgc accgactggg ttagccaaaa caccagatgg aactgatttg   1080
gcaaaatatg ttgccccagg ttatgaatat aataaaactg aagcagcaaa actctttaaa   1140
gaagggttgg ctgaatcagg cttgactaag ctaaaattaa caattacagc agatgctgat   1200
gttctctgtg ccaaaaactc tgttgactat atcaagtcta cttgggaagc tgctcttcca   1260
ggacttactg ttgaagaaaa atttgtaacc tttaaacaac gcttagaaga cagtagaaaa   1320
caaaactttg atatcgtagt ttctgtttgg ggtggggatt atccagaagg gtcaactttc   1380
tacggcctct ttaagtcaga ttcacaaaat aacgatggaa aatttgctaa caaggactat   1440
gacgctgctt ataacaaggc aatttccgaa gatgccttaa aaccagaaga atcagcaaaag   1500
gactataaag aagcagagaa aattctatct gagcaaggcg cttataaccc actctacttc   1560
cgtagtggtg aagggtttaca aaatccaaaa ttaaaagggtg ttattcgtaa tactacaggt   1620

```

GBS patentin.ST25

ttgtcaatag actttacaca tgcttataaa aaataa

1656

<210> 15

<211> 729

<212> DNA

<213> Streptococcus agalactiae

<400> 15

atggaactct taaaaacacc catctttggt atttgctttt ctttaatact ctatacgata	60
ggacaacatt tatttaagaa gagtaaaggt ttcttccttt tgcagcctct tttctttgca	120
atgggttagtg gtattgtcat tctttggctt atgtcaaaag gtttaggaac cgatgttaag	180
acattttata cacaagctta taaaccaggt ggcgatttaa ttttttggtt tttaaatcca	240
gcaacaattg cttttgcagt tcctctctat aagaaaaatg acgttggtta aaaatattgg	300
gtagaaattc tcagcagttt agtaatcggg atgattgttt cccttatgct tatcgtcgct	360
atttctaaaa tggttgggct tagtcaagtc ggaattgctt caatgttgcc acaagcagca	420
acaacagcaa ttgctcttcc aataacagca gcaattggag ggaacacagc tgtgacagca	480
atggcgtgta tcttaaatgc agttattatt tatgcattag gtaaaaaatt agtgtcattt	540
ttccatttga atgatagtaa gattggtgca ggattaggtc tagggacctc tggtcataca	600
gtcggagcag cttttgcatt ggaattggga gaactgcaag gtgcgatggc agctatagcg	660
gtggtgggta tcggtttggt agttgatttg gttattccta tctttagtca tttgattggg	720
ttgctataa	729

<210> 16

<211> 1629

<212> DNA

<213> Streptococcus agalactiae

<400> 16

gtgactaaat atttgaagta catctctttt gttgctttgt ttctggcgag tatcttttta	60
gtagcttgctc aaaatcaaaa ttcacaaaca aaggagcgaa cacgaaaaca acgacccaaa	120
gatgaattgg ttgtttctat gggggcaaag cttcctcatg aattcgatcc aaaggaccgt	180
tatggaatcc ataatgaagg taatattact catagtaccc tattgaaacg ttctcctgaa	240
ctagatataa aaggagagct tgctaaaaaa tataaaatct ctaaggatgg cttaacgtgg	300
tcgttcgact taaatgatga ttttaaatc tccaatggtg agcctgttac tgctgacgat	360
gttaagttta cttatgatat gttgaaagca gatggaaaag cttgggattt gacctttatt	420
aagaatgttg aagtagttgg gaaaaaccag gtaaatattc atttgactga ggcgcattcg	480

GBS patentin.ST25

acattttacag cacagttgac agaaatccca atcgtcccta aaaaacatta caatgataag	540
tataagagca atcctatcgg ttcaggacct tacatggtaa aagaatataa ggctggagaa	600
caagcaatct tcgttcgaaa tccatattgg cacggtaaaa agccttattt taaaaagtgg	660
acttgggtat tacttgatga aaatacagca ctagctgctt tagaatctgg tgatgttgac	720
atgattttacg caacgccaga gcttgctagc aagaaagtca aaggaacacg tcttctagat	780
attgcttcaa atgatgttcg tgggttatcg ctaccttatg tgaagaaagg tgttgtgaaa	840
aattcaccag acggttatcc agtaggaaat gatgtcacta gtgatccagc aatcagaaaa	900
gccttgacta ttggtttaaa tagacaaaaa gttctggata ctggtttaaa tggttatggg	960
aaaccagctt attcaattat tgatagaaca ccattctgga atccaaaaac agcaattaaa	1020
gataataaag tagctaaagc taagcaactt ttgacaaaag ctggatggaa agaacaagca	1080
gacggtagcc gcaaaaaagg aaatctttaa gcggaatttg acctttacta ccctactaat	1140
gatcaattac gagcaaacct agccgttgaa gtagcggagc aagctaaagc cttaggtatt	1200
actattaaac tcaaggctag taactgggat gaaatggcaa ctaagtcaca tgattcagcc	1260
ttactttatg cgggaggacg tcatcatgcg cagcaatttt atgaatcaca ttaccaagt	1320
ttagctggta aaggttggac caatattact ttttataaca atcctactgt gactaagtac	1380
cttgacaaag caatgacatc tcccgcactt gataaagcta acaaatattg gaagttagct	1440
cagtgggatg gcaaaacagg tgcttcact cttggagatt taccaaagt atggttggtg	1500
agtcttaacc atacttatat tgggtataaa cgtatcaatg taggtaaaca aggtgtccat	1560
agtcatggtc atgattggtc attattgact aacattgctg aatggacttg ggatgaatct	1620
gctaagtaa	1629

<210> 17

<211> 1146

<212> DNA

<213> Streptococcus agalactiae

<400> 17

atgggccaaag aacctatcat cgaatatcaa aatatcaata aagtgtatgg ggaaaatggt	60
gcggttgaag atattaacct taaaatttac cctggtgatt tcgtttgttt catcggtacg	120
agtggatcag gtaaaacaac attaatgcgt atggttaacc atatgttaaa accaacaagt	180
ggtactctat tatttaaggg aaaagatatt tctactatta accccattga attagacgc	240
agaattggat atgttatcca aaacattggg ttaatgcctc atatgaccat ttacgaaaat	300
atagttcttg taccaaaatt attgaaatgg tcagaagaag ctaaaagagc taaagcaagg	360
gaacttatta aattagttga attacccgaa gaatatttgg atcgctaccc tagtgagttg	420
tctggcggtc agcaacaacg tatcgggtgct attcgcgctc ttgcagcaga ccaagatatt	480

GBS patentin.ST25

attttaatgg atgagccttt tggagctctg gatcctatta ctagagaagg tattcaagac	540
ttagtcaagt ctcttcagga agaaatgggg aaaactatca tcttagttac tcatgatatg	600
gatgaagccc tcaagttagc aacaaaaatt attgttatgg acaatggtaa aatgggtccaa	660
gaagggacac ccaatgatct cttacatcat cctgctacca gtttcgttga acaaattgatt	720
ggggaagagc gtcttcttca tgcgcaggct gatattaccc ctgttaaaca gataatgtta	780
aataatcctg tttcaataac tgctgaaaaa acactaactg aagctattac actaatgcgc	840
caaaaacgcg ttgactcact tctagtaacc gataacggta aattaattgg ttttattgac	900
ttagaatctc taagcagtaa atataagaaa gaccgacttg tttctgatat cttaaaacat	960
actgattttt atgttatgga agacgactta cttagaaata ctgctgagcg tatttttaaaa	1020
cgtggtttaa aatacgtcc agttgttgac catgagaata acctaaaggg cattgttact	1080
cgtgcatccc tagttgatat gttatacgat attatttggg gcgatactga aacggaggat	1140
caataa	1146

<210> 18

<211> 708

<212> DNA

<213> Streptococcus agalactiae

<400> 18	
atgaaaatag ataaaaaaga attttttagca cttattgcta gtattatttt attaatTTTT	60
gcttctgtta cgTTTTtctt atttaaagat catggcacta ctcaaattgga tactgtagaa	120
agcagtgtta accatgtcag tgatttctcaa ttaactgagg cacaagatat gttagataaaa	180
tttgagaaga aaccttcaga aaaattattg aaggatgtcg aacttgcttt aaataaattg	240
tccaattctt ctaaaaaaga agctttgcaa aaacgtttta agaaagcaaa agataagtat	300
cttaaagacg aagcagataa gaaagctacc aaagatgcta cagatttagt agaaattcta	360
gaacaagccc cttcagaaga aaatgtgtta aaagctgaag cagcagtcaa taagttaact	420
gtcaaagaat ctaaagaagc ttacaaaaa cgtattgata ctgttaagac acaatatggt	480
ttgattggga atcaaactcc ctctagttca gtagctgaaa ctacagaaca agggacagct	540
aatcctgcta gtcaggatac ttctagttac gttaatcaga atgtagcacc aacttatgag	600
caaccgcaaa cgaataatac accagttact ccaggggtta acaatactgt tccgactcca	660
ggaactggta ctgcacctgc tactaatggg acgggtgttg cttagtaa	708

<210> 19

<211> 2040

<212> DNA

<213> Streptococcus agalactiae

<400> 19

atgactaaag	atttattatt	ggagcttggc	cttgaagagt	tgccagctta	tgttgtgaca	60
ccgagtgaga	agcaattggg	ccaaaaaatg	gtcaagtttt	tagaggatca	tcgtttatca	120
tttgaaactg	ttcaaacttt	ttcaactcca	cgtcgtttgg	ctgttcgtgt	taaaggattg	180
gcagaccagc	agacagattt	aacagaagat	ttcaagggtc	cttctaagaa	aattgctttg	240
gatgcagaag	ggaatttttc	taaagcagcc	caaggttttg	ttcgcggaaa	aggtttaagt	300
gttgatgata	tcgaatttcg	tgaagttaag	ggagaagaat	atgtttatgt	cactaagcat	360
gaaactggaa	aaagtgcgat	tgatgtttta	gcaagtgtga	cagaggattt	aacagaattg	420
actttccag	tgaacatgca	ttggggcaaat	aatagttttg	aatatatctg	tccagttcac	480
acttttagtg	tattattaga	tgatcaagcc	ttagagctag	acttccttga	tattcattca	540
gggcgtatta	gtcgagggca	ccgtttcttg	ggttctgaca	ctgaaatttt	atctgctagt	600
tcgtatgaag	atgacttgcg	acaacaattt	gttattgctg	atgcaaaaaga	acgccagcaa	660
atgatcgttg	atcaaattca	tgctatcgaa	gaaaaggaaa	atatttcagt	tgaaattgac	720
gaagattttac	taaatgaagt	gcttaattta	gttgagtatc	cgacagcatt	cttgggttct	780
tttgacgaga	aataccttga	tgtacctgaa	gaagtttttag	tcacttcaat	gaaaaatcat	840
caacgctatt	ttgtttgttcg	cgacagggat	ggaaaaattgt	taccaaactt	tattttctgtg	900
cgtaatggaa	atgctgagca	tatcgaaaat	gttataaaaag	gtaatgaaaa	agtttttagtg	960
gctcgtctcg	aagatgggtga	attcttcttg	caagaagatc	agaaacttaa	tattgcagat	1020
ttagttgaga	aattaaaaca	agtaactttc	catgaaaaaa	ttggttcact	ttatgaacat	1080
atggatcggtg	taaaagttat	ttcacaatat	ttggctgaga	aggcagatct	ttctgatgaa	1140
gaaaaattag	ctgtgcttcg	agctgcaagt	atttataaat	ttgacctctt	aactggaatg	1200
gttgatgagt	ttgatgaatt	acaagggtatt	atgggtgaga	aatatgcctt	acttgcaggg	1260
gaacagccccg	cagtagcagc	agcgatacgt	gaacattata	tgccgacatc	ggccgatgga	1320
gagcttccag	aaaccagagt	tggtgcaatt	ctagcgttag	ctgataaatt	tgacacctta	1380
ctttcattct	tctcagttgg	tttgattcca	agcggttcaa	atgatccata	tgctcttcgt	1440
cgagctactc	aggggattgt	ccgtattttg	gaagcttttg	gttgggatat	cccacttgat	1500
gaattagtaa	ctaaccttta	tggtctatcg	tttgctagtt	tagattatgc	taatcaaaaa	1560
gaggtcatgg	cctttatttc	agctcgtatt	gaaaagatga	ttggctctaa	ggcccttaaa	1620
gatattcgag	aagccgtttt	agaatcagac	acttatattg	ttagccttat	tctagaagct	1680
agccaagcat	tggtgcaaaa	gagcaaggat	gctcaatata	aagtttccat	tgaaagtttg	1740
tcacgtgcat	ttaatttagc	tgaaaaagtt	actcattctg	tatcggtgga	ctattcattg	1800
tttgaaaata	atcaggagaa	ggcgctatat	caagctattt	tgtcacttga	actgactgag	1860
gatatgcatg	acaacttaga	taagcttttc	gcacttagtc	caattattaa	tgatttcttt	1920

GBS patentin.ST25

gataatacaa tggtaatgac agatgatgaa aaaatgaaac aaaatcgtct ggctttactc 1980
aatagccttg ttgcaaaagc aagaacagtc gctgctttta acttattaaa cacaaaataa 2040

<210> 20

<211> 1986

<212> DNA

<213> Streptococcus agalactiae

<400> 20

atgacatttg acaccattga tcaattagcg gttaatacag tccgcacgct ttctattgat 60
gctatccaag cagcaaattc tgggcaccca ggtcttccta tgggagctgc gcctatggct 120
tatgtgcttt ggaataaatt cttaaagtga aacccaaaaa caagtcgcaa ttggacaaac 180
cgtgaccggt ttgtgctatc agctgggcat gggttcagctc ttctttatag cctacttcat 240
ttagctggct atgatttatc aattgatgat ttaaaacaat tccgccaatg gggatcaaaa 300
acacctggac atccagaagt taaccatact gatggtgtag aagcaacaac tggaccttta 360
gggcaaggta ttgctaatgc tgttgggtatg gcaatggctg aagctcattt ggctgctaaa 420
tttaataaac caggctttga tttagttgat cattacactt atacacttca tggatgatgg 480
tgtttgatgg aggggtgttag ccaagaagct gccagtcctg ctggacactt aaaacttgg 540
aaattgggtcc ttctttatga ttcaaatgat atctcacttg atggtccaac gtctcaatca 600
tttacagaag atgttaaagg gcgttttgaa tcatatgggt ggcaacatat cttagttaaa 660
gatggtaatg atttagaagc gattgctgca gcaattgaag ctgctaaagc tgaaactgat 720
aaaccaacca ttattgaagt taaaactatt attggatttg gcgcagagaa acagggaaca 780
tcttcagttc atggagcgcc acttgggtgca gaagggtatta cttttgcca gaaggcttat 840
ggatgggaat atccagactt tactgttcct gctgaagttg tagctcgatt tgcctcagat 900
cttcaagcgc gtgggtgcga ggcagaagag gcatggaatg atctttttgc taaatatgaa 960
gttgagtatc cagaattagc agctgaatac aaagaagctt ttgctggcca agctgagaca 1020
gttgaattga aagctcatga cctaggttca tcagtggcta gtcgtgtttc aagccaacaa 1080
gctattcaac aattatcgac tcaattaccg aacctctggg gagggtcagc agacctctca 1140
gcttctaata acacaatggg agcagcagaa acagatttcc aagcaagtaa ttacgctggg 1200
cgtaacattt gggttgggtg acgtgaattt gcaatggctg ctgcaatgaa tgggaattgcg 1260
cttcacgggtg ggactcgtgt ttatgggggt acattctttg tcttctcaaa ctacttggtta 1320
ccagcagtac gtatggctgc acttcaaaac ttgccaactg tctatgttat gacacatgat 1380
tctattgctg ttggagaaga tgggccaact catgagccaa tagaacaatt agcatcagtg 1440
cgctcaatgc ctaatttgaa cgttatccgt cccgcagacg gtaatgaaac aaacgctgca 1500
tggcaacgag ctgtatcaga gacagatcga ccaacgatgc ttgttttaac acgtcaaaac 1560

GBS patentin.ST25

ttaccagttc ttgaagggaac atcagaatta gccaagaag gggttaataa aggtgcttat	1620
atattatcag aagctaaagg tgaacttgat ggtatcatca ttgcaacagg ttcagaagtt	1680
aaattagctt tagatactca agacaaactt gagtcagagg gcatccatgt tcgctcgta	1740
tctatgccag cacaaaacat ttttgatgaa caagaggctt catatcaaga gcaagtgctt	1800
ccatcagctg ttacaaaacg tcttgctatt gaggcaggat caagcttcgg ttggggtaaa	1860
tatgttggtt taaatgggct aacacttact attgatactt ggggagcatc agcaccaggt	1920
aacagaattt tcgaagagta tggctttaca gttgagaatg ctgtatcgct atataaagaa	1980
ctttaa	1986

<210> 21

<211> 822

<212> DNA

<213> Streptococcus agalactiae

<400> 21

atgactttgc aagatcaaat tatcaaagaa ctcggtgtaa aacctgttat taatccaagt	60
caagaaatcc gtcgttccgt agaattttta aaagactatc tattaaaaca tagttttcta	120
aagacctatg tactgggtat ttcagggggg caagattcaa ctttagcagg acgtctagct	180
caactagcag ttgaagagtt gcgtgctgat acaggggaaa actatcaatt tatagctatt	240
cgtttaccat atggtattca ggccgatgaa gaagatgcac aaaaagcatt agattttatc	300
aagccagata ttgctttgac cattaatatt aaagaagctg ttgatggcca agttagagct	360
cttaatgcag caggagtaga gattacagac ttttaataag gaaatattaa agctcgtcaa	420
agaatgatta gtcaatatgc agttgcaggt caatatgctg gagcgggttat tggtagctat	480
catgctgcag aaaatattac aggttttttc accaaatttg gtgatggagg tgctgactta	540
ttacctctct ttagacttaa taaaagtcag gggaaacagt tattagctga acttggtgct	600
gataaagcct tgtacgaaaa gattccaacc gcagatttag aagaaaataa accaggaatc	660
gctgatgaaa tagcccttgg agtaacctac caagaaattg atgcttatct tgaagggaag	720
gtggtttcgg acaagtctcg aggtatcatt gaaaattggg ggtataaggg tcaacataaa	780
cgatcatctc caatcacaat ttttgatgat ttctggaaat aa	822

<210> 22

<211> 2238

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 22

attaaaaagg aatctgttat caaactattg aagtatgctt ttggcattat aatgggattt	60
attatcttag ctattgtaat aggtgggctc ctatttgcat actacgtag tcgttctccg	120
aaattaaccg atcaagcttt aaaatccggt aactctagtt tggtttatga tggtaataat	180
aaacttattg cggatttagg ctcagaaaag cgtgaaagtg ttagtgcgga tagcattcca	240
ctaaatttgg ttaacgctat cacttctatc gaagataaac gtttctttaa acatagaggt	300
gtcgatattt atcgtatttt aggtgcagct tggcataatc ttgttagtag taatacgcaa	360
gggtggttcaa cccttgatca acagttgatt aaactggctt acttttctac caataaatct	420
gaccaaactg taaaacgtaa atcacaggaa gtttggcttg cgcttcaa at ggagcgtaaa	480
tacaccaaaag aagaaattct tactttctat attaataaaag tttatatggg aaatgggaat	540
tatggtatga gaacaacagc taaatcatalc tttggtaaag acctaaagga attatctatt	600
gcacaacttg ctttgctcgc tgggtattcct caagcaccta cacaatatga cccttataaa	660
aaccagaat ctgctcaaac aagacgtaat accgttcttc agcagatgta tcaagataaa	720
aacatttcta aaaaggaata cgaccaagct gttgcaactc cagtaactga tggcttaaaa	780
gaattaaagc aaaaatctac ttatccaaaa tatatggata actacttaaa acaagttatt	840
agtgaagtta aacaaaaaac tggtaaagat atctttactg ctgggctaaa agtggtatact	900
aatatcaaca ctgatgcaca aaaacaacta tatgacatct acaacagtga cacttacatc	960
gcttatccaa acaatgaatt acaaatagca tctaccatca tggatgagac taatggtaaa	1020
gtcattgcac aattaggcgg gcgtcatcag aatgaaaata tttcatttgg gacaaatcaa	1080
tctgtcttaa cagaccgca tttgggttctt acaatgaaac ctatctcagc ttatgcacct	1140
gctattgata gtggtgtcta taattcaaca ggtcaatcat taaacgactc agtttactac	1200
tggcctggta cttctactca actatatgac tgggatcgct aatatatggg ttggatgagt	1260
atgcagaccg ctattcaaca atcacgtaac gtccttgctg tcagagcact tgaagccgct	1320
ggattagacg aagcaaaatc tttccttgaa aaattaggca tatactatcc agaaatgaac	1380
tattcaaag ctatttcaag taacaacagt agcagtgatg caaaatatgg tgcaagtagt	1440
gagaaaatgg cagcggctta ctcggtttt gcaaacggcg gaacttacta taaaccgcaa	1500
tatgttaata aaattgaatt tagcgatgga accaatgata cttatgcagc gtctggtagc	1560
cgtgcatga aagagactac tgcctacatg atgacggata tgctgaaaac agtactaaca	1620
tttggtactg gtactaaagc agctatccct ggtgttgac aagctggtaa gactggtact	1680
tccaactata cggaagatga gttagctaaa attgaagcaa ctactggtat ctacaatagc	1740
gccgttggta caatggctcc tgatgaaaac tttgtcggct atacttctaa gtacacaatg	1800
gcaatttggga ctggttataa aaatcgctt acaccacttt atggtagcca actggatatt	1860
gctactgagg tttatcgtgc aatgatgtcc tacctaactg gcggatacag tgcagattgg	1920
acaatgccag aagggtctta tcgaagcgga agctacttgt atatcaatgg gacaactaca	1980
accggcactt actcttcttc tgtctataag aatatctatc aaaattctgg acagtcaagt	2040

GBS patentin.ST25

caaagcagta gttcaacatc ctctgagaaa caaaaagagg ataagaatac agcaaatgat	2100
gccaatccat catccccaca agtcgaaaca cctaataatg gtaatgctac taccctaata	2160
aattccaatc aaactgtgcc aggaactgga catggtaatg gtaatggtaa caacaatata	2220
gtacctaacg gtaattaa	2238

<210> 23

<211> 1278

<212> DNA

<213> Streptococcus agalactiae

<400> 23	
atgttagact taaaacgtat tcgtacagat tttgatgttg tcgctaaaaa attggccacg	60
cgtggtgttg accaagaaac attaacaacc cttaaagaac ttgatataaa acgccgtgaa	120
ctacttatca aagctgaaga ggcgaaagcg caacgtaatg ttgcttctgc tgccattgct	180
caagcaaaac gaaataaaga gaatgcagac gagcaaatcg cagctatgca aacactttcc	240
gctgatataca aagcaattga tgcggaattg gcagatgtgg atgctaattt acaatcaatg	300
gtgaccgtac ttcctaatac accagctgat gatgtgccgc ttggagcaga cgaggatgaa	360
aatgttgaag ttcgtcgtcg gggaaactcct cgtgaatttg attttgagac caaagctcac	420
tgggatttag gtgaaagcct tggaattctc gattgggaac gtggtgcaaa agttactggc	480
tctcgcttcc tcttctacaa aggtctaggt gctcgtttag agcgtgctat ctacagcttc	540
atgctggatg aacacgctaa ggaggggtac actgaagtga tccctcctta tatggttaac	600
cacgattcaa tggtcgttac gggacaatat ccaaagttca aggaagatac tttcgaatta	660
gcagatagcc cattcgtact tatcccaaca gctgaagttc cttaacaaa ctattatcgt	720
gatgaaatta tcgatgggaa agaattacct atatacttta ctgccatgag tccatcattc	780
cgttcagaag caggctctgc aggacgtgac acacgtggat taattcgcct tcatcaattc	840
cataaagtag aaatggtgaa atttgccaaag cctgaggaat cataccaaga attagaaaaa	900
atgacagcaa atgctgaaaa tattcttcaa aaacttaatc tcccataaccg tgtcattacc	960
ttgtgtacag gagatatggg attctcagca gctaaaacgt atgacttaga ggtatggatt	1020
cccgtcaaaa atacttatcg agaaatttct tcatgttcta atactgaaga tttccaagca	1080
cgtcgtgctc aaattcgta ccgtgacgaa gttgatggca aagttagggt gcttcatact	1140
ttaaattggtt caggacttgc agttggacgt actgtacgag caatcctcga aaattatcaa	1200
aatgaagatg gttctgtgac tatcccagaa gttcttcgtc catatatggg taatatcgat	1260
attattaaac caaattag	1278

<210> 24

GBS patentin.ST25

<211> 801

<212> DNA

<213> Streptococcus agalactiae

<400> 24

```

gtgacaatat caaatcaaga attgacgctt actcccttaa gaggaaaaag tggcaaagcc      60
tatattggta cttatccaaa tgggtgaacgt gtctttgtca aatataatac gacacctatt    120
ttgccagcct tagctaagga acagattgcg ccacaactac tgtgggcacg ccgtagaagt     180
aatggcgata tgatgagtg tcaagaatgg ttagatgggtc gaacattgac taaagaagat     240
atgggtagta aacagattat tcatatttta ttgcgcctgc acaagtctcg tcccttagta     300
aatcagctgt tacaattagg gtataaaatt gaaaaccctt atgatttggt gatggattgg     360
gaaaaacaaa ctctatttca aatccgggaa aacacttatt tgcaatctat tgtgactgag     420
ttaaagcgta gtttacctga gtttcgaaca gaggttgcaa caatcgttca cggagatatc     480
aaacatagca actgggttat tacaacaagt ggtttaattt atttggttga ttgggattct     540
gttcgtttta cagatcgcat gtatgacgtt gcatatatat taagtcatta tattccacaa     600
aaacactgga aagattggct gtcttactac ggttataaag ataatgagaa agtctggagc     660
aaaattatct ggtatgggca attttcatat ttatcacaga taatcaaag ttttgataaa     720
cgagatatgg agcatgtcaa tcaagaaatt tatgaattac gaaagttag agagttaatt     780
aaaaagcata atgcgagtta g                                     801

```

<210> 25

<211> 1566

<212> DNA

<213> Streptococcus agalactiae

<400> 25

```

atgaaaaatat cacaatacaa taaatgggtca attcgccgat tgaaagttgg agctgcatct     60
gtaatgattg ctagtggaag cattgttgct ttagggcaat ctcatattgt ttcagcagat    120
gagatgtccc aacctaaaac aaccattaca gctccaacag ctaaaccttc tacaaatgta     180
gaaagtagta ctgataaggg attatcaaaa gttactacga tggagacaag ttcagaaatg     240
cctaaaatgc aaaatatggc aaaagttgaa aaaacgagtg acaaacctat gatgggtggct     300
acctctgtta gaaaaatgat ggcaacgccg acacctgtag cgatgaccaa aacgactagt     360
gtagatgagg taaagaaatc aactgatact gcttttaaag agacagtaga cgttccggct     420
cattatgtta atgcagcaaa agggaaatgg ccatttctag cagggtgtaa tcaaacgatt     480
ccatatgaag cgtttggtgg agatggcatg ttaacgcgtt taatccttaa atcttctgaa     540
ggagcaaaat ggtcagataa tgggtgttgat aaaaatagtc cattattacc attgaaaggc     600

```

GBS patentin.ST25

ttaactaaag gtaaataatctt ctatcaagtt tctttaaatg gtaatacgac aggtaaagag	660
ggacaagctc tcttagatca aattaaagct aatgataaac atagctacca agccacaatt	720
agagtttatg gtgctaaaga tggtaaagtt gatttaaaaa acatgattag caaaaaatg	780
gtaaccatta acattcctca cattacaact gatatggaag taaaaaattc tctaaagatg	840
gccttttaaag aaaaagtaga cgtcccagca aaatatgtta gtgctgcaa agctaaaggt	900
ccatttttag caggtgttaa cgaaacgatt ccatatgaag cgtttggtgg ggatggcatg	960
ttaacgcggt taatccttaa agcttcagag ggagcaaaat ggtcagacaa tgggtgttgat	1020
aaaaatagtc cattattacc gttaaaagat ttaactaagg gtaaatactt ctaccaagtc	1080
tctcttaatg gcaatacagc cggtaaaaaa ggccaagctc tcttagatca aattaaggca	1140
aatggaagcc atacttatca agcaactatc actatttatg gtacgaaaga tggcaaagtt	1200
gatatgaata ctatttttagg acaaaagaca gtgatgattc atattaatgt cgctaaaaaa	1260
gatatgaata gcacatcaat gatgatgaaa aaagataaga tgacaatgcc tatgaagaaa	1320
gaaatgactt catctaaaat aaataccggt atgatgatgt ctaacaacaa gatgtcagct	1380
aatatgcaaa tgtcatcaca agccaaatca aatgataaag ctggtaaaaa aatgtctatg	1440
atgtctaaaa atttacctaa tacagggtgaa acaaagcaac aaaatgtagg tgtgctaggt	1500
atgcttagtc tagcctttgc gacagggtcta actgcgctag gccttaaaaa atctaaacaa	1560
agatag	1566

<210> 26

<211> 1350

<212> DNA

<213> Streptococcus agalactiae

<400> 26	
atgacacata ttacatttga ctattcaaaa gtcttgggtc aatttgtagg cgaacacgag	60
ttagactacc tacaaccaca agtaagtgc gcagatgctt tccttcgtca agggactggt	120
cctggctcag attttctcgg atggatggac ctcccagaaa actatgacaa agaagaattt	180
tctcgcattc aaaaagccgc tgaaaagatt aaatcagata gcgaagtact cgtgggttatt	240
ggatttggtg gttcgtacct tggcgcaaaa gcagcaattg actttttgaa taatcatttt	300
gctaatttgc aaaccgcaga agaacgtaaa gcgcctcaga ttctttatgc tggaaattct	360
atttcatcta cttaccttgc cgatttagtt gaatacgtcc aagataaaga attctcagta	420
aatgtcattt caaaatcagg tacaacaact gaaccagcga ttgctttccg tgtatttaaa	480
gaacttctag ttaaaaagta cgggtcaagaa gaagctaata aacgtatcta cgctacaact	540
gataaagtta aagggtgccgt aaaagttgaa gcagatgcta acaattggga aacatttgta	600
gttcctgata atgttggtgg tcgtttctca gtactgacag ccgtaggtct tcttccaatt	660

GBS Patentin.ST25

gctgcttcag gagcagatat tactgctctt atggaaggcg caaatgctgc tcgtaaagat	720
ttatcttcag ataaaatctc tgaaaacatt gcttatcagt acgctgcagt tcgtaatggt	780
ctttatcgca aagggttatat cacagagatt ttagctaact acgaaccatc attacaatac	840
tttggtgaat ggtggaaaca attagcaggt gaatcagaag gtaaagatca aaaagggtatc	900
tatcctacat cagcaaactt ctcaactgat cttcactcac ttggtcaatt tattcaagaa	960
ggttaccgta acctctttga gacagttggt cgcgttgaga aacctcgtaa aaatgtgact	1020
attcctgaat taaccgaaga tttagatggt cttggttatc ttcaaggaaa agatgtagat	1080
tttgtaata aaaaagcaac agatggtgta ctccttgctc atacagatgg tggggttcca	1140
aatatgtttg taacgcttcc tacacaagac gcttacacc ttggttacac tatttacttc	1200
tttgagttag caattggcct ttcaggttat ctttaactcag taaatccatt tgatcaacca	1260
ggggtagaag catataaacg taatatgttt gctcttctag gtaaacctgg attcgaagag	1320
cttagcgctg aattgaatgc acgtctttaa	1350

<210> 27

<211> 318

<212> DNA

<213> Streptococcus agalactiae

<400> 27

atgaaagaaa aacaaacagc cggacgtcgt caattagaag aatttgcacc tgaatttgcc	60
agatataatg atgatatttt atttggtgag gtttgggcaa aagaggatca tttaacagat	120
aaaacacgtt ctattattac tatatctgcc ttaattagcg gaggaaatct tgaacagtta	180
gagcatcatc ttcaatttgc caaacaacac ggagttacta aagaagaaat tgctgacatt	240
atcactcacc ttgcttttta tgttggatgg ccaaagcgtt ggtcagcctt taataaagct	300
aaggaaattt ggatataa	318

<210> 28

<211> 471

<212> DNA

<213> Streptococcus agalactiae

<400> 28

gcttgagag ctttagagga tgctcaaaaa tctggaagg taaaatccat cgggtgtctca	60
aacttttttag aaaaagactt agaaaatatc ttaaaaaatg gtcattgttaa acctgctgtc	120
aatcaaatct tagctcacat cggaaataca cctttcgact tgattgatta ctgtcaaagt	180
aaaggatttc aagttgaagc ttattcacca attgcacatg gacaagcatt gaaatctgat	240

GBS patentin.ST25

ggtattcaaa aaatggctga aaaatatggg gttagtgttg ctcaattatg tattcaatat 300
 ttactacaat taaacctgat cgttttacca aaggcttcta gtaaagaaca ttacagctct 360
 aatctagact ttgactttgt aattagtgac gaagatatgt cgatattaaa atcacttatg 420
 ttgacgatt atggggaatt ttctaacttc cctgttttta gtgaaaaatg a 471

<210> 29

<211> 3381

<212> DNA

<213> Streptococcus agalactiae

<400> 29
 atgttttagaa ggtctaaaaa taacagttat gatacttcac agacgaaaca acggtttttca 60
 attaagaagt tcaagtttgg tgcagcttct gtactaattg gtcttagttt tttgggtggg 120
 gttacacaag gtaatcttaa tatttttgaa gagtcaatag ttgctgcatc tacaattcca 180
 gggagtgacg cgaccttaaa tacaagcatc actaaaaata tacaaaacgg aaacgcttac 240
 atagatttat atgatgtaaa gaatggattg attgatcctc aaaacctcat tgtattaaat 300
 ccatcaagct attcagcaaa ttattatata aaacaagggtg ctaaataatta tagtaatccg 360
 agtgaaatta caacaactgg ttacagcaact attactttta atatacttga tgaaactgga 420
 aatccacata aaaaagctga tggacaaatt gatatagtta gtgtgaattt aactatatat 480
 gattctacag ctttaagaaa taggatagat gaagtaataa ataatgcaaa tgatcctaag 540
 tggagtgatg ggagtcgtga tgaagtctta actggattag aaaaaataaa aaaagatatt 600
 gataataatc caaaaacaca aatagatatt gataataaaa ttaatgaagt caatgaaata 660
 gagaaattgt tagttgtatc gctaccagat aaaattaagt attcaccaga ggctaagcat 720
 aggactgttg aacaacacgc ggaattagat gcaaaaagata gcattgcaaa tacagatgaa 780
 ttgccatcaa attcaacgta taactggaaa aatgggtcata aaccagacac ctcaacatca 840
 ggtgaaaaaag acggaattgt tgaagttcac tatccagatg gtactgttga tgatgtgaat 900
 gttaaagtaa ccgtttacatc gaaaaaaaact gataatacag ctccaacatt aaccgtcact 960
 ccagagcaac agactgttaa agtggatgaa gatattacct ttacggttac agctgaagac 1020
 gaaaatgaag ttgaactagg tttagatgat cttaaagcta agtatgaaaa tgatatcatt 1080
 ggagctcgtg ttaaaattaa gtatcttact aaagaaccta ataagaaagt catggaagtg 1140
 acaattatga aagctacttt agcagataag ggcgcaatta cctttactgc aaaagataaa 1200
 gcaggtaatc aagcagaacc taagacagtt accatcaatg ttcttccgcc agataaaatt 1260
 aagtattcac cagaggctaa gcataggact gttgaacaac acgcggaatt agatgcaaaa 1320
 gatagcattg caaatacaga tgaattgcca tcaaattcaa cgtataactg gaaaaatggg 1380
 cataaaccag acacctcaac atcagggtgaa aaagacggaa ttgttgaagt tcactatcca 1440

GBS patentin.ST25

gatggtactg ttgatgatgt gaatgtttaa gtaaccgtta catcgaaaa aactgataat	1500
acagctccaa cattaaccgt cactccagag caacagactg ttaaagtgga tgaagatatt	1560
acctttacgg ttacagctga agacgaaaat gaagttgaac taggtttaga tgatcttaaa	1620
gctaagtatg aaaatgatat cattggagct cgtgttaaaa ttaagtatct tactaaagaa	1680
cctaataaga aagtcatgga agtgacaatt atgaaagcta ctttagcaga taagggcgca	1740
attaccttta ctgcaaaaga taaagcaggt aatcaagcag aacctaaagac agttaccatc	1800
aatgttcttc cgccagataa aattaagtat tcaccagagg ctaagcatag gactgttgaa	1860
caacacgcgg aattagatgc aaaagatagc attgcaaata cagatgaatt gccatcaa	1920
tcaacgtata actggaaaaa tggtcataaa ccagatacct caacaccagg agagaaaaac	1980
gctgttggtg ttgtgacctt tccagataag tcaacagatg aagttcctgt aaaagttaca	2040
gtgggtgacc cacgtacaga cgcagagaaa aatgatccag caggtaaaga tcaaactgtc	2100
aaagtgggtg aacaaccaga tccgacaaaa tctcttgaag cagtaccagc tggaagtaca	2160
gtagcgtaca aagaaccagt tgatactaag acaccaggag agaaaaacgc tattgttggt	2220
gtgacctatc cagataagtc aacagatgaa gttcctgtaa aagttacagt ggttgacca	2280
cgtacagacg cagagaaaaa tgatccagca ggtaaagatc aaactgtcaa agtgggtgaa	2340
caaccagatc cgacaaaatc tcttgaagca gtaccagctg gaagtacagt agcgtacaaa	2400
gaaccagttg atactaagac accaggagag aaaaacgcta ttgttggtgt gacctatcca	2460
gataagtcaa cagatgaagt tcctgtaaaa gttacagtgg ttgaccacg tacagacgca	2520
gagaaaaatg atccagcagg taaagatcaa actgtcaaag tgggtgaaca accagatccg	2580
acaaaatctc ttgaagcagt accagctgga agtacagtag cgtacaaaga accagttgat	2640
actaagacac caggagagaa aaacgctggt gttgttggtga cctatccaga taagtcaaca	2700
gatgaagttc ctgtaaaagt tacagtgggt gaccacgta cagacgcaga gaaaaatgat	2760
ccagcaggta aagatcaaac tgtcaaagtg ggtgaacaac cagatccgac aaaatctctt	2820
gaagcagtac cagctggaag tacagcagcg tacaaagaac cagttgatac taagacacca	2880
ggagagaaaa acgctgttgt tggtgtgacc tatccagata agtcaacaga tgaagttcct	2940
gtaaaagtta cagtgggtga cccacgtaca gacgcagaga aaaatgatcc agcaggtggg	3000
gaaacaacag taccacaagg cacaccgatc agtgatgaag aaattacagg attagtgaag	3060
attccagaag gatcaaacgg cgtaccgaaa gtagtaggag accgtccgaa tacagacgta	3120
ccaggagatt ataaagtaac ggtagaagta acgtatccag atggaacaaa ggatacagta	3180
gcagtaacgg ttcattgtgac accaaaacca gtaccggata aagataaata tgatccaaca	3240
ggtaaattct agcaagtcaa cggtaaagga aataaactac cagcaacagg tgagagtgc	3300
actccattct ttaatgttgc agctttgaca attatatcat cagttgggtt attatctgtt	3360
tctaagaaaa aagaggatta a	3381

GBS patentin.ST25

<210> 30

<211> 570

<212> DNA

<213> Streptococcus agalactiae

<400> 30

atgcagattc tcgaagacta tgatggtaga gcattaccca agctagaaac ggatcgactt	60
atcttgcgtc agcgaacggt gggggatgtc ccagccatgt ttgattacgt ttgcttgga	120
gaggttgctt atccagcagg gctcagccca atagcatctt tagaagatga gtatgattat	180
tttgaaaatc gctactatca aaatctggaa aaggcaaaat taccatctgg ttatggtatt	240
acgggttaaag gaagtgaccg gattatcgga tcctgcgctt ttaaccatcg ccgtgaagac	300
gatgttttcg agattggcta tctgcttcat cctgactact ggggtcatgg ctatatgaca	360
gaagctgtcg ccgctttgat tgaagtcggt tttacccttc tcaatctcca caaaatcgaa	420
atccgctgct atgactacaa taagcaaagc cagcgctgtg cagaaaaact aggattcacc	480
cttgaagcaa ccatccgtga tcgtaaggat aatcaaggca atcgctgtgt caatttgata	540
tatggtttgc tgaggagtga gtgggagtaa	570

<210> 31

<211> 2655

<212> DNA

<213> Streptococcus agalactiae

<400> 31

atgtcaaaag aactatcacc aaaatacaat cctgccgagg ttgaggaagg ccgttatcaa	60
acttggttg accaagatgt tttcaagcca tcaggggata ctgaggctaa gccctattct	120
atcgtgattc caccaccaa cgttacgggt aaattacact tgggtcacgc ttgggataca	180
actctacaag atatcattat tcgtcaaaag cgtatgcagg gctttgatac actctggctt	240
ccaggatagg accacgctgg tatagccact caagctaagg ttgaggagcg ccttcgtgag	300
caaggatatt cacgttatga tcttggtcgt gaaaaattcc tagataaagt ttgggaatgg	360
aaagacgagt atgcagcaac tattaaatct cagtggggga aaatgggtct ttcggttgat	420
tatagccgtg agcgttttac ccttgatgag ggactttcaa aagcggtaag aaaagtcttt	480
gttgatttgt acaataaagg ttggatctat cgtggggaat tcatcattaa ctgggatcca	540
gcagctcgta cagccctttc agatattgaa gttattcaca aggatgttga gggtgctttc	600
tatcatatga attatatgct ggaagatggc tcacgcgccc tagaagtagc aacaactcgt	660
cctgagacta tgtttggaga tgtggctgta gcggtaaadc cagaagatcc acgttacaaa	720
gatttgattg gtcaaaatgt tatccttcct atcatcaata aacctattcc aatcatcgct	780

GBS patentin.ST25

gatgaacacg ctgatccaga atttgggaaca ggtgtggtta agattacgcc ggctcacgac	840
cctaatagact tcgctgtagg tcaacgccac aacttaccac aagttaacgt tatgaacgat	900
gatggtacta tgaatgaact tgcggatgaa tttaatggta tggatcgttt cgaagctcgt	960
aaggcagtag tcgctaaatt agaatcgta ggaaacttag taaaaattga aaaaatgact	1020
cattctgttg gtcattcaga acgaacaggc gttgtggttg aaccacgttt atctactcaa	1080
tggttcgtca agatggatca attggctaag aatgccattg ccaaccaaga tacagaagac	1140
aaggtagagt ttatccacc acgatttaac gatactttta tgagctggat ggaaaatgtc	1200
catgactggg ttatctctcg tcaattatgg tggggacacc aaattcctgc atggtacaac	1260
gtcaatggtg agatgtatgt tggagaagat gccccagagg gtgacggatg gacacaggat	1320
gaagacgttc tagacacatg gtttagttct gctttatggc cgttttcaac aatgggatgg	1380
ccagacaccg aagcagctga cttcaaacgc tacttccaa catcaacctt ggtaactgga	1440
tacgatatca tcttctctg ggtatcgcg atgattttcc aatctcttga atttacagga	1500
cgccaaccat tctcaaatgt tcttattcat ggactcatcc gtgatgaaga aggacgtaaa	1560
atgtctaaat cacttggcaa cgggattgat ccgatggatg tcattgagaa atatggtgcg	1620
gatgcccttc gttggttcct ctcaaatggt tcagcccctg gtcaagatgt gcgtttttca	1680
tacgaaaaaa tggatgcttc gtggaatttc attaataaga tttggaacat ttcacgctat	1740
atccttatga ataacgaagg tttaacgttg gatcaagcca gagaaaatgt ggaaaaagtt	1800
gttaatagtc aagttggaaa tgtaacagac cgttggattc tccacaattt aaatgagact	1860
gtgggtaaag ttactgaaag ctttgacaag tttgaatttg gtgttgctgg tcacatcctt	1920
tacaacttta tctgggaaga atttgcta attggtacgttg agttaacaaa agaggttctt	1980
tatagtga atgaagatga gaaagttgtt acacgttctg ttcttcttta taccttagat	2040
caaattcttg gttcttctta tccaatcatg ccatttgtga cagaagaaat ttttggacaa	2100
tacgcagaag gatcaattgt ccttgcaagt tatccacaag ttaacgcgac atttgaaaaat	2160
cagacagctc acaaaggcgt tgaaagcttg aaagatttga ttcgttcagt gcgaaatagc	2220
agagcagagg tcaatgttgc tccatctaaa ccaatcacta tcttgggtta gacaagtgc	2280
agcgaactcg aaagcttctt caaagacaat agtaactaca tcaaacgctt cacaaccca	2340
gagacgcttg aaatcagctc agcgattact gccccagAAC ttgccatgac tagcattatc	2400
acaggtgcag aaattttcct cccacttgct gacctcctta acgttgaaga agagttggca	2460
cgacttgaaa aagaacttgc taaatggcaa aaagaactaa atatggtcgg caaaaaactc	2520
agcaacgagc gctttgtagc taacgctaaa ccagaagtcg tccaaaaaga aaaagacaaa	2580
cagaccgact accaaactaa atacgacgca actatagcac gtattgaaga gatgaaaaaa	2640
ttaaataatg attga	2655

GBS patentin.ST25

<211> 735

<212> DNA

<213> Streptococcus agalactiae

<400> 32

atggttgagc caattatttc aatacaagga cttcataaaa gttttgggaa aaatgaggtt	60
ttaaaaggca ttgacttgga tattcatcaa ggagaagtgg tggttattat tggcccttct	120
ggctctggta agtcaacatt tttaagaaca atgaatctct tggaagtacc aacaaaggga	180
acagtgactt ttgaagggat tgatataaca gacaaaaaga atgatatttt taaaatgcgc	240
gaaaaaatgg gcatgggttt tcaacagttc aatctatttc ccaatatgac tgtactagaa	300
aatattactt tatcacctat taagacaaag ggactttcta agcttgatgc tcagacaaaa	360
gcatacgagc tacttgaaaa agttggactc aaagagaagg ctaatgctta tccagctagc	420
ttatctggag ggcaacaaca acgaattgct attgcaagag gtcttgcaat gaatcctgat	480
gtccttcttt ttgatgaacc tacttcagct cttgatcctg aaatggtagg tgaagtcttg	540
actgttatgc aagatttagc taaatctggt atgacgatgg ttattgtcac tcatgaaatg	600
ggttttgcac gtgaagtagc ggatcgtgtc atttttatgg atgcaggcat tattgttgag	660
caagggaccc ctaaggaagt atttgagcag acaaaagaaa tccgcacaag agatttctta	720
agtaaagtat tataa	735

<210> 33

<211> 1695

<212> DNA

<213> Streptococcus agalactiae

<400> 33

atgaattata aagagattta tcaagagtgg ttagaaaacg actcactcgg taaagatatt	60
aagtcagatt tagaagctat taaaggcgat gaatctgaaa ttcaggatcg tttttacaaa	120
acattagaat ttggaacggc gggattgaga ggtaaacttg gagcaggaac caatcgtatg	180
aatacttata tgggtggggaa agcagcacaa gcattagcta atacgattat tgatcatggc	240
cctgaagcta ttgcacgtgg aattgcagtt agttatgatg tccgttatca atctaaggaa	300
tttgcagaat taacttggtc cattatggca gcaaattggt ttaagtctta tatttataaa	360
gggattcgcc caacaccaat gtgctcatat gctattcgtg ctctaggatg tgtttcgggt	420
gtgatggtta ctgctagtca taatcctcaa gcttataatg gttataaggc atattggaaa	480
gaaggatctc agattttaga tgatattgct gatcaaattg ccaatcatat ggatgctata	540
accgattatc agcaaattag gcaaataccc tttgaagagg ctctggcaag tggtttggca	600
agttatattg atgagagtat tgaagaagca tataaaaaag aagtgccttg ttttaaccatt	660

GBS patentin.ST25

aatgatacta acattgataa gtcagtccga gtagtttata ctcctttaaa tggcgtagga	720
aattttacctg tgcgcgaagt ttttaagacgc cgtgggtttg aaaatgttta tgtggtacct	780
gagcaggaaa tgcccgatcc tgattttaca acggttggct atccaaacc tgaagttcct	840
aaagcatttg cctattcaga atctctagga aagtcagttg atgcagatat cttacttgcc	900
acagatccag attgtgaccg agtagcattg gaagtcaaag atagtaaggg agaatatatt	960
ttcttaaatg gtaataagat aggggcactt ctttcctatt atattttttc acaacgatgt	1020
gccttaggga atttgccaca tcctcctgta ttggtaaaat ccattgtaac tggatgatcta	1080
tcaaaagtta ttgcagataa atataatatt gaaactgttg aaactttaac cggatttaaa	1140
aatattttgtg gaaaagctaa tgaatatgat atctcaaagg ataaaaactta tctctttggc	1200
tatgaagaaa gtattgggtt ttgctatggc acttttgtac gtgataaaga tgctgtgagt	1260
gcttcaatga tggtagtaga aatgactgcc tattataaag aacgagggca aacactttta	1320
gacgttttgc aaaccattta cgatgaattt ggctattaca acgagcgcca attttctctt	1380
gagtttagagg gtgctgaggg gcaagaacgt attagtcgta ttatggagga ttttagacag	1440
gaccaatat tacaagtagg tgagatgaga ttggagaatt ctattgattt caaggatggt	1500
tataaggatt ttccaaagca aaattgttta aaatattatt ttaatgaggg ttcattggtat	1560
gctttaaggc cgtcagggac ggaacctaaag ataaaatgtt acctttatac gattgggtgt	1620
acagaagcag atagttttatc gaaacttaat gcaattgagt cggcttgtcg tgctaaaatg	1680
aatagtacta aataa	1695

<210> 34

<211> 1212

<212> DNA

<213> Streptococcus agalactiae

<400> 34

atgtatagag aaattaccgc tgtcgaacac gatcgctttg tgagcgaatc caaccaaaca	60
aaactacttc aatcttctaa ttggcccaaa gtaaaagaca actggggtag tcaattactt	120
ggcttttttg acggtgaaac ccaaattgcc agcgctagta ttctcatcaa atcacttcct	180
cttggcttct ccatgctata tattccgcgt ggaccaatca tggattactc caatctagat	240
attgtaacta aggtccttaa ggaccttaaa gcttttggca aaaaacaaag agctctcttt	300
atcaagtgtg atcctctcat ctatttataa atgggtcaatg ccaaagattt tgaaaattcg	360
cccgatgaaa aagaagggtt aatcgccatt gatcatttac agcgtgcagg tgctgattgg	420
actggtcggg caacagattt agctcatact atccaaccac gttttcaggc aaacctatat	480
gctaataaat ttggacttga taaaatgtct aaaaaaactc gtcaagctat tcgaacttcc	540
aaaaataagg gagtagatat acaatttggg agccatgaac tacttgaaga ttttgcagag	600

GBS patentin.ST25

ttgatgaaaa	aaacggaaga	ccgtaaaggg	ataaatctta	gaggaattga	ctactaccaa	660
aaactccttg	atacgtatcc	taataactca	tacatcacia	tggcttcgct	agatgttgca	720
aaacgattag	aaaaaataga	aaaagaatgt	cagatagccc	aatctgaaag	aataaaatca	780
cttgaactta	atcgtgagaa	aaaagttaaa	caacaccaag	gtacgattga	tcgattaaat	840
aaagaaattg	attttctcaa	agaagctcaa	aaagcctatg	accgagacat	tattccattg	900
gctgcaaccc	tcactctaga	atttggtaat	acatcagaaa	atatttatgc	tggtatggac	960
gattacttta	aatcttattc	tgctcctatt	tacacttggt	ttgaaacagc	tcaaagggct	1020
tttgaacgtg	gaaatatttg	gcaaaatatg	ggggggattg	agaatgactt	atctggtggt	1080
ttatatcatt	ttaagtctaa	gttcgaacca	atcattgagg	aattttattg	agaatttaac	1140
attccagtga	acagattgct	ttataaagcc	tctaattatg	tctatgcctt	acgcaaaaaa	1200
cgtaatagct	ag					1212

<210> 35

<211> 1398

<212> DNA

<213> Streptococcus agalactiae

<400> 35

atggcttgta	caacaatatt	ggttggtaaa	aaggcttctt	atgatgggtc	gactatgatc	60
gctagaacgg	aagactctgt	taatggcgat	ttcacacca	aaaaattaaa	ggtaatgaca	120
tctaaagatc	aaccgcgtca	ttacaaatca	gttttatcaa	attttgaagt	agatttacca	180
gataaccac	ttccttatac	ttcagtaccg	gacgcattgg	gaaaagatgg	tatatggggt	240
gaagccggta	ttaacagtaa	aaatgtagcg	atgagtgcta	cagaaactat	tacaacgaat	300
tcccgcgttt	tgggtgcaga	tcctttgggt	tcagatggta	taggggaaga	ggatatactc	360
acttttagtg	ttccctatat	tcagtcagcg	cgagaagggt	tggagcggtt	aggtgctatt	420
ttggaaaaat	atggaaccta	tgaatcaaat	ggtattgctt	tttcagatac	cgaagaaata	480
tgggtgggttag	aaacaattgg	tgggcatcat	tggattgctc	gtcgcgtacc	tgatgatggt	540
tatgttacta	atcctaacca	actaggaatt	gatcattttg	aatttaataa	ctgtgatgac	600
tacatgtgct	ctagtgattt	gaaagagttt	atcgaacaat	accatttaga	tttgacctat	660
tctaattgagc	atttcaatcc	tcgatatgct	tttggtagcc	aacgtgataa	agatcgtcac	720
tacaacacac	caagaagtgg	ggcaatgcag	cgttttttta	atcctgaaat	tgaacaggat	780
ccacgtagct	tgtttattcc	ctgggtgtcaa	aagccttacc	gaaaaattac	tgttgaggat	840
attaaatatg	tgttgagtga	tcattatcaa	gacagtgtgt	atgaccata	tggaccagaa	900
ggggatgcgg	taagtaggag	agcttttcgt	tcagttggta	tcaaccgaac	tagtcaaacg	960
tctattctac	aattacgacc	aaataaatca	cttgaaacga	caggtgttca	atgggttatct	1020

GBS patentin.ST25

tatggctcta tgccatttgc aaccatggtg ccgttggtta cacaagttga gactgtacca	1080
aactatTTTT cgaatacaac caaggatgct tcaacagata atTTTTattg gaccaatcgt	1140
ttaattgcag ctctagcaga tccacacttt tatcaacatg aagctgatat tgaaagctat	1200
atcgagagaa cgatggctca aggacatgca catattaacg gtgttgatag agaagttgct	1260
gagaataaag agattgattt tcaacagaaa aatcaagaaa tgagtgacta tatccaaaaa	1320
gaaagccaag aattgttaaa tcgtattcta tttgatgcaa gtaatttaat gacaaatcgc	1380
ttttcaatgg gagattaa	1398

<210> 36

<211> 1521

<212> DNA

<213> streptococcus agalactiae

<400> 36

atgagaaaga aatttctttt attgatgagc tttgtagcta tgtttgcagc ttggcaactt	60
gttcaagtta aacaagtttg ggctgatagt aaacttaaag tggtacaac tttttacca	120
gtttatgagt ttacaaaaaa tgtcgttggt gataaagctg atgtatctat gttaattaaa	180
gcaggtacag aaccgcatga ttttgaacca tcaactaaaa acatcgctgc catccaagat	240
tcaaatgctt ttgtttacat ggatgataac atggaaactt gggctccaaa agtagctaag	300
tcagttaaat ccaaaaaagt aacaactatt aaagggtactg gcgatatgtt acttactaaa	360
ggcgtcgaag aagaaggtga agaacatgaa ggacatggtc atgaagggca tcatcatgaa	420
cttgaccac acgtatgggt gtctccagaa cgtgcgattt ctgttgtaga aaacatccgt	480
aataaatttg tcaaagctta tccaaaagat gcagcttcat ttaacaaaaa tgcagatgct	540
tacattgcaa aattaaaaga gcttgacaaa gaatacaaaa atggtttgct aaatgctaaa	600
caaaagagtt ttgtgactca acacgcagcg tttggttaca tggcgcttga ttacggttta	660
aatcaagttc caattgctgg tcttactcca gatgcagaac cttcatcaaa acgttttaggc	720
gaattagcta aatacatcaa gaaatataac atcaactaca tttattttga agaaaatgct	780
tcaaataaag ttgctaaaac tttagcagat gaagttggcg tgaaaacagc tgtgcttagt	840
ccacttgaag gactttctaa aaaagaaatg gcagctggcg aagattactt ctgagttatg	900
agacgtaatt tgaaagttct taaaaagaca acagatgttg caggtaaaga agtagctcct	960
gaagaagata aaactaaaac agttgaaaca ggttacttta aaactaaaga tgtaaagac	1020
cgtaaattga cagattactc tggttaattgg caatcagtat atcctcttct tcaagatggg	1080
acacttgatc cagtttgggg ttacaaagct aaatctaaaa aagatatgac tgctgcagag	1140
tacaaaaaat attatacagc aggttacaag actgacgtag aatcaatcaa gattgatggg	1200
aaaaaacatc aaatgacctt tgtacgtaat ggtaaatac aaacatttac atacaaatat	1260

GBS patentin.ST25

gcaggttaca aaatcttaac ttataaaaaa ggtaatcgtg gaggtagtta tctctttgaa	1320
gctaaagaaa aagatgctgg tcaattcaaa tatatccaat ttagtgacca tggattataaa	1380
ccgaataaag ctgaacactt ccatatcttc tgggggttcag aaagccaaga aaaattattt	1440
gaggaaatgg aaaactggcc aacatacttc ccagctaaaa tgtctggacg tgaagttgcc	1500
caagacctta tgtctcatta a	1521

<210> 37

<211> 1665

<212> DNA

<213> Streptococcus agalactiae

<400> 37

atgaaattat cgaagaagtt attgttttcg gctgctgttt taacaatggt ggcgggggtca	60
actgttgaac cagtagctca gtttgcgact ggaatgagta ttgtaagagc tgcagaagtg	120
tcacaagaac gccagcgaa aacaacagta aatatctata aattacaagc tgatagttat	180
aaatcggaaa ttactttctaa tgggtggtatc gagaataaag acggcgaagt aatatctaac	240
tatgctaaac ttggtgacaa tgtaaaagggt ttgcaagggtg tacagtttaa acgttataaa	300
gtcaagacgg atattttctgt tgatgaattg aaaaaattga caacagttga agcagcagat	360
gcaaaagttg gaacgattct tgaagaagggt gtcagtctac ctcaaaaaac taatgctcaa	420
ggtttggtcg tcgatgctct ggattcaaaa agtaatgtga gatacttgta tgtagaagat	480
ttaagaatt caccttcaaa cattaccaaa gcttatgctg taccgtttgt gttggaatta	540
ccagttgcta actctacagg tacaggtttc ctttctgaaa ttaatattta ccctaaaaac	600
gttgtaactg atgaaccaa aacagataaa gatgttaaaa aattagggtca ggacgatgca	660
ggttatacga ttggtgaaga attcaaatgg ttcttgaaat ctacaatccc tgccaattta	720
ggtgactatg aaaaatttga aattactgat aaatttgcag atggccttgac ttataaatct	780
gttggaaaaa tcaagattgg ttcgaaaaca ctgaatagag atgagcacta cactattgat	840
gaaccaacag ttgataacca aaatacatta aaaattacgt ttaaaccaga gaaatttaaa	900
gaaattgctg agctacttaa aggaatgacc cttgttaaaa atcaagatgc tcttgataaa	960
gctactgcaa atacagatga tgcggcattt ttggaaattc cagttgcatc aactattaat	1020
gaaaaagcag ttttaggaaa agcaattgaa aatacttttg aacttcaata tgaccatact	1080
cctgataaag ctgacaatcc aaaaccatct aatcctccaa gaaaaccaga agttcatact	1140
gggtgggaaac gattttgtaa gaaagactca acagaaacac aaacactagg tgggtgctgag	1200
tttgatttgt tggcttctga tgggacagca gtaaaatgga cagatgctct tattaaagcg	1260
aatactaata aaaactatat tgctggagaa gctgttactg ggcaaccaat caaattgaaa	1320
tcacatacag acggtacgtt tgagattaaa ggtttggtt atgcagttga tgcgaatgca	1380

GBS patentin.ST25

gagggtacag cagtaactta caaattaaaa gaaacaaaag caccagaagg ttatgtaatc 1440
 cctgataaag aaatcgagtt tacagtatca caaacatctt ataatacaaa accaactgac 1500
 atcacggttg atagtgtctga tgcaacacct gatacaatta aaaacaacaa acgtccttca 1560
 atccctaata ctggtggtat tgggtacggct atctttgtcg ctatcggtgc tgcggtgatg 1620
 gcttttgctg ttaaggggat gaagcgtcgt acaaaagata actaa 1665

<210> 38

<211> 2673

<212> DNA

<213> Streptococcus agalactiae

<400> 38

atgaaaaaga gacaaaaaat atggagaggg ttatcagtta ctttactaat cctgtcccaa 60
 attccatttg gtatattggt acaagggtgaa acccaagata ccaatcaagc acttgaaaaa 120
 gtaattgtta aaaaaacggg agacaatgct acaccattag gcaaagcgac ttttgtgtta 180
 aaaaatgaca atgataagtc agaaacaagt cacgaaacgg tagagggttc tggagaagca 240
 acctttgaaa acataaaacc tggagactac acattaagag aagaaacagc accaattggt 300
 tataaaaaaa ctgataaaac ctggaaagtt aaagttgcag ataacggagc aacaataatc 360
 gagggtatgg atgcagataa agcagagaaa cgaaaagaag ttttgaatgc ccaatatcca 420
 aaatcagcta tttatgagga tacaaaagaa aattacccat tagttaatgt agagggttcc 480
 aaagttggtg aacaatacaa agcattgaat ccaataaatg gaaaagatgg tcgaagagag 540
 attgctgaag gttggttatc aaaaaaatt acaggggtca atgatctcga taagaataaa 600
 tataaaattg aattaactgt tgagggtaaa accactgttg aaacgaaaga acttaatcaa 660
 ccactagatg tcgttgtgct attagataat tcaaatagta tgaataatga aagagccaat 720
 aattctcaaa gagcattaaa agctggggaa gcagttgaaa agctgattga taaaattaca 780
 tcaaataaag acaatagagt agctcttgtg acatatgcct caaccatttt tgatggtact 840
 gaagcgaccg tatcaaaggg agttgccgat caaaatggta aagcgctgaa tgatagtgtg 900
 tcatgggatt atcataaaac tacttttaca gcaactacac ataattacag ttattttaat 960
 ttaacaaatg atgctaacga agttaatatt ctaaagtcaa gaattccaaa ggaagcggag 1020
 catataaatg gggatcgac gctctatcaa tttggtgcga catttactca aaaagctcta 1080
 atgaaagcaa atgaaatttt agagacacaa agttctaatt ctagaaaaaa acttattttt 1140
 cacgtaactg atggtgtccc tacgatgtct tatgccataa attttaatcc ttatatatca 1200
 acatcttacc aaaaccagtt taattctttt ttaataaaaa taccagatag aagtgggtatt 1260
 ctccaagagg attttataat caatgggtgat gattatcaaa tagtaaaagg agatggagag 1320
 agttttaaac tgttttcggg tagaaaagtt cctgttactg gaggaacgac acaagcagct 1380

GBS patentin.ST25

tatcgagtac	cgcaaaatca	actctctgta	atgagtaatg	agggatatgc	aattaatagt	1440
ggatatat	atctctattg	gagagattac	aactgggtct	atccatttga	tcctaagaca	1500
aagaaagttt	ctgcaacgaa	acaaatcaaa	actcatgggtg	agccaacaac	attatacttt	1560
aatggaaata	taagacctaa	aggttatgac	atctttactg	ttgggattgg	tgtaaacgga	1620
gatcctgggtg	caactcctct	tgaagctgag	aaatttatgc	aatcaatatc	aagtaaaaca	1680
gaaaattata	ctaattgttg	tgatacaaat	aaaatttatg	atgagctaaa	taaatacttt	1740
aaaacaattg	ttgaggaaaa	acatttctatt	gttgatggaa	atgtgactga	tcctatggga	1800
gagatgattg	aattccaatt	aaaaaatgggt	caaagtttta	cacatgatga	ttacgttttg	1860
gttggaatg	atggcagtc	attaaaaaat	gggtgtggctc	ttggtggacc	aaacagtgat	1920
gggggaattt	taaaagatgt	tacagtgact	tatgataaga	catctcaaac	catcaaaatc	1980
aatcatttga	acttaggaag	tggacaaaa	gtagttctta	cctatgatgt	acgtttaaaa	2040
gataactata	taagtaacaa	atcttacaat	acaaataatc	gtacaacgct	aagtccgaag	2100
agtgaaaaag	aaccaaatat	tattcgtgat	ttcccaattc	ccaaaattcg	tgatgttcgt	2160
gagtttccgg	tactaaccat	cagtaatcag	aagaaaatgg	gtgagggtga	atttattaaa	2220
gttaataaag	acaaacattc	agaatcgctt	ttgggagcta	agtttcaact	tcagatagaa	2280
aaagattttt	ctgggtataa	gcaatttggt	ccagagggaa	gtgatgttac	aacaaagaat	2340
gatggtaaaa	tttattttta	agcacttcaa	gatggtaact	ataaattata	tgaaatttca	2400
agtccagatg	gctatataga	ggttaaaacg	aaacctgttg	tgacatttac	aattcaaaat	2460
ggagaagtta	cgaacctgaa	agcagatcca	aatgctaata	aaaatcaaat	cgggtatctt	2520
gaaggaaatg	gtaaacatct	tattaccaac	actcccaaac	gcccaccagg	tgtttttcct	2580
aaaacagggg	gaattgggtac	aattgtctat	atattagttg	gttctacttt	tatgatactt	2640
accatttggt	ctttccgtcg	taaacaattg	taa			2673

<210> 39

<211> 606

<212> DNA

<213> Streptococcus agalactiae

<400> 39

ggagcaaaaa	aggcaggggtg	gactgaatac	gctaggatgt	tagaagtcag	agagcagggtt	60
gaccatgtga	tgattccaaa	aatcaatcag	gattttacca	tctacgctgg	tccagaagag	120
gacaatctgc	aacggggagt	tggtcatcta	gaagggataa	gtttgccgat	tggaggggct	180
tctacacatg	cggctcttgag	cggtcaaaga	ggtatgccag	ctgctcgggt	gtttgcggat	240
ttggataaga	tgaaaaaagg	tgattatctt	tatgttacca	atctgaaaga	aaccttggct	300
tatcaagtgg	atcgtatcat	gggtgattgaa	cctagccaat	tggatgccgt	gagcattgaa	360

GBS patentin.ST25

gaggataaag attatgttac ccttctgacc tgtacacctt atatgggctc tttgtcaact	420
gtaatgggtg acttatcatt aacaacgaga gagaatcagc ttggttctct ctcttttttg	480
atgttcaaag cgatgagaat tttgctttta aaatttttaa agttgcgaaa gccaaaggct	540
tgtcgcttga tgtctttgat aagcttgttg gtcgcttcta atttggcatt ggaaagggat	600
agctga	606

<210> 40

<211> 1059

<212> DNA

<213> Streptococcus agalactiae

<400> 40

atgtcggatg ttgtcgaaaa acaaacagct aaatcgttta taatgaacgt attaaatggt	60
ttagcttttag ggactgttat tgtcttgata ccaggagcaa tccttgagaga attaatgaaa	120
gctttactgc caatgtggag cggatttgca actttaatcg ctgcaacagc agttgcaaca	180
agtatgatgg ggcttgttat tggattatg gttggtctca attttaaatt taatccatt	240
caatcagcat cactaggatt agcggttatg tttgcagggtg gagctgcaac cttccttaaa	300
ggcgctatta tgctaaaagg aacaggcgat atcattaata tgggaattac tgctgcctta	360
ggtgtccttt tgatccaatt tttatctgac aagacgaaat cattcacttt gattgtcatt	420
ccaacagtaa cactcttact agttggagga gtaggtcatg tgttattacc ttatgtcaaa	480
atgattacca ccatgattgg acaagggtt gcttcattac ttggtttaca acctgttttg	540
atgtcaattt taattgcgat gatcttctgt ttcttgatcg tatctccaat cacaacagtt	600
gggattgctt tggcaattag tttgtccgga attggttctg gtgctgctaa tttaggtatc	660
tgtgctgcta gttttgggct ttgtatggct ggggtgtcag tcaattctaa ggggacagcc	720
ttagcgcagc ttttaggggtc tcctaagatt tcgatggcta atgtattagc aaaaccgaag	780
attatgctac ctatgatatc ttcagcagca atactaggaa ttctcggagc tctctttaat	840
attcaaggaa caccagctag tgcaggtttt ggtatcagtg gtttgattgg accgattaat	900
gctcttaatt tagcaaaagg tggatgggtca gttatgaata tgttattgat aattataata	960
tttgttgctg caccaattat attgaatttt atttttaatt acctctttat aaaagtactt	1020
aaaattattg atccaatgga ctataaatta gatatttaa	1059

<210> 41

<211> 672

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 41
atggctagac ccttagtaga acaaacagca gatcgtctat tgcatttaat tttagaaaga 60
gaataccctg ttggtgctaa gctccccaat gaatatgaat tagcggaaga tctagatggt 120
ggtcgcagca caatccgaga agcagtcaga agtttagcaa cgcgtaatat tttagaagtc 180
agacagggct ctggaacata tattagttct aaaaaggggtg tttctgagga tccattaggg 240
ttctctctaa taaaggacac agatagggtg acatcagatc tctttgaact acgcctttta 300
ttggaacctc gaatagcgga gctggttagct tatagaatta cagatgatca gttacaatta 360
ctcgaaaagc ttgttggaga tattgaagat gctgttcacg caggcgatcc gaaacattta 420
cttttagatg tggaatttca ttccatgcta gctaaataca gtggtaatat tgcaatggat 480
agccttttgc cagtcaccaa ccagtcaatt catctgataa atgcgaatta tacaaatcgt 540
cagatgaagt cggatagttt agaagcacat agagaaatta tcaaagcaat ccgagaaaaa 600
aatccagtag ctgcacatga tgctatgctt atgcatatca tgagtgttag acgttcagca 660
ttgaaagctt aa 672

<210> 42

<211> 567

<212> DNA

<213> Streptococcus agalactiae

<400> 42
atgattaaga aaaataaagt ttttttagga gttcttttag tccttggtgt tacccttgga 60
ggtggtgtat tattttacca atcacaattc caaaagacaa ctaatcaagc gtttagctatt 120
gcttataaag atgctaaagt ggctaagaag gatgtcatat atcaaaaaat tgacaaagaa 180
tttgaaaact ttagagggag ctacgaaatt gagttcaata ccaaaagcgc agaatacagc 240
tatcatgtag atgctaagac tggacaaatc cttgagcggg acatggataa taatggcttt 300
tcaaaatcga cttctcagtc aagttcatcg tcaagtcaaa aatctcataa aataagtcaa 360
gaagaagcca aaaagattgc atttaaagat gctaatatag aggaatcaga agtcagtaat 420
cttaagatca aagaagaaat tgaaaatgga aaatcagttt atgatattga ctttgtggac 480
ctgaaaaata aaaatgaagt tgattatcaa attgatgcag aaactggaaa aatcattgaa 540
cgttctagag atcatatgaa tgattaa 567

<210> 43

<211> 2043

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 43
 ttgaatcgta aaaaaaggta tcgtctcact gtaaaaaagc aaaatgctag catacctaga 60
 cgattaaatc ttctattttt tattattggt ttattattta ctgttctaata tcttcgttta 120
 gagcaaatgc agattgggca acaatcattt tacatgaaaa aactgacagc tcttacgagt 180
 tatacagtga aagaatcaaa agcgagaggt cagatttttg atgctaaggg agtagtcta 240
 gttgaaaatg atgaacgtcc tactgtggcg ttttctagag gaaacaatat ttcattctcag 300
 tctatcaaag agtttagcgaa taaattatca cattacatta ccttaaccga agttgcttca 360
 agcgatagag caaagagaga ttattattta gcagataaag ccaactacaa aaaagttggt 420
 gaaagtttac cagattctaa acgttacgat aaatttggt accatctagc cgaatcaacc 480
 gtatatgcaa atgcagttgc tgcagttcca gtgagcgcta ttaactattc tgaagatgag 540
 ttaaaagtgg ttgccattatt taaccaaatg aatgcgacac caacgtttgg ttcagtga 600
 ttaagtacag gcgaattaag tgatgatcaa atcaagaaac tggatgctga taagaaggaa 660
 ctgttaggaa tttctgtaac aagtaattgg catcgtcgta aaaaaggaac ttttttatcg 720
 gatataatag gtactatttc tacagaaaag gcaggtttac caagagaaga agttaaaaaa 780
 tatttgaaaa aaggctattc actgaatgac cgagtgggaa cttcttacct tgaaaaacaa 840
 tatgaagatg acttacaagg aatcagacaa attcgcaaag tagttgttaa taaaaaagg 900
 aaagttgttt cagataatat tacgcaagaa ggtaagtcag gaagaaatct taaattaacg 960
 attgatctta attacaaaaa caaagtagaa agtatcttga aacaatacta tggcagtgaa 1020
 ttatctagtg gacgcgctag tttttccgaa gggatgtatg cagttgctat agaaccttca 1080
 actggtaaa gtttagcaat ggctggctg aaaaatgatc atgggaattt agttgatgac 1140
 agcctaggca ctattgctaa gaatttcacg ccaggatctg ttgtgaaagg tgcgacgcta 1200
 tcatcaggat gggaaaataa agttcttaga ggaaatgaag tgctttatga ccaagaaatt 1260
 gctaataatc ggtcatggtt tacacgaggt ttgactcaa tatctgcggc acaagcgcta 1320
 gagtattcat ctaatactta tatggttcaa gtagcacttc gtttaatggg acaagactat 1380
 aatacaggag atgctttaac tgatcgaggc tatcaagaag caatggctaa actaaggaaa 1440
 acttacggcg aatatgggtt aggggtttct acaggattag atttacctga atcagaagg 1500
 tatgtacctg gaaaatacag cttaggaaca actctaattg aatcgttcgg tcagtatgat 1560
 gcctatacac caatgcaact tggtcagtat atctcaacta ttgcgaataa tgggaatcgt 1620
 tttagcacctc acgtggtttc agatatctat gaagggaatg attctaataa gttcgtcaa 1680
 ttggttcgtt caatcactcc taaaacacta aataagatag ctatctcaga tcaagagtta 1740
 gccattattc aagaagggtt ttataacgtt gtcaatagtg gaagtggcta tgcaactggt 1800
 acgtcaatga gggggaatgt gacaaccatt agtggtaaaa ctggtaccgc tgaaacattt 1860
 gctaaaaatg taaatggaca aacagtttct acctacaact taaacgctat tgcctacgat 1920
 actaatcgta aaatagcagt agcggtaatg tatccgcatg ttacaactga tacaacaaaa 1980

GBS patentin.ST25

tcccatcaat tagttgcacg agatatgatt gatcaatata tttcacagtt cacaggacaa 2040
taa 2043

<210> 44

<211> 1428

<212> DNA

<213> Streptococcus agalactiae

<400> 44

atgacggttt ttcctaaaca ttttctatgg ggagggtgcag ttgctgccaa tcaggtagag 60
gggtgcattta gaacagatgg caaagggtta tctgtacaag atgtacttcc aaatgggtgg 120
ttaggcgatt tcaccgccaa acctactcca gacaatttga agctagaagc aattgatttt 180
tatcataact ataaaaatga tataaaactg tttgcagaga tgggctttta agtttttaga 240
acctctattg cctggtctcg aatttttcca aatgggtgat atagtgtcc aaacgaagct 300
ggcttacaat tttatgataa tttatttgat gagttgctta aatataatat cgagcccttg 360
gttaccttat ctcatatga aacaccgctt catcttgcaa aaacttataa tggttgggct 420
gatagacgtt tgatagcatt ttttgagaaa tttgctcaa cagtcatgga gcgttataaa 480
gataagggtga aatattgggt gacttttaaat gaagtgaatt ctattttaca tatgcctttc 540
accagtgggt ctattatgac cgacaaatca caactaagtc ctcaggagct ttatcaagct 600
attcatcatg aattagtagc atcggctaga gtgacaaaat tagggcgttc tatcaatcct 660
aattttaaaa ttggctgtat gattctggct atgccagctt atcctatgac atctgatcca 720
agagatgtcc tggctgcaag acaatttgaa caacataatc tgctattttc agatatacat 780
gtcagaggta aatatccac ttatatcag tcctatttca aaaataatgg tattaataatt 840
aaatttgaag aaggagatga ggaagtattg gcacaaaata cagtagattt tctatcgttt 900
agttactata tgagcgtgac acaagcttat gactttgaaa attatcaaag tggtcaggga 960
aatatccttg gaggcctaac taatcctcat ttaacaactt cagaatgggg atggcaaadc 1020
gatcccatcg ggctacgcct agtctttaat cagtattatg aacgttatca gattccgttg 1080
tttattgtag aaaatggatt gggagcaaaa gatcaattga tagaaacact agacggtgat 1140
tatactgtcg aagatgatta tcgtattgat tatatgaatc aacatttagt tcaagttgct 1200
aaagctattg aagatgggtg tgaaataatg ggatatacat cttgggggtg tattgattgt 1260
gtatccatgt ctacagctca actaagtaaa cgttatggtc taatatatgt tgatcgaaat 1320
gatgatggaa cagggagtct acaacgttac aagaagaagt catttggttg gtacaaaaaa 1380
gtgattaaga caaatggcca atcattgttt gaacatcata acagataa 1428

<210> 45

GBS patentin.ST25

<211> 486

<212> DNA

<213> Streptococcus agalactiae

<400> 45

atggctactt ttcaaattaa agaaaaaatg ttttctctag gcggtaaatt tactattaca	60
gaccagactg ggcttccctg ttatcacgtt gaaggaagtt tgttccctct acctaagact	120
tttaaagtct ttgacgaaga ggggcatctg attagtcaga ttgagaagaa ggttttaagt	180
tttttaccaa agtttaaatgt gacattagcc aatgggaatc atttcacgat taagaaagat	240
ttctcatttt tgaaacctca ttacaccatt gaagacctg atatggaagt taagggaaat	300
ttttgggata tagatttcca actcttaaaa gacaatcaag ttatagcaaa catatctcaa	360
cagtggtttc gtatgacttc aacttatcag gtagaagttt acaatgaaac ttacaacgat	420
ttgacaattt cgcttgatcat agcgatcgac tatgtcaaag agttagaaaa aaatgcatca	480
aactaa	486

<210> 46

<211> 546

<212> DNA

<213> Streptococcus agalactiae

<400> 46

atgaaaaaaaa taacaacttt aatcttagct agtagcttat tactagttgc aacgacatcg	60
gttaaagctg atgataactt tgaaatgcc aacggttatg ttaaaatgag tgaaaaatca	120
aaagcatttt atcaaagact acaagaaaa caacgtaagg cacatactac tgtgaagact	180
tttaataatt cagaaataag gcatcaacta cctcttaaac aagaaaaggc tagaaatgat	240
atctacaatt taggcattct tttttctcag gagtctaaag ggttcatcca acgtattgat	300
aatgcctatt ctttgaaaaa tgtctcagat attgttaatg aagctcaggc tttgtataaa	360
cgtaactatg atttatttga aaaaatcaaa tctacacgtg ataagggttca agtcttactt	420
gcatcgcatc aagataatac agacttaaaa aacttttatg ctgagttaga tgatatgtat	480
gaacatgttt atctcaatga aagtagagtg gaggcgataa acagaaatat ccaaaaatat	540
aattag	546

<210> 47

<211> 921

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 47

atgaaattaa	aaaaattctt	tgaggatttg	ctggctaaac	tagaatatag	accattcaa	60
gtttttatgc	gtcattttca	aagtgcagag	atggacttat	cagccatagc	agttgcttat	120
tatctattag	tgacagcttt	tccattacta	gttattgctg	ctaataat	tccttatttt	180
catattaatg	tgctcggattt	attgtcactt	atgcaaaaaa	atcttccgaa	aaatatttat	240
gaacctgcct	cacgcttagc	agtagatgct	ttttcgaaac	cgtctaccgg	cattttggga	300
ttcgtttcat	taacagcttt	ttggacaatg	tctaaaagtt	tgacctctct	tcaaaaagcc	360
attaataaag	catacgggtg	tgaccaacac	agagactttg	tgattagtcg	tttagtgggt	420
gtggggactg	ggctgatcat	cctattttta	ctgacttttg	ttttaatttt	ttcaactttt	480
tcaaaaccag	ttttacagat	aattgtaa	atgtatgatt	tgggagatac	tctaacggcg	540
tggcttttaa	atcttgcaca	accagttaca	tttttgacta	tatttttagg	tattggaatt	600
ttatacttta	ttttaccta	cgcacgaatt	agaaaagtac	gttatgtcat	tccagggaca	660
ttattttcaa	cgtttgttat	tgggtttttt	agtaatttaa	ttagccaata	cgtcttaa	720
agggttgaga	aatggtaga	tattaaaacg	tttggttcg	tcgttatctt	tatcttaatg	780
ctatggttta	ttttcttagc	ccacattatg	attttaggtg	caatactgaa	tgccagcggt	840
caagaaattg	cgacaggaaa	aattgaatca	aggcgtggag	atattatgtc	tcttatccaa	900
aatccaaag	aagaaaaata	a				921

<210> 48

<211> 3234

<212> DNA

<213> Streptococcus agalactiae

<400> 48

atgaaattac	tttatactga	tattaatcat	gatatgacag	aaatcttagt	caatcaggcc	60
gcgcattgctg	ctgaagctgg	atggcgtatt	ttttatattg	ctccaaactc	tttatctttt	120
gaaaaagagc	gtgcagtatt	agagaacctt	cctcaagaag	cctcttttgc	tattacaatt	180
actcgctttg	ctcaattggc	acgttat	actttaaac	agcctaata	aaaagaaagt	240
ttaaacgata	ttggattagc	aatgatcttt	tatcgctgctt	tagcaagttt	tgaagatgga	300
caattaaaag	tttttgagc	attgaagcaa	gatgcttcct	ttatcagtca	attggtagac	360
ctatacaag	aattgcagac	agcaaactg	agtatttttag	atttaaaata	tttacattct	420
cctgaaaaat	ttgaagattt	attagctatt	tttctagtgg	tttcagatct	tttaagagaa	480
ggagaatacg	acaatcaatc	taaaattgcc	ttttttacag	aacaagtaag	gtcaggccag	540
ctagatgtgg	atttaagaa	cactatcctt	atagtcgatg	gttttaccg	tttctcagct	600
gaagaagaag	ctttaattaa	aagtctgagt	tcacgttgct	aagagattat	catcggagct	660

GBS patentin.ST25

tatgctagcc	aaaaagcgta	taaggctaac	tttactaatg	gaaatattta	ttctgcaggg	720
gttgattttt	taagatatct	agcaacgaca	tttcaaaca	aaccagaatt	tatcttgtct	780
aagtgggaaa	gtaagtctgg	ttttgaaatg	atttcgaaaa	atatcgaagg	taaacatgat	840
tttacaata	gtagtcacat	tttagacgac	actgctaag	attgtataac	aatttgagg	900
tgcattaatc	aaaaagatga	agtggaacat	gtggctagag	ctatacgtca	gaaactttat	960
cagggatatc	gctacaaaga	tatttttagtt	ttactaggag	atgtagatag	ttataaacta	1020
caattaagca	agatttttga	gcagtatgat	attccttatt	atttcggtaa	agctgaaaca	1080
atggctgctc	acccttttagt	tcatttttatg	gattccttgt	ctcgaataaa	acgttatcga	1140
tttagagctg	aagatgtttt	aaatcttttt	aagacaggta	tttatggaga	gattagtcaa	1200
gatgatttag	attattttga	ggcttatatc	tcatatgcag	acattaaagg	tcctaagaag	1260
ttctttacag	attttgttgt	gggggctaaa	aaatttgatt	tagggcgtct	taacactatt	1320
cgtcagtcct	tccttgctcc	actggaaagt	tttggttaaaa	cgaaaaaaca	agacggtata	1380
aaaacactca	accaattcat	gtttttcctt	actcaggtag	gtttgagtga	caatttatcg	1440
cgattagtgt	gtcaaagtgc	tgaaaatgaa	caagaaaaac	atcaagaagt	ttggaaaaca	1500
tttacagata	ttttagagca	gtttcaaaca	atatttggtc	aagaaaaatt	aaatttagat	1560
gaatttttat	cgttattaaa	ttcaggtagt	atgcaagccg	agtatcgtat	ggtccttgct	1620
actgttgatg	tggttactgt	taagtcttac	gacttggtag	aaccacatag	taatcaattt	1680
gtctatgccc	taggcatgac	acaatcacat	tttcaaaga	ttgctcaaaa	caaactctta	1740
atatctgata	ttgaacgtca	gcttataaat	gatgccaatg	acactgatgg	tcattttgac	1800
attatgacgc	gagaâaattt	gaagaaaaac	cattttgctg	ctctctctct	ttttaatgct	1860
gctaaacaag	cattagtgtt	gactatacca	caattattga	atgagtctga	agatcagatg	1920
tcaccatata	ttatcgaact	aagagatata	gggtgttcctt	ttaatcataa	aggacgccaa	1980
tcgttaaaag	aagaagctga	taatattggg	aattacaaag	ctttattatc	gcgtgttggt	2040
gacttgatc	gctctgctat	tgacaaagag	atgactaaag	aagaacaaac	tttttggtca	2100
gttgctgttc	gttattttgcg	tcgtcaatta	acttctaaag	ggattgagat	accaataatt	2160
acagatagtc	ttgatactgt	gacagtttca	tcagatgtga	tgaccagacg	cttcccagaa	2220
gatgaccac	ttaaattatc	ctcatctgct	ttgacaactt	tttataataa	tcaatataag	2280
tattttttac	aatatgtgtt	aggtttgga	gaacaagact	caattcatcc	agatatgcgg	2340
caccatggaa	cgtaacctca	tcgtgttttt	gaaattctga	tgaaaaacca	agggatagaa	2400
tcttttgaag	agaaactcaa	ctctgcaatt	aataaaacca	atcaagaaga	tgttttcaaa	2460
tccttgatatt	cagaagatgc	agaaagtcgt	tattcttttag	aaattttaga	agatatcgcg	2520
cgtagcaactg	caaccatatt	acgacaagat	agtcagatga	ctgttgaaag	tgaagaagaa	2580
cgatttgaac	taatgattga	taatactata	aaaattaacg	gtattattga	ccgtatcgat	2640
cgtttatctg	atgggttcttt	gggtgtcgtg	gactataaat	caagcgctca	aaaattcgat	2700

GBS patentin.ST25

atccaaaaat tttataacgg tctaagtcca caattagtta cctacattga tgctatcagt	2760
cgtgacaagg aggttgaaca aaaaccaccg atttttggag ctatgtatgtt acatatgcaa	2820
gaacctaaac aagacttgct taaaattaaa aatttagatg atttagtaac aaaaaatcat	2880
caagctttaa cttataaagg attattttca gaagctgaaa aagaattttt agcaaatggg	2940
aaataccatc tcaaagattc cctttattca gaggctgaaa ttgctatgtt acaagcacat	3000
aaccaattgc tttacaaaaa agcatctgag actattaagt caggtaagtt tttgatcaat	3060
ccatatacag aagatgctaa aacagttgac ggtgatcagt ttaagagtat tacgggggtc	3120
gaggcggata ggcatatggc gcgtgccaga gcgctttata aattacctgc taaggaaaaa	3180
cgtcaagggt tcttaacatt aatgcagcaa gaggaggaaa atgatgacct ttaa	3234

<210> 49

<211> 999

<212> DNA

<213> Streptococcus agalactiae

<400> 49

atgagcgaaa ctaaagttat ggctttgcgc gaagcgatta atgtcgctat gagcgaagaa	60
atgcgcaaag atgaaaaagt atttttaatg ggtgaagatg taggtgtata tggaggagac	120
ttcggtagat cagttggtat gttagaagag tttggtgcta agcgcgttcg cgacacacca	180
atctcagagg ctgcgattgc aggttcagct atcgggtgctg cacaaacagg tttgcgtcct	240
atcgttgatt tgacattcat ggatttcgta acaatcgcaa tggatgctat cgttaaccaa	300
ggtgctaaaa cgaattatat gtttggtgga ggtctatcaa ctccagttac tttccgtgtg	360
gcatcagggg caggtattgg ttcggctgca caacactcac aatcattaga agcttggtta	420
acacacattc caggtctaaa agttgttgca cctgggtactg ttaatgagtc aaaagcactt	480
ttgaaatctt ctattcttga caataaccca gttatcttct tagagccaaa agctctctat	540
ggtaagaaag aagaagttaa catggatcct gatttctata ttccacttgg taaaggggat	600
attaagcgtg agggtagtga cttacaatt gtttcttatg gccgtatgct tgagcgtgtt	660
atgcaagctg ctgaagaagt tgctgaggaa ggtattaacg ttgaggttgt tgatccacgt	720
acacttattc cgcttgataa agaattaatt atcgattctg ttaagaaaac tggtaaattg	780
attttggtta acgatgctta taaaactggg ggtttcactg gtgaaattgc aactatgggt	840
gctgaaagtg aagcatttga ttaccttgat catcctatcg tgcgtcttgc aagtgaagat	900
gttccagtac cgtattcacg tgtacttgaa caaggaatct tacctgatgt agcaaaaatt	960
aaagatgcta tctacaaagt agttaacaaa ggtaaataa	999

<210> 50

GBS patentin.ST25

<211> 1758

<212> DNA

<213> Streptococcus agalactiae

<400> 50

atggcctttg atgtaattat gccaaaactt ggggttgaca tgcaagaagg cgaaatcctt	60
gagtggaaaa aaaatgaagg tgacaccgtt aatgaagggtg atgtccttct tgaaatcatg	120
tctgataaaa ccaatatgga aattgaagca gaagacactg gtgtactttt aaaaattgta	180
catcaggcag gagatgttgt tcccgtcact gaagtgattg cctatatcgg agaagaaggt	240
gaagaagtag gtacgtcatc accttcagct gatgcaacta tcacagctga agatgggtcaa	300
tcagtttctg gacctgctgc tccttcacaa gagacagttg cagcagcaac tcctaaagaa	360
gaacttgtag ctgatgagta cgatatcgta gtcgtagggtg gtggacctgc aggttattac	420
gcagcaatcc gcggtgctca acttggagga aaaattgcc a ttgttgagaa aactgaattt	480
ggtggtacgt gtttgaatgt tgggtgtatc cctacaaaaa catatcttaa aaatgctgaa	540
atcctagatg gtttgaaagt agcagctgga cgtgggtatca accttgcttc aactaactat	600
gcaattgata tggataagac tgttgccctt aaaaattctg tagttaagac actgactggc	660
ggtgtacgtg gtctcttgaa agcgaacaaa gttgaaattt tcaatggact tggacaagta	720
aaccctgata agtctgttgt tattggcgat aaagtatatca aagggtcgtaa cgctcgttctt	780
gcgactgggt ctaaggtatc tcgtattaat attccaggta ttgaatcacc attagtatta	840
acatcagatg atattcttga ttacgtgaa attcctaagt cacttgctgt tatgggtggt	900
ggtgtcgtag gtattgagct tgggtcttga tgggcttcat atgggtgtga cgtaactggt	960
attgaaatgg ctgatcgcat cattccagca atggataaag aagtatcgct agaacttcaa	1020
aaaatccttg ctaagaaggg aatgaagatt aaaacatcag ttggtgtttc tgaaattggt	1080
gaagccaata atcaattaac gcttaaatta aacaacggcg aagaagttgt tgctgataaa	1140
gctcttctt caattggacg tgttccacaa atgaatgggtc ttgaaaatct tgagcctgaa	1200
cttgagatgg aacgtggacg tattaagtt aatgcttatc aagaaacttc aattccaggt	1260
atctatgcac cagggtgatgt taatggaact cgtatgttag ctcatgctgc ataccgtatg	1320
ggtgaagtag ctgctgaaaa cgcaactcggc ggtaataagc gtaaagcaca tctagatttc	1380
actccagcag ctgtttatac tcctcctgaa gtagcaatgg tggggatgac agaagagcaa	1440
gcacgtgaac aatatgggtga catattagtt ggtaaaaata gctttacagg caatgggtcgt	1500
gctatcgctt caaacgaagc acatgggtttt gtaaaagtaa ttgctgaacc taagtataaa	1560
gagattcttg gtgttcacat tattgggtcca gctgcagcgg aattgattaa tgaagcttct	1620
acgattatgg aaaatgagtt gactgtctat gatgtagcac aatctatcca tgggtcaccca	1680
acattctctg aagttatgta cgaagctttc ttagatgttc tcggtgaagc tattcacaac	1740
cctccaaaac gcaaataa	1758

GBS patentin.ST25

<210> 51
 <211> 1353
 <212> DNA
 <213> Streptococcus agalactiae

<400> 51
 atgggaaaat attttggtag agatgggtgt cgcggtgaag ctaatgttga actgacgcca 60
 gaattggcctt ttaaattagg acgttttggga ggatatgttc taagtcaaca cgaaactgat 120
 cgtccgagag tttttgtagc tcgtgatact cgtattttctg gtgaaatgct ggaatctgct 180
 ttgattgctg gtctactttc agtaggtatt gaggtttata aacttgggtgt tttagccact 240
 cctggagtgt cttaccttgt ccgtacagaa aaagctagtg caggggttat gatttcagca 300
 agccacaatc cagcacttga taatgggtatt aagttctttg gtagtgatgg ttttaaactt 360
 gatgatgatc gtgaattaga aattgaagct ttacttgatg cgaaggaaga cactttacca 420
 cgtccatcag cacaagggtt aggtacttta gtagattatc ctgaaggact tcggaaatat 480
 gagaagttaa tggaatcaac tggtattgat ttagaaggta tgaaggttgc gttggataca 540
 gcaaatggag cagcaacagc ctcagctcgg aatatctttt tagacttgaa tgctgatata 600
 agtgttattg gtgatcaacc agatgggttg aatatcaatg atgggtgttg ttcgacacat 660
 cctgagcaat tacaaagttt agttagagaa aatggttccg atatcggtct agcttttgat 720
 ggtgatagtg atcgtttgat cgctgttgat gaaaatggag agattgtaga tgggtgataaa 780
 attatgttta tcattgggaa atatctttct gataaagggc agcttgctca gaatacaatc 840
 gtaacaacgg ttatgtcaaa tctcggcttt cataaagcgc tcgaccgtga aggtattcat 900
 aaagcgatta ccgctgtagg agaccgctac gtggttgaag aaatgcgtaa atcaggatat 960
 aatcttggcg gggagcaatc aggccacgtt attatcatgg attacaatac tacaggggat 1020
 ggacaattaa cagccatcca attgactaag gtcattgaaag aaactggtaa gaaattatca 1080
 gagtttagcta gtgaagtgaac gatttatcct caaaaattag taaatattcg ttttgaaaat 1140
 aacatgaaag ataaagcgat ggaagttcct gcaattgcgg aaattattgc taaaatggaa 1200
 gaagagatgg atggcaatgg tcgtattcta gtacgtccta gtggtactga gcctcttctt 1260
 agagttatgg cagaagcgcc aacaaatgaa gcagttgatt attatgttga tactatcgca 1320
 gatgtcgttc gtacagaaat tggtttagat taa 1353

<210> 52
 <211> 2634
 <212> DNA
 <213> Streptococcus agalactiae

GBS patentin.ST25

<400> 52
 atgaaaggtc aaaaaattat tgctctagct ggtcttgtcc tgtcatgccca ttttgctctt 60
 acggcatgtc atactcaaga acacaaaaat tctcatcata ttaaaacaaa gcaggttgct 120
 aagaaaaaag ctaataaaaa gaaagtctct gttaaggaaa gtcataaaaa acgcaagggg 180
 gttgcagggg ttgactttcc aactgatgat ggctttttac tgactaaaga ttcgaagatt 240
 ttatctcatc ccgattctgg aatcgttgta gcacatggaa atcattctca ttttattttt 300
 tactctgatt taaaagggtc aaaatttagc tatttaattc ctaatgcaaa tgcaaaaact 360
 aataaaaagc aagcggtaag aaactttaaa gcagggggcg tagctgttaa tacattaaat 420
 gatggctatg tttttaatcc cgcagatatt gtttcagaag atgctaattg ctacgtgggc 480
 agacatgggtg atcattttcca ctatattcca aaagcaagtt tatctcagca aaagcaagta 540
 caagcaagta gagctgtttc acgttttagga aatcaaaata atagccatta cagagttaat 600
 agttctaaaa ttgcagggct tcaccacca acaagtgatg gtttcttatt caatggacaa 660
 ggaataaaaag gcactacccc aacaggtatt ttagtagaac atcataatca tctgcatttt 720
 attagttttg ctgatttaag aaaaggggga tggggatcaa ttgctgaccg ttaccaacca 780
 caaaagaaag ttgattctaa aaaacagtca ccatcaagta aaaagccaag aactgaaaat 840
 actttaccta aggacatcaa agataagcta gcttaccttg ctcgtgaatt acatttagat 900
 atttcacgta tcagagtcct taaaacacta aatggtgaaa ttggatttga ataccacat 960
 gatgatcata cacatgttat tatggccaaa gatattgatc taagtaagcc aattccaaat 1020
 ccacatcatg atgacgaaga tcatcaciaa ggtcatcacc atgatgagtc cgaccataag 1080
 catgaagaac acgagcacac taagtcaa ataaattatctg atgaagatca aaagaaatta 1140
 atttatttag cagagaagct tggtttaaat cctaataaaa ttgaagtatt aacgtcagag 1200
 gatgggagta tcatctttaa atatccacat gatgaccact cacacactat agcaagtaag 1260
 gatattgaaa ttgggaagcc tatcccagat ggacaccacg atcactctca tgcaaaagat 1320
 aaagttggta tggcaactct aaaacaaatt ggttttgatg atgagattat tcaggatatt 1380
 ctgcatgcag atgctccaac accattccca tccaatgaaa ctaatcctga aaaaatgcgt 1440
 cagtggcttg caactgttac taagattaac attggacaaa gaaccaatcc attccagcgt 1500
 tttggctctat cattgatgcc taatattgaa gttctaggaa ttgggtttac tccgattaat 1560
 gatatgacgc cagttttgca attcaaaaaa cttaaacagc tttggatgac aaatactggg 1620
 attacagatt attctttcct tgataagatg ccactattag aaggattgga tatttcacaa 1680
 aacggtatta aggatttatc tttccttaca aaatataaac aattaagtct tattgctgca 1740
 gctaataatg gcattacttc gctaaaacca ttggctgaat taccaaacct tcaattctta 1800
 gttttgagtc ataacaatat ctctgacttg acaccgttat caaacttgac aaaactccaa 1860
 gaattgcacc ttgatcataa taatgtgaag aatttaagtg cactttctgg taaaaagat 1920
 ttgaaagttc tagatttatc aaacaataaa tccgcagact tatcgactct aaaaacaact 1980

GBS patentin.ST25

agtcttgaga	cgcttctttt	aaatgagacg	aatacaagca	atctaagttt	cttaaagcaa	2040
aatcctaagg	tatctaattt	aacaattaat	aatgcgaaat	tagcatcatt	agatggtatt	2100
gaagagagcg	atgaaattgt	taaagtagaa	gctgaaggga	accaaattaa	gtcactagta	2160
ttgaaaaata	aacaagggtt	gttaaaattc	ttgaatgtga	ctaataatca	gttaacatca	2220
cttgaagggt	ttaataatta	tacttcactt	gagaccttaa	gtgtttctaa	aaataaactt	2280
gaatcttttag	atattaaaac	acctaacaaa	acagttacaa	atcttgattt	tagccataac	2340
aatgttccaa	catcacaatt	gaaattgaat	gaaaaaaata	ttcctgaagc	agtagctaag	2400
aattttccag	cagttgtaga	aggttcaatg	gttggaatg	gtagtcttgc	tgaaaaagca	2460
gctatggctt	ctaaagagga	caaacaagtt	tcagataata	ctaataacca	aaaaaacact	2520
gaaaaatctg	ctcaagcgaa	tgctgatagt	aaaaaagaaa	accctaaaac	acatgatgaa	2580
catcatgacc	atgaagaaac	agatcatgca	catgtaggtc	atcatcacca	ttaa	2634

<210> 53

<211> 1503

<212> DNA

<213> Streptococcus agalactiae

<400> 53

atgaataaac	gcgtaaaaat	cgttgcaaca	cttggtcctg	cggtagaatt	ccgtggtggt	60
aagaagtttg	gtgagtctgg	atactggggg	gaaagccttg	acgtagaagc	ttcagcagaa	120
aaaattgctc	aattgattaa	agaagggtgct	aacgttttcc	gtttcaactt	ctcacatgga	180
gatcatgctg	agcaaggagc	tcgtatggct	actgttcgta	aagcagaaga	gattgcagga	240
caaaaagttg	gcttcctcct	tgataactaaa	ggacctgaaa	ttcgtacaga	actttttgaa	300
gatggttcag	atttccattc	atatacaaca	ggtacaaaat	tacgtgttgc	tactaagcaa	360
ggtatcaa	caactccaga	agtgattgca	ttgaatgttg	ctgggtggact	tgacatcttt	420
gatgacgttg	aagttggtaa	gcaaactcctt	gttgatgatg	gtaaactagg	tcttactgtg	480
tttgcaaaaag	ataaagacac	tcgtgaattt	gaagtagttg	ttgagaatga	tggccttatt	540
ggtaaacaaa	aaggtgtaaa	catcccttat	actaaaattc	ctttcccagc	acttgcagaa	600
cgcgataatg	ctgatatccg	ttttggactt	gagcaaggac	ttaactttat	tgctatctca	660
tttgtacgta	ctgctaaaga	tgттаатgaa	gttcgtgcta	tttgtgaaga	aactggcaat	720
ggacatgtta	agttgtttgc	taaaattgaa	aatcaacaag	gtatcgataa	tattgatgag	780
attatcgaag	cagcagatgg	tattatgatt	gctcgtgggtg	atatgggtat	cgaagttcca	840
tttgaaatgg	ttccagttta	ccaaaaaatg	atcattacta	aagttaatgc	agctggtaaa	900
gcagttatta	cagcaacaaa	tatgcttgaa	acaatgactg	ataaaccacg	tgcgactcgt	960
tcagaagtat	ctgatgtctt	caatgctggt	attgatggta	ctgatgctac	aatgctttca	1020

GBS patentin.ST25

ggtgagtcag ctaatggtaa ataccagtt gagtcagttc gtacaatggc tactattgat	1080
aaaaatgctc aaacattact caatgagtat ggtagccttag actcatctgc attcccacgt	1140
aataacaaaa ctgatgttat tgcattctgcg gttaaagatg caacacactc aatggatata	1200
aaacttggtg tgacaattac tgaaacaggt aatacagctc gtgccatttc taaattccgt	1260
ccagatgcag acattttggc tgttacattt gatgaaaaag tacaacgttc attgatgatt	1320
aactgggggtg ttatccctgt ccttgacagc aaaccagcat ctacagatga tatgtttgag	1380
gttgacagac gtgtagcact tgaagcagga cttgttgaat caggcgataa tatcgattatc	1440
gttgacaggtg ttcctgtagg tacaggtgga actaacacaa tgcgtgttcg tactgttaaa	1500
taa	1503

<210> 54

<211> 990

<212> DNA

<213> Streptococcus agalactiae

<400> 54

atgactgcaa ctaaacaaca taaaaaagtt atcctcgttg gtgatgggtgc cgtaggttct	60
tcttacgctt ttgcatttgt taaccaaggt attgcgcaag agttaggtat cattgaaatc	120
ccagctttat ttgataaagc tgttggtgat gctgaagatc tttcacatgc ccttgattt	180
acatcaccta aaaaaatcta cgcagctact tatgcagact gcgcagatgc tgacctgtt	240
gtcattactg ctggcgcacc tcaaaaacca ggtgaaactc gacttgacct tgttggtaaa	300
aacttagcaa ttaacaaatc aatcgtaact caagttgttg aatcaggttt caacggtatc	360
ttcttagtag cggctaacc tgtagatgta cttacatatt caacttggaa attctcaggt	420
ttccctaagg aacgcgttat tgggttcaggt acttcacttg actctgcacg tttccgtcaa	480
gcttttagcag ataaaattgg tgttgatgct cggttcagttc acgcatacat catgggtgaa	540
cacgggtgact cagaatttgc cgtttgggtca catgctaacg ttgctgggtgt ccaacttgaa	600
caatgggttac aagaaaaatcg cgatattgat gaacaaggac ttgttgattt gtttatttca	660
gttcgtgacg ctgcatactc aatcatcaac aaaaaaggtg ctacatatta cggatttgct	720
gttcgcacttg ctcgtattac taaagctatc cttgatgatg aaaatgcagt tcttccatta	780
tctgtatatc aagaaggcca atacgggtgat gttaaagatg tctttatcgg tcagcctgca	840
atcgtaggtg cacatggtat cgttcgtcca gttaatatcc cattaaatga tgctgaactt	900
caaaaaatgc aagcctcagc tgaacaatta aaagatatta ttgacgaagc ttggaaaaac	960
ccagaattcc aagaagcatc aaaaaactaa	990

<210> 55

GBS patentin.ST25

<211> 2460

<212> DNA

<213> Streptococcus agalactiae

<400> 55

atgcaagata	aaaatttagt	agatgttaat	ctaactagt	g	aaatgaaaac	gagttttatc	60
gattacgcca	tgagtgtcat	tgttgctcgt	gcacttccag	a	tggttagaga	tggtttaaaa	120
cctgttcac	gtcgtat	at	atatggtatg	a	aatgaactag	gtgtgacacc	180
cataagaaat	cagcacgtat	tactggtgat	g	t	ggttatgggta	aataccatcc	240
tcattctatt	acgaagcaat	ggtg	cgtatg	gc	cacaatggt	ggtcatatcg	300
gttgatggtc	atggaaactt	tggttcaatg	gatggggatg	gtg	ctgcccgc	acagcg	360
acagaagcac	gtatgagtaa	aattgctctt	gagatgcttc	gtg	atatcaa	taaaaataca	420
gttgat	tttc	aagataacta	tgatggcagt	ga	acgtgaac	ctcttg	480
ttccctaatt	tattagtcaa	tggtgcaact	ggtattgctg	tag	gtatggc	aacaaatatt	540
ccaccacata	atctaggtga	gtctatagat	gctgtcaagt	tg	gttatgga	taaccctgat	600
gttactacac	gggagttaat	ggaagttatt	cctgggtccag	at	tttctctac	tggtgccttg	660
gtgatgggac	gttcaggtat	tcaccgtgcc	tatgaaactg	gaa	agggatc	aattgtctta	720
cgttcacgga	ctgaaattga	aacaacttca	aatgggaaag	ag	cgtattgt	gtcacagag	780
ttcccatacg	gtgttaataa	aacaaaagta	cacgagcata	tt	gtacgttt	agcacaagaa	840
aagcgtattg	aaggtattac	tgctgttcgt	gatgaatcaa	gt	cgtgaagg	cgttcgtttt	900
gttattggaag	ttcgtcgtga	tgcttcagca	aatgtgattt	t	aaataatct	tttcaaatta	960
actagcttgc	agacaaattt	tagcttcaat	atgcttgcta	tt	gaaaaagg	tggtccgaaa	1020
at	ttt	gttcat	tacgacaaat	catt	gataac	tattattgaac	1080
cg	tcgtactc	ag	tttgacaa	ag	ctaaagca	gaagctcgtg	1140
ct	gtg	ggcgc	ttgatcactt	ggat	gaagtt	atcacgatta	1200
acc	attgctc	aagcagagtt	gatgtcacgt	ttt	gaattat	cggagcgtca	1260
at	tttagata	tg	cgtcttcg	tc	gtttaact	ggattagaac	1320
taca	atgact	tg	ctagcttt	aatt	gctgat	ttagcagata	1380
gtt	gtttacca	ttataaaaga	agagatggat	gag	gttaagc	gtaagtatgc	1440
cgt	acagaat	taatgattgg	tgaagtttta	tc	acttgaag	atgaagacct	1500
ga	agatgttc	ttattactct	ctcaaacaag	gg	atatatca	agcgtctcgc	1560
tt	tagagcac	aaaaacgtgg	aggacgcgg	att	caagggga	ctggaggttaa	1620
ttt	gttcgtg	aattggtttc	aacaagtact	cac	gatactg	tgcttttctt	1680
ggg	cgtgtgt	atcgtttgaa	agcatatgaa	att	ccagaat	atggacgtac	1740
ct	ccctatcg	ttaacc	tttt	aaa	acttgac	gaaggtgaaa	1800

GBS patentin.ST25

gctagaaaag aagatgtcgc taataaatat ttctttttca caactcagca aggtatagt	1860
aaacgtacaa gtgttttctga atttagtaac attcgtcaaa atggacttcg tgctattaat	1920
ttgaaagaga atgacgagtt gattaacgtc ctcttgattg acgaaaatga agatgttatt	1980
atcgggacac gtacaggcta ctctgttcgc ttcaaagtga acgctgtacg taatatggga	2040
cgcacagcga ctgggggtacg aggcgttaat cttcgtgaag gtgataaagt tgtgggagct	2100
tctcgtatcg ttaatggaca agaagtactg atcatcactg aaaaagggtta tggcaagaga	2160
acagaagctt cggaatatcc tacaaagggc cgtggtggta aaggaataaa aaccgcta	2220
attactgcta aaaatgggcc attagcacgc ttagtgacga ttaatggaaa tgaggacatc	2280
atggtcatta cagatacagg cgttattatt cgaaccaatg ttgctaatat ttctcaaact	2340
ggtcgttcta ctatgggtgt taaagtgatg agacttgatc aagaagctaa aatcggtact	2400
gttcgcgtag tggaacaaga aattgaagat aagtctaata tagaggatac aaaagaatag	2460

<210> 56

<211> 1329

<212> DNA

<213> Streptococcus agalactiae

<400> 56

atgacaatct ttgatgaaag agagttaaaa gaacgattta ctcataaaaa taggggttagt	60
ttttatgagt ttgtggctaa atatgatgct caaatgggtc ctgtgatgaa agcaaagggc	120
tatcgatgta ttcatccaat ggagcgtaca gtgggttttta cttttgggga attcacgatt	180
aggcgacgtc ggtggcaaaa aggagaacat tgggtggtgc cagttgatga aaagctagga	240
ctgaaaaaga atgttcgcta ctcttttagaa ttcatgtatc aaattgctag tttagcaacc	300
atgatgcctt atgaaaaagt gattaagggt gttcagatga tgtattgtat tgtgattacc	360
aaacctactg ttgtgaaggc cgtaagatt agtcgtgaat tgcttaaaga aaaggaagcg	420
tatcgttttt ttgatgaaga tataccagta gataaagaac cagttgatat gatttatctt	480
gaaggagatg gagtcatggt caaagctcga gaagaaggat tagataatcg caatgttgat	540
ttgtctcatt tcgtgggtca tacgggtagt cagaaagtag gaagcaatcg ctttgtctta	600
caaaataaaa aagagtttgt gtcccttgat aatcgtcaaa cgcgtcaaaa gattttggac	660
tacctttaca atcattttta cattgcccc aacaccttgc ttattaccaa ttcagatggg	720
ggccatggct ataccccata tgtttttaaa gagattgcga aagcactcaa agtgaagcaa	780
cacgaacact tttgggatag gtatcatgtc aatgaaaaga tcaaaagtgt ttttaaactc	840
tatccagtgg aactgatgac tggcgctttt cagagcatta aacagcatga taaagaaaag	900
cttagaactg ttttggtatc gacagaagca ttgatactga tggaagaaga aatggaaggg	960
tttaaccagt tcaaacgaaa gttgttaaac aattttcaat atactaaatc agctgaattg	1020

GBS patentin.ST25

agaggtttca gtcgtgcagg aataggtggt atggagtcac aacatcgaaa aattacctat	1080
cggatgaaaa agcgcgggat gtattggaca attcagggag ctgagacgat gagtcaatta	1140
attgtcctat cgtatgaagg acagctaaga gatctcttct ttgggttcttg gcgtgaagac	1200
tatcagaaat atcaagagct agaaaacctt agtgcgggaa aaatcaaaca tgaacagaat	1260
aaaatcaata agagatatga tctccagaca cttggtcggc ttaggtacgg taggcatcgt	1320
aatttatag	1329

<210> 57

<211> 384

<212> DNA

<213> Streptococcus agalactiae

<400> 57	
atggcatatt tatcaaaatt atccgatttg gatccatcgt tgatggatgc ggattctgaa	60
caaatttata ttcctaaagt cttgtttgag cataatgact ttaaaggctt gacctacaaa	120
gagattttat tatattcttt tttgttaa at cgtttaagag agccattaga ttttattcaa	180
aaaggctatg atgataatga agatacctat gttcacttta aggtcgaaga tttatgtgaa	240
ctactcaacc agagtaagac aaccgttatt tccttgaaga aaagggttagc tcaatatggt	300
ttgatagaag aagtgaaagc aggtagtcac cagccgaatc gtatttattt aacagataaa	360
ttagttccat atattaaggg gtaa	384

<210> 58

<211> 279

<212> DNA

<213> Streptococcus agalactiae

<400> 58	
atgacagata atcgctttgc ccaattaaaa gaaaactttg aaaagggatc tcctaaaagg	60
cgagttccaa cgtctcgccc aatcgcagct caaaaagcgc ctgagagcta taacaaaaag	120
ggacgggtatc cattttcgct ccaccaagat gtgcgttatg ataaattaga agcattagta	180
gcttatcatg gagctaagtc tgcatacagat tatctggaga gggtgattgt tcaggaatgg	240
gaaaagatgc agcgggaagct taagaacaaa gaaaaataa	279

<210> 59

<211> 3150

<212> DNA

GBS patentin.ST25

<213> Streptococcus agalactiae

```

<400> 59
atgttttagtt ggttggaagc tctttattac actctgatac aactggcaaa agtgaaccgg 60
ttgaatgctc ttttcttagt tagcgttggt gggttatcttt gttaccaggg aataaaactc 120
gtcagaaaaa ccataagaaa cttttttcag ctgatgaagg gtttcatagg tgatagagag 180
aacatcaaga aatgcatcaa aaacaagaaa gaggcactag tccattcttg gaaacatcgt 240
caagatattg attggaaatc aactggaaaa gataagagta aacagttatg gaatcttatg 300
aagcgacttg cgacagttgc tccttcattt ttgttcttat tattgggaaa tgttctcttt 360
cgtctcattt atcaactgcc ttttgtaaag caagacagaa agcgatttga caaggaaatg 420
aagcccttgc tctacttcaa gaactatcgt agttttgtgt tcatgggaat aggtttcagt 480
ttcatagcgt ttattctcac aaactatttt gtgacggttt taagggtctgc tattcgtttt 540
ctatatttct caatcatgac gttaagagat aatagccaag tcgttagctt taacgttgat 600
agtttgctca tccagaattt attcaatgct agggattttg tgatagctcc cattctagca 660
gtgccaatct ttctcattgg tttagtcgta gcttggcggg ctgcttgggt taactttgaa 720
cagtaccgtg attataatca taatgaagaa ggggatgacg gctttgagac tgtcaaagaa 780
atccaccagc aatataagaa agttcctaataaaaacggaaa cttatccagg tgaaggaggt 840
gtgcccgttc ttcataaagc aagaaagaat ttgacagggt taacgcttaa atctcaaag 900
ctttggcaaa accgtacctt tagtcgctat ttaacgaatg cggaaaggat tttagggtc 960
ttatcgacgc cttcaggaga ttattacatc gatgatagca ccacaaactt gatcaccatg 1020
gggattactc ggtcaggtaa gggagaagct catattgccc ctattattga tattaatagc 1080
cgtgcggaaa ttcaaccgtc actgattatt gcagacccta aaggggaaca ttaccagtcc 1140
tcttataaaa ccatgcgtcg gcgtggctat gatgttaatg tcctttcttt ccaaactatg 1200
gattgggtcca tgcctataa cccttagct cttgcgattg cagcagctaa gaagggttac 1260
tatgaaatga cacagacaag ggttaatgct gttgcagaag ccatttatcg taaaacgaaa 1320
cctggtagcg gtaatggcaa tgcaaaatac tgggaagata cctccatttc cctctttaat 1380
gccattgcta tggccttaat ggaccgtgct aatgaaaccg tcaggaatgg tgaaaccgat 1440
gcttgggata ccgttacagt tcgtaacatt gccaaagttt tgactgactt gggttctgaa 1500
gaagtctttg tcaatgattt tggagagatt gttgagaatc ctgataagaa ccaacaagtg 1560
aagaagaaat ctaaaatcac ggtttacttt gataacttgc gtaaaatcaa tcaagaacaa 1620
ttttccaaat ttagagatat ggctgattta aacttttaggt cttctgactt cgcttcagaa 1680
gaaactaagg gaaatgtctt ctctagcatg atgtcaggta ttaacttatt cttgcaagat 1740
aatattgcta aactaacctc taaaaactct attgacctag aatcggttgg tttcccacgt 1800
cgcttgctta tcaagtttcg ttctagttcc aatgtcgtta tgcgtaacga atacactcat 1860
aagacggcta aggttaccat tactagtcaa gctgtttggg gtaaaaccac taaacaagtt 1920

```

GBS patentin.ST25

atccacgtag atgctgcaac agctctgatt gatggtgaag gctatctaac ctatgtgatt	1980
gaaccccagc ttcctgatca attcttggtta acaattgact ttaatcacga aaacaatggt	2040
ggttcagcta ttcgtcacia aactttccaa ttctcagctg agaaagtcta taagaaacgt	2100
ggtaacgtta ttacgttggga tgactacacg aaaaaaccag ttttggatca tatcaaagtt	2160
actgtttctca acaagcaaga tgataacctt ctccagaaaag aagatattga cctgatttat	2220
tcagataatc ctaaagtgat ttacttggta acacctccaa ataggactga atataatagt	2280
attgtatctc tgtttttgga tcaattgttt aatgccaaat atgagtttagc tctgtcaa	2340
ggtcgcaagt gtgtcaatcg aattcttcat atcctcgatg aattcacaaa cattccagct	2400
attcctcaca tggataccaa gatttccatt ggtcttggtc aaaatattct ctactatctc	2460
tggattcaga acttgaaaca gttagtcagt gaatatggcg agaatacagc ggaaaccatt	2520
cggggagaact gttctttgaa agtttatatc aaatctactg cccagcgcac caacgagtac	2580
ttcagtaaag agttggggac tcggaccatt acacgtcgca gaaggccaag taatattcta	2640
gatgaagcta atccaaatgt ttccattgaa aatcctagac aggaactctt aacaccgaca	2700
cagctctcga aactccaaga aggggaagcg gttattttgc gtggtgttaa aggtcgagac	2760
aatgcagggtc ggaaaatcac aacggatccg attttcttgc atgagaaaac gagccttcct	2820
tatcgctaca tgttcttaca agaagaattt gaccagtcga tggctttggc agatattcca	2880
gtggaaaagtg ggcataggga ccttgacctg caagatatag cagtaggggc acaaagcact	2940
tttaataaga ttattgattg gcggatggct ctaactgacc gtatgagAAC aaatgggaag	3000
atacctcaat tagcatcaag aaaacaaacg attaaagctc taagtcaatc tcaatttact	3060
tctccagcag acctaacaca agctgtgatt gcagaggtat ttgatgagga agatgatgac	3120
gatcttttct ttgtggatga tgtcatgtaa	3150

<210> 60

<211> 2802

<212> DNA

<213> Streptococcus agalactiae

<400> 60

atgaattcta acacaaaagg tcacggattt ttccgcaagt caaaagcata cggcttagta	60
tgtgctattg cattagcagg tgcatTTACA ttagctacta gtcaagtgtc tgctgatcaa	120
gttacaactc aagcaacaac tcaaacagta acgcaaaatc aagcagaaac agtaacatca	180
actcaacttg ataaagcagt agctacagct aaaaaagcag ctgtagctgt tacaaccaca	240
cctgcagtta atcatgcgac aactactgat gcacaagctg atttagctaa tcaaacacaa	300
gctgttaaaag atgttactgc aaaagcacia gctaatacac aagctattaa agatgctact	360
gctgaaaatg caaaaattga tgctgaaaac aaagcagagg cagagcgtgt tgcaaaagaa	420

GBS patentin.ST25

aacaaggaag	gtcaagcagc	cgtagatgca	cgtaacaaag	caggtcaagc	agccgtagat	480
gcacgtaata	aagcgaaaca	gcaagcgcaa	gacgatcaaa	aagcaaaaat	tgatgctgaa	540
aacaaagcag	agtctcaacg	tgtaagtcag	ttaaatgcac	aaaataaagc	aaaaattgac	600
gcagaaaata	aagatgcgca	agctaaagca	aatgcgacta	atgcacaatt	acaaaaagat	660
tatcaagcta	aattagcggg	aatcaaata	gttgaagctt	ataatgcagg	tgtacgtcaa	720
cgtaataaag	atgcacaagc	taaagcagat	gcgactaacg	cacagttaca	aaaagactat	780
caagctaaat	tagcacttta	taatcaagct	ctaaaagcta	aagcagaagc	agataaacag	840
tctattaata	atgttgcttt	tgatatcaaa	gctcaagcta	aaggtgttga	taacgctgaa	900
tatggaaact	caatcatgac	tgcaaaaact	aaacctgacg	gaagtttcga	gtttaaccat	960
gatatgatcg	atgggtgtgaa	gacaatcggc	tatgggaaat	tgacaggtaa	agttaatcat	1020
cattatgttg	ctaacaagga	tggtctctgtg	acagcatttg	ttgattctgt	cactctttac	1080
aagtacgagt	atcgtaatgt	tgctcaaaat	gctgctgtta	acaaaaatat	tgtatttaga	1140
gttttaacaa	aagatggctg	tcctatTTTT	gaaaaagctc	ataatggtaa	caaaactttt	1200
gcagaaactt	taaacaaaac	tttacaactc	aatcttaaata	atgagcttaa	accacatgct	1260
tccagcggta	acgtcgaagt	ctttaagatt	catgatgact	gggtacatga	cacacatggg	1320
tctgctttag	tgtcttatgt	taataataat	gatgctgttc	ctaattgtgg	catcccagaa	1380
cggccaactc	caccaaagcc	agtgaaggtt	acacctgaag	cagaaaaacc	agtacctgaa	1440
aagccagttg	agcctaaatt	ggtaacgcct	acattaaaaa	cttatactcc	agtcaaattt	1500
attccgcgag	aatacaaac	agaaccaatc	accttgaga	cgtttacc	tgagaaattt	1560
actccagctc	aaccaaag	gaaaccacat	gtgtctattc	ctgaaaagat	taactactca	1620
gttagtgttc	atcctgtttt	agttccagct	gctaattcct	caaaagctgt	cattgatgaa	1680
gcaggtcaat	ctgttaatgg	taaaaccgta	ttaccaaatg	caacattaga	ctatgttgct	1740
aaacaaaact	ttagtcaata	caaaggtatt	aaagcttctg	cagaagcgat	cgcaaaaggt	1800
tttgcatTTG	tagatcaacc	aaatgaagcg	ttagctgaat	tgactgttaa	gtctatcaaa	1860
gcatctaattg	gtgatgatgt	atcaagcttg	ttagaaatgc	gtcatgtttt	atcaaaagat	1920
acttttagacc	aaaaacttca	atctcttatt	aaagaggcag	gaattagtcc	agttgggtgag	1980
ttttacatgt	ggactgcaaa	agatccacaa	gctttttata	aagcttatgt	tcaaaaagga	2040
ctagatatca	cttataatct	atccttttaa	atcaaagcta	actttactaa	aggtcaaatc	2100
aaaaatggtg	ttgcacagat	tgattttggg	aatggatata	caggtaatat	tgtagtcaat	2160
gatgttactg	ttccagaagt	acataaggat	atacttgata	aagaggatgg	taaatcaatt	2220
aataatagta	cggttaaagt	aggtgatgaa	gtgacctaca	aacttgaagg	atgggttgta	2280
ccagcaaacc	gtggttacga	tctttttgaa	tacaaatttg	tggtatcaatt	acaacacaca	2340
catgatcttt	acttacgtga	taaagtggct	gctaaagttg	atgtgacatt	aaaagatggg	2400
acagtcatta	aaaaagggac	taatttagga	gagtacacag	aaacagttta	caacaaaacg	2460

GBS patentin.ST25

acaggtcatt atgagcttgc ctttaaaaaa gagtttttag ctaaggtttc tcgtgaatca	2520
gaatttggtg cagatgattt tattgtagtt aaacgtatta aggcaggtga tgtttacaat	2580
actgctgatt tatatgttaa tggatataaa gttaagtcag aagcagttgt gactcatact	2640
actgagaaat caaaaccagt tgaaccacaa aaagcaactc caaaagctcc agctaaagga	2700
ctgccatcaa ctggtgaagc tagtatgacg ccacttactg caattggagc aattatctta	2760
tcagctctag gcctcgcagg ctttaaaaag cgtcaaaaat aa	2802

<210> 61

<211> 2262

<212> DNA

<213> Streptococcus agalactiae

<400> 61	
atgaaacaaa taaaaattat cacaggactt acagtcgcaa cactatccgc agtggtaggg	60
aatgtatacg cagaagatat cacaccgaca gcaccagtta atgagccaca agtttcaagc	120
gaaaccgcaa aaacgcctca agttacagaa agtcaagtta atagcgcaaa agttactgcc	180
gatcaagcaa taagtgatgt taataaccaa caaattgtag ttgatgaggc tcaaaagcag	240
aaagatcaat cacaacaaaa tcttgtaaaa gccacatcaa cagtaactga agctgaaaaa	300
gtcgctgctg aggcaacacc tgaagttgtt aaagaagcta ttaaagctgt cactgaagca	360
aaggaagctg ttacggatgc tgaagctaata gtagtcgatg cacaaaagac ggaacaaaaa	420
gctaatacaag aagtacaatc gcaagctaag actgttgatg aaaatgttaa agttgttgct	480
gataaagaat ccgaagtga acaagcagag ggtgttgtaa ctacagctca agaagctatt	540
gatagcaaaa ccgctaacac taatgcatca gaagcagaaa aagcagtgac tgagaagcaa	600
acaaagcttg aaactgctga aacaaatctt acagaggcac aaaaacaaga tgccaaaatc	660
gctgaagaaa aacgacttgc agaacaagaa gttgttaata aacaattagc tgtgacagat	720
acacaaactc ttttgaagaa gcttgttact gagattaata acgagaaagt aagcactagt	780
ttagaaaacc aagcctatct taaccaacgt gacggttcat gggcgggcta ttatggcaat	840
tatacttttg ccgctactgg ctgtgtacca agtagtttag caatggtatt tacggagtta	900
gctagacgcc aaattactcc aactgaaatc gccaatatc tttggaacaa ttcaaatgag	960
tttaataaaa actatggtgg aacaagtggc aaagggttag tacaagctac taaacatttc	1020
ggttttgtac caactcattt agcatctcaa tctgctattg tggaagcctt acaggcagga	1080
caccatgtcc tagcagctgt ccaacaagat aaattttctc cttgggggtat caattacagc	1140
catgagattg tcttacgtgg ttactcaaat ggcaatactt atgtttacga tccttataat	1200
cgagctaaca ttgggtggta ccctgttgct aatttatgga atgaacaaag tagagacgca	1260
attgacacat ctagtgtagg cgtaccattt ttcaaaatta caacacaaa aatggcccaa	1320

GBS patentin.ST25

ttagaagctc agaaagcaca agttcaatct tctctaaata cagctaaaaa tcagtttagct	1380
aaaacacaag acgtattaag aacactagaa gcaacacctc ttaaaacacc agaagcacia	1440
gctaagctta atcaagccaa agaagctcta gctcttgac aagcagacta tactaaagcg	1500
caagaagctg ttaagtttagc tagtcaagac ttagctgtta aagaagaaac acttaaaaaat	1560
gctcaggctg atttattaac gaaacaaaca gccttgaaag atgctcaaac tgttctcgtg	1620
gctagtcaag ttaaatttagc tgatcttaaa gcaacttttag ctactgttga aaataacggt	1680
aagaaagctc aagctacttt aacagatgcc aaagcaattg ttggtcaaaa acaagcaaaa	1740
ttacttgctt tacaaaatgc ccctaaaatt ctagcagatg ctcaagctaa acttgtaact	1800
gctaaaaatg attttagctaa taaaatggct atttttagatg aagcagtcgc aaaactaaaa	1860
tccttacaag ccgttcaagc cgaagcccaa aaacaatacc atgttgtttt tgaagcctat	1920
aaagcagtac gagatgccaa agaacaagct aaacttgacg aaagctataa ccatattatc	1980
gcacgaggcg gtgaggctat cccagttggt gacgaaacag ataaaataac tggatatgta	2040
gatggttagcc agaaagcagt tgctaataaa gtgactcttg ccttaactag taacggtgca	2100
ccccttgaaa gtccagttaa taaagaaaac caaaacgtaa caaatcatc tcaagcttta	2160
ccacatactg gtgaagctgg attatccatt ttatcagtat taggtgtagg tcttatctca	2220
actttagggc ttactagttt gaaaaaacgt cgccacatt aa	2262

<210> 62

<211> 1920

<212> DNA

<213> Streptococcus agalactiae

<400> 62	
gtgagattaa cccacgtgag tttgtggatg ccatcaaaga gaagttggcc gctcaaattg	60
cagttgttaa ggaaaggagt gattgagttg gaagatgaac tgaagacccc ttatcttgat	120
caatacacag acaatttaac ggctaaagtc actaaaaaat cggatgacta ccaagtttat	180
ggacgaaaca aggaggttca atccgtcatc atctctcttc tcagacgaac caaaaataac	240
cctatttttag taggagaagc aggggttggt aaatcagcca ttgtggaagg tataacgctt	300
gctatcttac gtggccaagt tcctgaacct ttaaaagggt taacgggttcg ttccctggag	360
ttgtctagtt tgatgagtga agatgacgaa ggctttattg ctaagtttaa gaagattatt	420
gaagagatgg ttgctacacg tggtcataat cttctctttg tagatgaatt tcatacgatt	480
attggtgcgg gtagccagaa tggccaagcc cttgatgcag gaaatgtgat taaacctgtc	540
ttagcacgtg gtgatattca gctgattgga gcaaccacct tagatgagtt ccatgagtat	600
attgaaacag atagagcctt ggaacgtcgg atgcagcctg ttatggttga agagccaacg	660
atttcacaag ctattacat tattgaacaa gctaaagtca ttatgagaa gtttcatggg	720

GBS patentin.ST25

attcaaattt cctcagatgc tgtgcatcaa gcaatccgtt tatctgttcg ctatttgaca	780
gatcgattct tgccggataa ggcctttgat ttgatcgatg aagcggcgac gattgcttca	840
gttgaagggg aaagtaaggt gacagaaaaa gatattgctc aagttttaaa agataaaaacg	900
ggaattccag tcactactat cctaaagggg gatcaagagc ggtagagggg tttcaaagaa	960
aggctgatga atcgagtcaa aggtcaagaa gatgccattg aggccgttgt agatgcggta	1020
acgattgctc aagctgggtt acaaaatgaa aaaaggccgc ttgcatcatt ctttttcctc	1080
ggaccaactg gcgttgggaa aacagaatta gccaaagcaa ttgcagaagc actttttgat	1140
gatgaagctg ccatgattcg ttttgatatg tctgagtaca aacaaaaaga agatgtgact	1200
aaactcatcg gcaatcgtgc gacaagaata aaaggacaat tgactgaagg agtaaaacag	1260
aagccttatt gtgtcctgtt actagatgag attgaaaaag cacacagtga ggtaatggat	1320
cttttcttgc aagtgctaga tgatgggtcgt ttaacagata gttcgggtcg tttgattagc	1380
tttaaaaaca ccattgtgat tatgaccacc aatattggcg ctaaaaaat catcaataag	1440
tgggagttga aaggaaactt taaagattta accgatcgag atcggaaaca atttgaaaag	1500
tcgatggaca gtgagcttca aaatgagttt cgtccagaat ttctcaatag gattgaaaat	1560
aagctcatct tcaacctttt agaacgtgat gtgattgaaa aaattgcaga aaaaaatcta	1620
tctgagattg cggataggat gaagcgccaa aatttaacac tgtcatatga gcctagtctg	1680
attcagtatc tctctgatgt tgggtactgat gtgaaaaatg gcgcacgtcc cttagaacga	1740
ctgatgaaac gaaaagtgtc ggcacccatt tctgtaaaaa gcttacagtt agataagtca	1800
aagcaaggct ataacgttca tctctgggtt gagggacggg ctccagacgg caatcatcgt	1860
caagaacaac gtcaaattca catggagata gagggagaaa gagataactt ttttagctga	1920

<210> 63

<211> 4731

<212> DNA

<213> Streptococcus agalactiae

<400> 63

atggcagaag aaaatgcaca acagccatct ttacgtggaa aaagccgtcg agaacgtgtt	60
gaatttgctc gttcccgtga tatttttagat gtggcccatg aattgaatat ggaacttttt	120
cgagatggca aaaattatcg ttggaaagag cacgattcta tggttaattac acctgcaact	180
aatcagtggg actggttttc acaacgtcaa ggaggtgatg tgattgcgct tgtagagacg	240
ataaaagaaa tcggcttcaa tcaagcattt gaatacctga atgaaggtag atttaaagaa	300
tttactgtgg tcaatcaagt aaaagaacct ttttcttatt atttagaacc ttacgaacag	360
ctttttgttg aagcaagacg ttatttgaaa gagaatcgtg gcttatcaga tgacactatt	420
gatttttttt atgataaagg agtacttgct caagccaatg ccaaggtagg tgatatgatt	480

GBS patentin.ST25

gagcctgttt tgggtgttta aaacttggat aagaacggcc aagtggttgg cgctgctcta 540
 caaggccttag tagctgcccc cgataaatat ttcggtcggg gttacctcaa acaaatcatg 600
 aaaaattccc aaccttacaa cggcatgcat gttgatattg gcacaccaa cgcctagtc 660
 tttgcggaaa gtagtattga tcttatgagt tactatgaaa tccacaaaga tagcttatca 720
 gatgttcgtt tagtttcctt agaaggcttg aaaacaggaa caataggaag gcatctcatc 780
 caattaagag ctgaaatgga acgtcgtccc ctctcctcca gttggactga tgaaatactt 840
 gctcagggat tagatgaggc tgtaaagcaa ggctatttca aagatggtaa gaacagtcatt 900
 ctctttacgc tagctgtaga taatgatgta aaaggtaaac aattgattga agagttaaaa 960
 gataagagca tcccagtcatt tgatgccact cctcctaaag cagaagggtca atctaaaatg 1020
 gattggaatg cctattttgca ggaaaccaag gctacttttt ctactgaaaa atatcaagaa 1080
 aagattgatc acctaatatc agatgttatt ttaggtgatg aaacttatta tctttggcat 1140
 gatgatgagt tggtaaattt aggagcagga gactctatta tacaggcgtt tcatcatcag 1200
 ctggaagaca gacgttatgt tattaatcag gcagaacttt acgttgaaga gtccagtaat 1260
 gatggggcta ctggctatct atcaattgaa ggacatgtat tagataagga tggatttagt 1320
 gactatttat ctgatcaagc tttaacagat gcggaaaaag tagcattctt agaaacttta 1380
 cagacagaac taccagatat ttgggacgag atagtcaatc attatgacaa ggtctttgaa 1440
 gaagttgtcg ttaaataatg actcagagaa aaacatgcgg acataattca ggaacaagag 1500
 ttggatttag accctttagt tgttcagaa gcaaaagaaa agtcccttga aatgaatcaa 1560
 gagactaaca ctggcggcga actatttaac cgcaattcca gttttttagg agaagattct 1620
 ccggggacag caccgcagcc cgttgagcca actgctcaac ctgattttcc taccaatggt 1680
 cgcttacatt ttaccactga tgatggaaat atgtcaaata aagcatttag gaaaaacatg 1740
 cgaaccttga atttatatgc taatacgatg agagattcgg cacaatggta cttatcagaa 1800
 atagccgata ctacaatgag ttatgtttat aaaactcctc atgaagaggg agtacagggt 1860
 cttagtgtgc attttggtta aaagaattgg atgcacttaa caggagtgc accagtatat 1920
 gaaaattggg tagattcact ttctgaacaa ttatttgatg atattgctaa tagtaagggg 1980
 cattttaaaa atctaaagtt tgcactaggg actcctgata agttaaagggt tcttaactta 2040
 cttcctgaaa ttattgaatc agataccttt gtatttaatg atttatcatc tgttcaaaag 2100
 ttaataatc ttgatttatc acaggcgtt aatcctgaag atagcgattt acttttgcta 2160
 tttagagatg aggggcttca tcaagtgcct gcttcgttga tgaggataaa gggcgattta 2220
 gaagaaagat tatctcatat agatagtggg acagtgttag gagtttaccg agaaagaaat 2280
 ggccaacttg agcaagtttc tgtcaatgag gagtatgtca aagatagtgg tcaagaaatg 2340
 ctatctatct tacagaataa gcactatgaa gaggtccttg atagtggta agaaatgggt 2400
 caaacggatg gtttttcagc cgaagatttc aaaaagttt tggatgctgt ctatcatggt 2460
 ggtgttccag atgatttagc acgtgttcca gaaggagtct tacctgtttg gcaaaaatat 2520

GBS patentin.ST25

cttgaggtat	cagaagagaa	tcaatgggac	ttagaacaaa	tgattgatta	tgcgataag	2580
aacagtcttt	tagtaaaaga	ttctgccttc	tataaagagt	ggaaagagga	tatgatctat	2640
aaaaatgact	atcatgttcg	cttacaattt	gctgagaatt	gggataatgg	cgttgaactg	2700
cctttccgta	cagaacaatt	gattgattac	aaaacgtttg	tcacaggact	ttatgaagct	2760
aatcaagctc	atcatcaacg	cagacaagaa	agtcagcttc	cttatacaaa	aacagagttt	2820
gacatttatg	ctcctggcgg	acagctcatt	aaagataatg	tccattatgc	tattggagat	2880
gaaacaagac	ctgtttcaca	actcatgggg	ttaggttatc	gtcgcctacc	tggctatcag	2940
gaattagctg	tgatagataa	cagtattctt	tctcagctgg	aaaataagga	gctaaatcaa	3000
gaaattgctt	ctgaagctaa	tgaacattcc	ttaaattcac	aagaaatacc	taaagaagat	3060
aactatccaa	gagaagcttt	cacttctcct	aaacaagaca	tcaaaaaggg	gctagctcaa	3120
cgagtagaag	agattgtggc	agaagatgct	actaagattt	tagtatcttc	cattcctcaa	3180
gttcaagaga	atttatcagt	cgaaggaaac	ttggtcggta	ctccacaagc	ggataatcgg	3240
atgctataca	ctaacctaga	agattttggc	caagattatc	aattagagct	tgagttttat	3300
agtccaaaac	gggttgactt	tttagaagat	gtgcaggctc	cgtggacctt	ggccctaatt	3360
agaaaagaaa	aaaagatagg	ttatttagcg	tatggtagtg	attgggcaaa	agaatttcag	3420
attgaagaag	agctagaaca	tttagctgca	caaattggag	acgaaaaagt	accagagggga	3480
ctctataaac	aagctgaagt	agaggctttt	atagctagtc	atcagggaaa	tgaaagcctt	3540
caggaaccaa	tacctactat	tgtagctgaa	ccgtttgact	ataccagtgc	ctccgcctat	3600
gagatcagcg	aacacgcttt	ccaaaagatt	cgtgagtaca	cacaatcccc	tgaggacttg	3660
cttgagtaca	tggatttcat	gagtaagttc	ccacaacttt	cacctcgaaa	tgctgctctt	3720
atccatgaac	aatggcgtgg	cgcaaatgca	gtcgcaactt	acgaacaatg	gaaagccatg	3780
ggagaagctc	taggtattaa	accagacgat	gttggtccaaa	caaaagcaac	ttatgttaat	3840
aagcggacag	gagagacgaa	ggaagtcggt	catcaagggg	tatctgttaa	gactggcgaa	3900
aaatcgaaaa	ttacgctctt	tagaccgcta	atgggttaaaa	tgatcccagt	tcttgatgag	3960
aatggtcaac	agctgaaaaa	tgataaagg	aatccaaagt	ataagaagct	atcagaagcg	4020
tcacttcaag	agaaagcttt	agtaaaagac	ggtaaaacttc	cagttcgtca	atttcaggag	4080
agagattcaa	aaactggtca	accaagggtt	acgacttaca	aagtttttga	gttggtcacia	4140
actactctga	agccaggaag	ctatcctaag	gctatgcaa	accgtcattt	caactttaat	4200
gtggataaag	tcaagactaa	agaggtatta	gaagggtctt	gtgactatgc	ggaaaagatt	4260
ggggttagcc	taatgaaaga	tgatgctcat	gttttggata	atgccaaagg	agctttttat	4320
tcagaagaac	agctgattct	tattaatcct	aataatacac	ctggagaaaa	aattgcaact	4380
accattcatg	agttagcaca	tgcaaccctt	cataatccta	agttggaaaa	acagtataaa	4440
gagttgccga	aaggacaaaa	agaatttgaa	gctgagatga	ccagttactt	gttggtcaaaa	4500
cactttggcc	tagatacgtc	tgaaaaggca	atccattata	tggcaagttg	gacagataat	4560

GBS patentin.ST25

ctaaaagcgt tagaggataa acaattggca gactctctga aacgagttca tcaaacggtt	4620
tcgaaaatgt tgaagcaagt tgaaaaatat acgaaccctc accagctagg aagggggaaa	4680
gaacacggtc taaattttcc taaagcccca accaaagggt ctagtcgtta a	4731

<210> 64

<211> 2367

<212> DNA

<213> Streptococcus agalactiae

<400> 64

atggatgtat cgtctagtcc gaattattaca tttatgctgc aatacacaga ggctaattcct	60
caatatgtgg actatactaa cagagaagag gctgtcaaaa ttgatgaaga attgtcctta	120
gaaacgaaca ggcaaatgat tgaaggatta actgaagacg agttgactcg tattcaggaa	180
gctgtccctg aaacgcagtt gaatttttagg gaatacattg attatatgaa ccgctcgtat	240
gcaactgaag aacaatctaa agaactaaca gctatcttta ctcaagaagc agattatctt	300
cagaaactac gattaatcga tctaaaaaat aagttggaat cagcttatca aaatggttca	360
cttctctggc aaggagttat ttcgtttgat aatgcttttc ttgcggaaca gggattgtat	420
gatgttgcga ctggtcaagt tgatcaaaaa gcgattaagg cagtgatgcg tgatatgatg	480
ccaacactta tccagaaaga gggcctttct gattctgctt tttggtgggg gaatatccat	540
ctgaatacag ataatatcca tatccatttt gggctttctg aagttgaatc taaccgtgag	600
aaaatattct atcagccacg tggacgtatg gagtacaaag gtaacttctc tcagaaaacc	660
atcaaccggt ttaaaagtgg tgtgtatcat ggattgctga aagaagaaac aagatccaat	720
cttctcagaa aagaacagat tttagctaatt ctcaaagcgg acttcataac atctattttac	780
cagaaggaca agattacttc ttcagctgaa aaaaattttt tggaacaagc ctacaatcat	840
ttgccgctaa ataagaagtg gcgctatggt tctaatacca gagattttgc ggtagtaag	900
ttctttcttg atcgctattt agattcctat ttaacaatg aaggtagtgc tgcctatcaa	960
gaatttttga aagagactag agattttctt cagacttatg aaggggttta ttcagctgaa	1020
aaaaataaaa tctatgaaaa actacgtaaa gttgatgggc aaacgatcag aacgcttgca	1080
gaatcaaaag gatatgattt agaacatcat ttggcacgctc gtgtaatgga tttagagag	1140
cgttttagcca ataatatctt acgttcgttt agagaagctg caccctaaat tcaagacggt	1200
cagctggaaa aaaattttaga gagtttttct gttttgaacc agaagaaaat tttagaacaa	1260
catcctgaag caagtgtggt aaaaagtcag aaagcttggc agaagttagg ctactttgtg	1320
aaggctggag agcagccact tgaaattata aggccagtct ataaatctta tgataagcat	1380
ggtaaaggta taggacggcc agaatttgta tcagatactg tttatgatat tagtcagcta	1440
acagaaaata ttcagctgaa aagtctaacc ttgaaagacc tctctctggt ttcttctaac	1500

GBS patentin.ST25

gagttaaaag agttagtaga tgctgctaag ttaaagacta atccaacaga gagagaacgc	1560
cgtgaattag gtacctatcg ttatgcgttg aaacttagca tattagaatc tagtcagaag	1620
gaattgcagg ttcgtcaaaa gctactagaa caggtacagc cactagcgtc tgatcaacca	1680
tttttagatt ttaagaaaca gttaatagct caggaattac aagctatagc gctacaattg	1740
actcctaatt acaagctatc agaagatgat aaagccttga aaaatcgatt gaagaggcag	1800
tttgaagata gtgttgcgct acctgtttca aaagctactc ctggtgccat acaacttcct	1860
attaggcaac tttggactga gctaggattg gttcatcaca ttcaagatga aaacattcta	1920
acgcttctga aagggacatc aacgacgaaa caagcttata tagaagaact tcagactcat	1980
atctctatct ttcagttgaa atatcagatt aacaatagaa acaagcagat aagccagtta	2040
tcggatgaag caacaataaa ggagatgagg atagctaattg cttaaagggtt ctctgagcta	2100
aaacgtctat atgatacatt acagccatca gatgatggtc aaaatcagat tagtcaagct	2160
gtttctaaac aattacaaga acgaaaagtt atcaaaaaag ctcaattaca acagacgcag	2220
agaagcggaa aaatcaatac agacttcatg cgacaattga cagcttctct taatcgttca	2280
caacaagcaa gtaaaaaagc attgatggaa cgtgcacgta gtgatgaacg tgaggaacaa	2340
gaagaacgta ggcaagctca acgttaa	2367

<210> 65

<211> 801

<212> DNA

<213> Streptococcus agalactiae

<400> 65

atgaagaaga ataaatttct attagtcagc attgtattta tcatcatttt tgtggtacag	60
ccacaaaatt ttcaatcttt aaaaaatata ttactcaaa atgatatagc tagtcaattg	120
aatatatcaa gttcacctga agaaaaaat gatggcttag gaacggccta tcaaacgcaa	180
aatgaagatt tgaaatctaa aagttttgat ggtcaacatc aagtcatagt ggttaatgaa	240
aaagcacaat ttacggcaga agagttgagc atgagaaatg gttcatggga aaaatacgat	300
aacctagatt ttttaaatcg tgttggggtc gcagaagcta tgtaggaaa agagttaatg	360
ccaaaagagg cacgtcagga cttttcttca gtcaaacc aa ctggctggaa aaataaaaaa	420
attaccttca atggaaagca agattatctc tataatcgtt ctcaactaat tggatttcag	480
ttaagtgggtg agaatgccaa tgtgaaaaat ctctttacag gaacacgtgc ccttaatgca	540
aactttaacg atgataaatc gtccatgggtg tactatgaaa atgaggtcgc aaactacatt	600
aagaaaacaa atcatcatgt tcgttatcga gtgacccac ttttcaaaaa tgtggagtta	660
gtagctcgtg gcgtacgtat agaagcacia agtattgaag atgagaccat ctcatctgat	720
gtctatattt ttaatgggca accaggatat gacattgatt atttgacggg atcatctgaa	780

aaaataatga ttacaaaatg a

801

<210> 66

<211> 348

<212> DNA

<213> Streptococcus agalactiae

<400> 66

gtgactaaag aaattaaaat tagatccatt ccagaaaaaa catgggcaca gctacatatg	60
atttcggaag aatatgagta tccgtctttt aatgaattta tgcttgctca attgcaacgg	120
attgtcgaaa atggtggtct tgatttatat gataataaat ttgcggaaac cttggcagtt	180
attaaagaac aacaagcaca aatattggat cagctcctaa aaaacgaaat caagttactg	240
gcttatcatg caaagcaaga tatagtggaa gagctaaca ccgactgggtt acgatttatg	300
gatgatgttg atgcgctggc tgcggaaaga ggagcaggag gacgttga	348

<210> 67

<211> 843

<212> DNA

<213> Streptococcus agalactiae

<400> 67

ttgttatatt attttattta cttgataaaa gtaattggaa atggccttaa attatcactg	60
atttgtgggt taaattggct catcaaaata gtattcaaag gacaatttta tcttttctca	120
gctgtctttt gtggcttggt gacctactat atgccacaag atattcaatt atttacagt	180
agagtttttag agctaatscat catgctaaaa gtgataatag atgttaccga tacagctctt	240
tcaagagatt ttaaaccgat gaaaacgcct ctttttttag gaggatgta cgtcttcttt	300
ctagctggta acagttatat taaagcacat cttttgacag aagttatggt taatcatctt	360
atttcgtttt ggcttatcag cctgtttttt gccactcttg taatagttat tcagcccaga	420
ttatttaagc attatctggt aaaaaaagtc attgataagg aatacttggg tatccgaaaa	480
ttcacagact ctcttctcc agaaatcaat ttgtacaagg atgcggacga agaagatgag	540
gacaaacgga tgcgactgat caaccagaat gtcacaaac acccctatca agaagttggt	600
gaactgagct ttttgaatag agaagtgata acagctattg gctataaagc cgttccattt	660
gaaaaagaaa ctgaacgtac ttttatagac gatgatacca tctattatcc catttttacg	720
gttcaccctt tcagaaattt ggaagggaaa tcagattttt atcacatact aatgaaactt	780
aaactcagtc gaaaagcggc ctttacaaaa aatggtgagc gattattaat tagagatttt	840
taa	843

GBS patentin.ST25

<210> 68

<211> 495

<212> DNA

<213> Streptococcus agalactiae

<400> 68
atgattagaa atgaatttta taatcagtta atcaatagtg agccaatagg ttttattgat 60
cctttcactg acttaggaga atttgattct attcagatga agttcaaaca acctgttaga 120
aatctggtaa ataagtactc tggtaaacct tataatctta gttggcaaaa taagattgaa 180
cagatgagag tgctatatat taaatatcag aaaagcttga agctagaaga tgaagaacaa 240
gagggttcata accgagttaa aaataaaaag tctaaaaaat atgttcatga aatcggtaca 300
acatatattga agttaggatt cagggtttaa gaaattgaag caaggggtatc cctattcaat 360
actcgtcttc gtcggaactg gaaaagaagc gactatgtga caactgataa ccctgaattc 420
tatttgaaga aggatctaca gaatgggttat tgttctccaa attcatttct tcctcggagt 480
atgaaaataa actaa 495

<210> 69

<211> 1272

<212> DNA

<213> Streptococcus agalactiae

<400> 69
atgaacgaaa tcaaattgcc tcattgtgga acagcttttg ccatcaacga gtctgaatac 60
catcaattac tagaaciaat tcgtggagat gcttttgaca aagaagtaag tgaacggttg 120
gaaaaagaac gtctaattatt aggggagcaa gcaaaaaatc aattacagga agttgttgta 180
gaaaaagaca aggagatagc taaacttcag tacaaagtca aacaatttct tatagaaaaa 240
gacaatcttc tcaaagacaa tgagtaccaa ctcgctgagc aattaaatca aaaagacatg 300
atgcttcgcg accttgaaaa ccaaactgat agactacgtt tagagcatga aaatagcttg 360
caagaggcgc taacaaaagt cgaacgagaa agagatgcaa tacaaaatca gttgcacatt 420
caagaaaaag aaaaagattt agcttttagct tcagtaaaaa gtgattatga agtacaacta 480
aaggcagcca atgaacaagt agaattctat aaaaacttca aagctcaaca gtctactaaa 540
gcagtaggag aaagtttaga acattatgct gaaacagaat ttaataaagt gcgacatttg 600
gcctttccta atgcttattt tgagaaggac aatacattat caagtcgtgg ctcaaagggg 660
gactttatct atcgagaaaa ggatgaaaat gaccttgagt ttttaagtat catgtttgaa 720
atgaaaaatg agtctgatga tactatcaag aagcataaaa atgaagattt tttcaaagaa 780

GBS patentin.ST25

ttagataaag atcgtcgtga aaaatcttgc gaatacgcag ttttagtaac tatgcttgaa	840
gcagacaatg actattataa tactggaatt gttgatgtta gtcacaaata ccctaaaatg	900
tacgtttatac gtccacaatt ttttatccaa ttaattggta ttctaagaaa tgcagcactc	960
aataccttaa aatataaaca agagcttgct ttgatgaaag aacaaaatat tgacatcaca	1020
cattttgaag aagatttaga tattttcaaa aatgcatttg ctaaaaatta taattctgca	1080
agcaaaaatt tccagaaagc aatcgatgaa atagataaat ctattaaacg tatggaagct	1140
gttaaggctg ctttaacaac gtctgaaaat caactacgtc ttgcaaataa taaattagac	1200
gatgtttctg tcaagaaatt aacaagaaaa aatccaacaa tgaaagcaaa attcgatgct	1260
ctaaaagact aa	1272

<210> 70

<211> 843

<212> DNA

<213> streptococcus agalactiae

<400> 70

atgaatcatt ttgaactatt taagcttaaa aaagctggac taacaaatct taatatcaac	60
aatattatca actatctcaa aaagaatagt ttaacttctc tatctgttcg caatatggcc	120
gtagtatcaa aatgtaaaaa tcctactttc tttatagaaa attataaaca gctagacctt	180
aaaaaacttc gacaagaatt caaaaaattt ccagttctat cgattttgga ttctaactat	240
ccttttagagt taaaagaaat atataatcca ccagttctac ttttttatca gggtaatatt	300
gaacttctat ctaaacctaa attagctgta gtgggggcaa gacaggcatc tcagataggt	360
tgtcagtctg ttaaaaagat tatcaaggag actaacaatc aatttggtat cgtaagtggg	420
ttagcgcgtg gcattgatac agcagcacat gttagtgtt taaaaaatgg cggcagtagt	480
atagctgtta tcgggagtggt ttttagatgtt tattatccaa cggagaataa gaaacttcaa	540
gaatatatgt catataatca tctcgtatta tcagaatatt ttaccggaga acaacccttg	600
aaatttcatt tccccgaacg taaccgtatt attgcagggc tgtgtcaagg tattgtgggt	660
gccgaagcta agatgagatc tggaagttaa attacctgtg aaagagcatt agaagagggg	720
cgagaagttt ttgccattcc cggaatatatt atcgatggca aatcagatgg atgccaccat	780
cttatccaag aaggagctaa atgcattatt tcaggaaaag atatcctttc tgaatatcag	840
tag	843

<210> 71

<211> 357

<212> DNA

<213> Streptococcus agalactiae

<400> 71
 atgactgaac gaacattcga agatattgaa cttgacttaa agttattcca aataaagctt 60
 gataatgctg agaatagtaa aaggctctta caaaaattga aaaacgacgt catggagtta 120
 caaatagagt tactagaatc attaaaactc ggtgatgcct atttaacaga atcagaagaa 180
 ttagaagaga ataatgactt tattctaacg gtaaatagtg aaacactaag tttatcctat 240
 gacaatagga taaacttagt ttctaaagag attatggatt atgaaaatgc attagataag 300
 ttgtattatg aaaaacagag tttgatgcaa aaaagtaatg aaagaaaagg aggttaa 357

<210> 72

<211> 1233

<212> DNA

<213> Streptococcus agalactiae

<400> 72
 ttgttcaata aaatagggtt tagaacttgg aaatcaggaa agctttggct ttatatggga 60
 gtgctaggat caactattat tttaggatca agtcctgtat ctgctatgga tagtgttgga 120
 aatcaaagtc agggcaatgt tttagagcgt cgtcaacgtg atgcagaaaa cagaagccaa 180
 ggcaatgttc tagagcgtcg tcaacgcgat gcagaaaaca gaagccaagg taatgttcta 240
 gagcgtcgtc aacgtgatgc agaaaacaga agccaaggta atgttctaga gcgtcgtcaa 300
 cgtgatgcag aaaacagaag ccaaggtaat gttctagagc gtcgtcaacg cgatgttgag 360
 aataagagcc aaggcaatgt tttagagcgt cgtcaacgtg atgcggaaaa caagagccaa 420
 ggcaatgttt tagagcgtcg tcaacgtgat gcagaaaaca gaagccaagg caatgtttta 480
 gagcgtcgtc aacgcgatgt tgagaataag agccaaggca atgttttaga gcgtcgtcaa 540
 cgtgatgcag aaaacagaag ccaaggtaat gttctagagc gtcgtcaacg cgatgttgag 600
 aataagagcc aaggtaatgt tctagagcgt cgtcaacgcg atgttgagaa taagagccaa 660
 ggcaatgttt tagagcgtcg tcaacgtgat gcagaaaaca gaagccaagg taatgttcta 720
 gagcgtcgtc aacgcgatgt tgagaataag agccaaggta atgttctaga gcgtcgtcaa 780
 cgcgatgttg agaataagag ccaaggcaat gtttttagagc gtcgtcaacg tgatgcagaa 840
 aacagaagcc aaggcaatgt tctagagcgt cgtcaacgcg atgcagaaaa cagaagccaa 900
 ggtaatgttc tagagcgtcg tcaacgtgat gcggaaaaca agagccaagt aggtcaactt 960
 atagggaaaa atccacttct ttcaaagtca attatatcta gagaaaataa tcaacttagt 1020
 caaggtgact ctaacaaaca gtcatttctt aaaaaagtat ctcagggttac taatgtagct 1080
 aatagaccga tgттаactaa taattctaga acaatttcag tgataaataa attacctaaa 1140
 acaggtgatg atcaaaatgt catttttaaa cttgtaggtt ttggtttaat tttgttaaca 1200

GBS patentin.ST25

agtcgctgcg gtttgagacg caatgaaaat taa

1233

<210> 73

<211> 1722

<212> DNA

<213> Streptococcus agalactiae

<400> 73

atgaaaagac taacttatta ttttaagggg tatatcaaag aaactatctt tggacccctt 60
ttcaaattat tagaagcctc ttttgaactt ttggtacca tgcgttattgc aaaaatgatt 120
gacgagacca ttccacgagg ggatagaagt agtttactgt tgcaaattgg attgattttc 180
tttttggtcg cgggtgggtgt tgtagtagcg ataactgctc aatattattc ttcaaaagcc 240
gcagttgggt atacgagaca attgacagag gatctctacc aaaaagtcac gtcactgggg 300
aaaaaagaca gagatgaatt gggaactgct agtttgatta ctcgtttaac tgctgataca 360
tttcaaatcc aaactgggtt aaatcaattt ttacgtttat ttttgagggc tccgattatt 420
gtttttggtg ccataattat ggctttttcc attagcccct cattgactat ttggttcttg 480
gtaatgggtg tcacgttatt tatcattggt tttgtaatgt ctgactatt aaatcctatt 540
taccttaaaa tcagaacttc aaccgattat ttggtaaagt tgactaggca acaacttcaa 600
ggtgtacgag ttatccgtgc ctttaatcaa gtagatagag agagtgaagc atttaatgat 660
atcaattatc attatacgaa tttaacaatta aaagcaggta ggctttctag tttagtaacg 720
cctctaacat ttctagtgtg taatatcact ttggttggtg ttatttggcg tggttaattta 780
aatatagcta atcatctttt atcacaagga atgttggttg ctttaattaa ttacttattg 840
caaattcttg ttgaattggt aaaaatgaca atgttggtga catcactgaa ccaaagttat 900
atcagtgcta agcgaattat agccgttttt gaaagaccgt ctgaaataat tgatgacaaa 960
cttgagccaa aatattcgaa taaggcttta gaagtacaag aaatggcatt ttcttatcca 1020
aattcttctg aaaaagcttt atctgatatt actttttcta tgaatgtagg agaaacttta 1080
gggataattg gtggaactgg ctctgggaaa tcaaccttgg ttaatttact gcttcatatt 1140
tataaagtgc aagaagggga tattgatata tatcatcagg gaaaaagtcc agatacaatt 1200
tcaaattggc gtaccctggt aagagttggt cctcaaatg ctgagttggt taaaggaact 1260
attcgttcta acctttcttt gggacttgggt aaagttagtg aggaaaaact ttggactgct 1320
ttagaaatag cacaagctag tgattttgta aaagaaaaag atggtcaact tgatgcccct 1380
gtagagagtt ttggtagaaa tttctctggt ggtcaaaggc aaagggtgac gattgcaaga 1440
gcttttagttc aagataagat accatttttg attttagacg atgcaacatc tgcattggat 1500
tatttaacag aagctcgttt atttaaagcc ataactaaac atttcaacca aactaatctt 1560
attattgtat cacagagaat taatagtata caaatgacg atagaatctt actccttgat 1620

GBS patentin.ST25

aaggggaaac aagttggttt tgataatcat caatctttat tagctcataa caaagtttat 1680
aagtccattt accattcaca aaattttaag gaggaggagt aa 1722

<210> 74

<211> 1275

<212> DNA

<213> Streptococcus agalactiae

<400> 74

atgaaattta atgagcaaag taactcgcaa gcagcacttc taggcttgca acacctgtta 60
gctatgtatg caggatccat tcttgtagct atcatgattg ctagtgtctt tgggtataat 120
gctgagcaac taacttatct tattgcgaca gatattttta tgtgtgggat tgccacctta 180
ttacaattac aattaagtaa gcactttgga gtgggtcttc cagttgtatt aggggtgtgcc 240
tttcagtctg tagctccttt atcaattatt ggtgcacaac aagggtccgg ctatatgttt 300
ggagctttta ttgcttcagg aatatatgtc gttttagttg ctggcatttt ttctaaagtt 360
gcaaatttct ttcttccaat tgtaacagga tcagttatta ctacaattgg ttgacatta 420
ataccagttg cgatgggaaa tatgggtgat aatgcaaaag aaccgagctt acaatcttta 480
actttatcac tggtaacgat tgggtgttgt ttattaatta atattttcgc aaaaggcttt 540
ttgaagtcaa tttcaatcct tattggactc atatcaggta caattcttgc agcatttatg 600
ggcttagttg atgcttctgt ggtagcagaa gcaccacttg tacatattcc gaagccattt 660
tattttggag ctcttagatt tgaatttact tctattttta tgatgtgtat tattgcaaca 720
gtttctatgg tagaatcaac aggtgtttac cttgcgcttt cagatattac aaacgataaa 780
ttagacagta agagacttcg taatgggttac cgttcagaag gattggcagt attacttggc 840
ggcttattta atacctttcc atataccggt ttttctcaaa atgtgggact ggtacagata 900
tctgggatac gtacgcgtaa gccgatatat ttacagctc tcttcttagt tatacttggc 960
ttgttaccta aatttggcgc aatggctcaa atgattccaa gtccagttct tgggtgtgct 1020
atgttagttt tatttggtat ggtagcactt caagggatga aaatgcttaa tcagggtgat 1080
tttgagcata atgagcataa ctttatcatt gcagccgtat caattgcagc aggagtaggt 1140
tttaatggga caaatctctt cattagctct cctaatactt tacaaatgtt ttgacaaaat 1200
ggtattgtta tctcaaccct gacagctgtt gttttaaata tcattttgaa tggattgcct 1260
aaaaaattaa tatga 1275

<210> 75

<211> 3237

<212> DNA

GBS patentin.ST25
<213> Streptococcus agalactiae

<400> 75
atggctaata catacgattt aatttcacag cgtattgaag cacaacgaca gaaactcatc 60
gctatagata ttgtggccgt tgcgagctca ctaggactta acttgaaaca aggttcaggt 120
ggacatctct attgggatga acatgatagt ttcatattt acccccaaac taacaccttt 180
cgttggtggt caagaagcat ggggaccaat accattgatt tagtccaagt catccaagaa 240
gagctaacag gaaagaaacc tagctttcga gaaactgtca actttttaga aacagggcaa 300
tttgaatcgg ttacggtaac accagtcgtt agagaaccct ttaagcacta cctcgctcct 360
tatgaacatc acaattttga cttagggcga cagtatctta aagaagaacg agggctatct 420
gatgagacca ttgattttgc tttggcatca ggtagtatga gctctgcgac attgaaaaag 480
ggtgattatt ttgaacctgt tattatcttt aaaagttttg cggaagacgg ccgaatgatc 540
ggcggtagcc ttcaggggat cgttgaaaat aaagtccagc atcctgaacg tggccgtctc 600
aaacaaatca tgaagcattc agacggtcta gcagggtttc atttggacgt tggaacacct 660
aaacgtctcg tgttttcgga agctcctatt gaccttctct cttattatga attacataag 720
gagagtttac agaatgtccg cttagtcgct atggatgggg tcaaaaaagg ggtgattagt 780
cgctatacgg ctgatttatt gacagatggc cagtattctc aaaccatgcc cagagagtcg 840
attagaggag cgatagatgc cattaaccaa acgactagaa tccttaaaaa caatcccaat 900
atgattacca ttgccgttga taatgacgag gcaggccgaa actttattaa ggagttacag 960
gaagatggca ttccaattaa cgtagacctc ccaccacgga aagaacacca gagtaaaatg 1020
gattggaata attatctgaa acaaaagaaa ggattactaa aaatgccaca aacagaaggc 1080
acacaaaaag cccagaaca agttctggag catgaaaaaa tggataggag ccaaattagt 1140
tcgggctctt tagaggacga ccctcaaggc agtgccaaac ctgtatccaa aagggatacc 1200
tttgagcaag ctgttaccag ccacccgact ttctcctatc ctttactaca gtttagcaca 1260
gaagaagcct ttgtgtcaaa cgttagagat ggctaccaca tcgcaagtga ggaggatatt 1320
cggaatctca attactatgc ccctagtctc caacaaacgg ctaactggta tcgggataat 1380
ctggcagacc gtcaagtgaac ttatatgtta aaaggggata aggagataaa ggcgcttcag 1440
gtcagttttg ccaaggataa gtttgccac ttaaccggta ttcgtccgat tggaaaaggg 1500
ttgtcagctg aaaaactggt agatgatttt gcgaaaggct gaggttccta tcctaattctg 1560
accttatcaa atggttttaa tgacaagata caagttttgc caatgattca agaactatct 1620
caatccaagt cttttgtctt tacagattta gaggaagttc aaaaaatgag aaacttaaag 1680
gccagtcatg cgattcaatc caataatcgg agtttagtcg tcgctttaaa aactattgat 1740
gatgtcacct ttccttcgtc cctcctaaga ggaaaaaaga atctaaatga tgatctgatt 1800
caaaaggcga aagaaaatga agttctaggt gtactcagtg agaaagatgg gaacatcacg 1860
gtgctgtccg ttaacgataa gtacatccaa gatggtgggc aagccttaaa agatatgatt 1920

GBS patentin.ST25

aaaaatggcg	aacttgaacc	actccaaatg	gagacgatac	agcgacatgt	tcctcatgag	1980
aatgcctatc	ctaaggattc	tgacggtgat	ggcttaaccg	atgatgaaga	aatcgctcta	2040
ggcaccaatc	ccttttagttc	tgatagtgat	ggtgatggga	ctccagataa	tgtcgaaaag	2100
gcaaatggaa	cagaccccac	caatgcttct	gataatgagg	tgacaaggca	acaagaagcc	2160
aataaacgtg	acttcacttt	gtcagaaatg	attaaagcca	aaaataccgc	agcgctgaat	2220
caacacttac	aagacggcat	caaacagtat	tttgatagtg	atacctataa	gcaataacctg	2280
gaagggatgg	cccacttcaa	taactactcg	ccacgaaata	ttcaattgat	tatgtcacao	2340
tttcagaag	catcgatggt	tgcgtctttc	caagagtggg	ggaagcgaaa	tggttcgggt	2400
aaaaaaggtg	agaaggccat	ctatatccaa	gcccctgttt	ctgttatgaa	aaaagatgag	2460
aatgggaaac	ctatccttaa	tcctgaaacg	ggagaaaagg	agaccatcac	ttactttaaa	2520
cctgtccctg	tctttgacat	taaacaggtc	tctccccaag	aaggaaaaga	actcaatctc	2580
cctaaagcca	tgggaactat	tccagaacaa	ttggataaag	aatactacca	aatgtcttat	2640
cgtagcttaa	gagatatttc	tcagaataac	aataaggttc	ccattcgatt	tagagaactt	2700
ggacaagaag	atgggttcta	tagtccacag	acaaatgaaa	ttgttattaa	gaaagggatg	2760
tcttatgaac	gaaccttgtc	aacgctgatt	catgaaatgg	ctcattcgga	attacacaac	2820
aaacaaagtt	tgacggaacg	ctttgatggt	aaactaacia	gaagtaccaa	agaacttcaa	2880
gcggaatcca	ttgcttatgt	tgtatccagt	catctagggt	ttgataccag	tcaagagtca	2940
tttccttatt	tagcgtcttg	gtcaaaagaa	aaagacgggc	ttgccaaactt	aacagcacao	3000
ttggaaatcg	tgcaagaaga	agccaaaaac	ttaatggaac	ggattgatca	acagttaagt	3060
caatatcaaa	cagtaacact	gaataaagaa	acccaacaat	tgactaaaca	agaaatgaaa	3120
aagcagactc	atccctttta	tcaaagttta	gcagccgcta	aaacatcaag	agcacaagtc	3180
accactcagg	agaaggaagc	aagcgtaaaa	aaagacaatc	gacctacgat	gccgtag	3237

<210> 76

<211> 2799

<212> DNA

<213> Streptococcus agalactiae

<400> 76

atgaattcac	aagaaacaaa	aggtcacgga	ttttttagaa	aatcaaaagc	atatggttta	60
gtatgtggga	ttgactagc	aggtgcattt	acattagcta	ctagtcaagt	gtctgctgat	120
caagttacaa	ctcaagcaac	aactcaaaca	gtaacgcaaa	atcaagcaga	aacagtaaca	180
tcaactcaac	ttgataaagc	agtagataca	gctaaaaaag	cagctgtagc	tgttacaacc	240
acaacagcag	ttaatcatgc	gacaactact	gatgcacaag	ctgatttagc	taatcaaca	300
caagctgtta	aagatgttac	tgcaaaagca	caagctaata	cacaagctat	taaagatgct	360

GBS patentin.ST25

actgctgaaa atgcaaaaat tgatgctgaa aacaaagcag aggagagcg tgttgcaaaa	420
gctaataaag caggtcaagc agaagtagat gctcgtataa aagcaggtca agcagccgtt	480
gatgcacgta ataaagcaaa acagcaagcg caagacgatc aaaaagcaaa aattgatgct	540
gaaaacaaag cagagtctca acgtgtaagt cagttaaagt cacaaaataa agcaaaaatt	600
gacgcagaaa ataaagatgc gcaagctaaa gcagatgcga ctaatgcaca attacaaaaa	660
gactatcaaa caaagtttagc aaacattaaa tctgttgaag cttataatgc aggtgtacgt	720
caacgtaata aagatgcaca agctaaagca gatgcgacta acgcacagtt acaaaaagac	780
tatcaagcta aattagcact ttataatcaa gctctaaaag ctaaagcaga agcagataaa	840
cagtctatta ataatgttgc ttttgacatt aaagcccaag ctaaagggtgt tgataacgct	900
gaatatggaa actcaatcat gactgcaaaa actaaacctg acggaagttt cgagtttaac	960
cacgatatga tcgatgggtgt gaagacaatc ggctatggta agcttacagg taaagttaat	1020
catcattatg ttgctaacaa ggatggctct gtgacagcat ttgttgattc tgtcactctt	1080
tacaagtacg agtatcgtaa tgttgctcaa aatgctgctg ttaacaaaaa tattgtattt	1140
agagttttta caaaagatgg tcgtcctatt tttgaaaaag ctcataatgg taacaaaact	1200
tttgcagaaa ctttaaacaa aactttacaa ctcaatctta aatatgagct taaaccacat	1260
gcttcacgcg gtaacgtcga agtctttaag attcatgatg actgggtaca tgacacacat	1320
gggtctgctt tagtgtctta tgttaataat aatgatgctg ttcctaattgt ggtcatccca	1380
gaacagccaa ctccacaaa accagaaaaa gttacacctg aagcagaaaa accagtacct	1440
gaaaagccag ttgagcctaa attggtaacg cctgttttaa aaacttatac tccagtcaaa	1500
tttattccgc gagaatacaa accagtccca agtacccttg agacgtttac ccctgagaaa	1560
tttactccag ctcaacaaa agtgaaacct catgtgtctg tacctgaaaa aattaactat	1620
aaagtagcgg tgcattcagt acagatacca aaggccacac caactaagaa agttctagat	1680
gaaaacgggc aatctattaa cggtaaatct gtattaccaa atgcaacatt agactatggt	1740
gctaaacaaa actttagtca atacaaaggt attaaagctt ctgcagaagc tatcgcaaaa	1800
ggttttgcat ttgtagatca accaaatgaa gcgtagctg aattgactgt taagtctatc	1860
aaagcatcta atggtgatga tgtatcaagc ttgttagaaa tgcgtcatgt tttatcaaaa	1920
gatactttag accaaaaact tcaatctctt attaaagagg caggaattag tccagttggt	1980
gagttttaca tgtggactgc aaaagatcca caagcttttt ataaagctta tgttcaaaaa	2040
ggtctagata ttacttataa cttatcattt aaagttaaaa aagagtttac taaagggtcaa	2100
atcaaaaatg gtgttgacaa gattgatttt gggaaatggat atacaggtaa tattgtagtc	2160
aatgatttga caactccaga agtccataaa gacgtgtagt acaagaaga cggcaagtct	2220
attaacaatg gtactgtcaa actcggtgac gaagtcactt acaagcttga aggatgggtt	2280
gtaccagcga accgtgggta cgatcttttt gaatacaaat ttgtagatca cttacaacac	2340
acacacgatc tttacctaaa agataaagta gtcgctaaag tagcaattac acttaaagat	2400

GBS patentin.ST25

ggcactgtaa	ttccaaaagg	gacaaatcta	gttcaatata	ctgagactgt	ctataataag	2460
gaaacaggtc	gctatgagtt	agcctttaag	gcagacttcc	tcgcacaagt	ttcacgttct	2520
agtgcctttg	gggcagatga	ctttattgta	gttaaaccgta	tcaaagcggg	tgatgtttac	2580
aataccgcag	acttctttgt	caatggcaat	aaggtaaaaa	ctgaaactgt	ggtaacacat	2640
actcctgaga	aaccaaacc	agttatgccg	caaaaagtaa	ctcctaaagc	accagcttta	2700
ccatccacag	gagagcaagg	ggtatctgtc	ctaacagtac	ttggtgccgc	cttactctca	2760
ctcttaggcc	ttgtaggggt	taaaaagcgt	caacagtaa			2799

<210> 77

<211> 2232

<212> DNA

<213> Streptococcus agalactiae

<400> 77

atgaatcaga	taaaaattat	cacaggactt	acagtcgcaa	cactatccgc	agtggtaggg	60
aatgtatacg	cagaagatat	cacaccgaca	gcaccagtta	atgaaccaca	agtatcaagc	120
gaaaccgcaa	aaacgcctca	agttacagaa	agtcaagtta	acagcgcaaa	agttactgcc	180
gatcaagcaa	caagtgatgt	taatgcacaa	aaaaatgtag	ttaataatgc	tcaaaatcaa	240
aaaaatcaag	cacaacaaaa	acttggttaac	gcaactacaa	cgtaaataga	aacacaaaaa	300
ttagtgcgaag	aatctaccaa	tcaaaatcaa	gtacaacaaa	cagttgattc	cgcaaagcaa	360
aggttgctgc	agacagaagc	taatcaaaaa	attactcaaa	ctgaacaagt	caaagctcaa	420
aatcaagtta	atgcacaaca	aacagttggt	gttaacaatg	agcatgatgt	tgcaactaag	480
acagctgatg	ttaaacaagc	tcaagcatca	gtcgatacag	ctaaagatgc	tttgactaat	540
actatagtta	atagtgattt	aaataaagca	cagtcaaacg	tcacaactaa	gacagctgat	600
gttaaaaactg	cgacagatgc	acttacaaaa	gcacaagcga	ctgataaaac	acttactaat	660
caaaaagcaa	aagcacaaca	aatagttgat	tcagcaaaac	aaaacttatc	tgctaaagat	720
acacagcttt	cacaagctaa	tgctgaggtc	aatcatcaca	agtttaaaac	ggctctaggg	780
caaagtcatt	attacaatca	acgtgataat	gcttgggctg	gggtatatgg	agggcataca	840
tttgcttcaa	ctggatgtgt	cccacagca	ttagcaatgg	tttactctga	tttatcaaat	900
cggacaataa	cgccgagaga	gatagctgat	tacttataca	acaacacaga	tgaattcaat	960
aaacgtttcg	gtggcacaag	tgggaaagggt	attatttctg	ctactaaagc	gtttgggttat	1020
gttggtgactc	atttggctag	caaaaatgct	ataactgaag	cattaaaagc	aggtcatcat	1080
gttggttgctg	ctgtacaaaa	taataaattc	agtcctggg	ggcctcaata	cagtcacgaa	1140
attgtattga	gaggtagttc	taatggcaat	acgtatgttt	atgatccgta	taaccgtgat	1200
aacaatgggt	tttacagtgt	tgaccgcatt	tggaaatgaac	agtcacgaga	tagtattgat	1260

GBS patentin.ST25

actgctggtg taggtgtacc gtttttcgca attatgacta aaaatatggc taatgcttta	1320
actaagcagt cacaagcttt agcaagccaa caagttgctc aaaaacaatt aaatgatgca	1380
caagctaaag caacaggtct taatgcagta actatgcaga caccgattgc acaagctaatt	1440
ttgattaaag cacagtcaaa tttaaaagat gctcaaaagc gattagcaga agcacaagca	1500
tcagtcaaat tagctaataca agataatggt aaaaaacaag ctgacttaac aaaagcagag	1560
tctaaattaa aagatgctca aaagcaatta gcagcagcac aagctaaatt gacaacaagc	1620
aaaacaaaac ttaatcaatt aaaacaagtg ttagcagaag caagtcaaca agtagcccaa	1680
gcaaatacaag attacaagca agctaaagat aatctaacac aaaaaactgc ttatctaaca	1740
aatctacgca atgcacaagc taatttgatt aaagcacagt ctgatgtagc acaagctaaa	1800
gataacttag caaataagat tgctaagtta caaagagaag tagcttattt acaagagtta	1860
aaaactaaag cagtagatgc gcaatcacag tatcaaaaag ttttatcagc ttataagtca	1920
gttttatcag ctaaagcaag tttaaaatta gcggaagaga aagctcgact tgataaaaag	1980
ggtcacgaag cagtagcagt agttgacgaa acaggtaaaa ttactagcta tattacttct	2040
aaacacaaaa tagaaatgaa atctcttggt gcaactaaga caactgatgt taaacaagta	2100
tcagttgcta aagcaagcgt gttgccaagt actggtgatg ttaaacaagt atcagttgct	2160
cttctgggta tgttattaac gttctctggt tttttaggta tacgtaaaca aagtaaaaaa	2220
gttattaatt aa	2232

<210> 78

<211> 762

<212> DNA

<213> Streptococcus agalactiae

<400> 78

atgatatcac gtaaagttgc gcttgtgacg ggggcatctg ctgggttttg tgcagctatt	60
gttactaaat tagtttcaga tggttatagc gttattgggt gtgctcgctg aatggataaa	120
ttaaaatgct ttggagaaaa gttttcagag ggttactttt atccacttca aatggatatt	180
acaagtagag aatcggttga caaagcttta gaaagtctgc ctaaaaattt gcaatcaatt	240
gatttggttg ttaataatgc aggttttagca cttggattgg ataaatcata tgaagctgat	300
tttgaagatt ggatgactat gattaatact aacgtttagt gattaattta cttgacacga	360
tgcatTTTTAC cgaaaatggt agaagttaat agagggttaa ttatcaattt gggatcaact	420
gcaggaacaa ttccttatcc aggagctaatt gtctatggcg catcaaaagc ttttgtaaaa	480
caattttctc tcaacttgcg tgccgattta gctggaacta aaatcagagt tactaaccta	540
gaacccggtt tatgtgaagg gacagaattt tcaactgtac gtttcaaagg agatcataaa	600
agagttgaaa aactttatga aggtgcgcac gcaattcaag cagaggatat tgctaatacc	660

GBS patentin.ST25

gtgtcatggg ttgctagcca accagaacac attaatatta atcgcataga aataatgcc 720
gtcagtcaaa cttatggacc tcaacctgtt tatcgtgatt aa 762

<210> 79

<211> 1116

<212> DNA

<213> Streptococcus agalactiae

<400> 79

atgatttatt tagacaatgc tgctactacc gctctaacc catctgttat tgagaaaatg 60
accaatgtca tgacaagtaa ctatggtaat ccatctagta tacatacctt tgggcgtcaa 120
gcaaatacaac ttttacgtga atgtcgacaa attattgctg aatatctaaa tgttaattca 180
cgtgaaatta ttttacttct tgggggaact gagagcaaca atacagctat caaagggtat 240
gctcttgcaa atcagctaaa aggtaaacat attattacct ctgaaattga acatcattca 300
gtcctacata ctatgactta cttatcagag cgatttggtt ttgatattac ttacttaaaa 360
ccaaaccatg gacaaattac tgcaaaagac gttcaagaag ctttacgaga tgatactatt 420
atgggtatctc tcatgtttgc taataatgaa accggggact ttttaccat tcaagagatt 480
ggtcagcttc tcaggaacca ccaagctgtt tttcacgttg atgccgttca agtctttagc 540
aaaatggaac ttgatcctca ttcttttagga attgactttt tagctgcttc tgcccataaa 600
tttcacggtc caaaagggtg tgggatactt tactgtgctc cccatcactt tgatagtcta 660
cttcatggtg gagaccaaga ggaaaaaagg cgtgcttcaa ctgaaaatat aattgggtatt 720
gctggaatgt ctcaagctct tactgatgct acgactaaca cccttaaaaa ttggactcac 780
attagtcagc tgagaacgac ctttttagat gctatttcag accttgactt ctatcttaat 840
aacgggtcaag actgcttacc tcatgtactt aatatagggt ttcctagaca gaataatggc 900
ttgttattga cacagttaga tttagctgga ttcgcagttt caacagggtc tgcattgact 960
gcaggaacag tcgaacctag tcatgtctta acaagcttgt atggagccaa ctaccacgt 1020
ctaaatgaat caatacgtat tagtttttca gaactaaata cccaagaaga aattcttgaa 1080
ttagctaaaa ccttaagaaa aattatagga gattaa 1116

<210> 80

<211> 1344

<212> DNA

<213> Streptococcus agalactiae

<400> 80

atgtctagga aaacatttaa acatatacta tcgattggag tttgcacgct cgtactatcg 60

GBS patentin.ST25

atgagtcctt	attacactga	aaaagccac	gctattgctg	gtcctagtga	ccgccaatac	120
gtagaaaacc	caaatcctca	cattattgta	aatgttacag	gtactgatca	aaacggaaat	180
agcattttac	cgcattacat	cgaagtcaat	gtaaagatgg	gacaaacttt	aagtaaagaa	240
gaaattctag	attatattgc	tcgaaattta	aactctagt	ttggaggaga	aagtaaaaac	300
gttcaataca	gcaacatcga	gtttaaggaa	agtgttatc	tgaagcgtca	attagatgat	360
ggcaagacag	aagaaatagc	aattgataac	gacggtgtta	ctgtacctaa	agacggtcca	420
aacaaatttt	ggattgacgt	tccagtaact	tgtactgtta	ctcctatcgt	aacagaaaaca	480
catgaagttc	gatgggggac	tccagtcgct	atatcacacc	gtatttactt	tggtgaagaa	540
tcttctggaa	aagtttttaga	tgaatacaca	aatctacaca	ctgctgattc	ggaacttaac	600
ggttatcgtg	ttggagatta	tatcacagac	tatgcacttt	ctaagtctgc	ttacgaagct	660
tttttaaaact	ctcgttttaga	taaagaaggt	tacaaacttc	aacatcgtat	tagcacgaat	720
gtacgacaaa	accttcaaat	tgataaattg	attttcaatt	atgactttta	tgaggaaaat	780
atttactacc	aaatcgggaa	tatccgtcca	ctattaagtc	gctcatcagc	tgaagtagaa	840
tctgacatca	ttacagaacg	ctactatggt	tctaaaaatg	ctaaaagttt	agcacgtaca	900
gaatcaacca	tttcgattaa	aatgggtgat	gccaaaactg	aacaaccgct	atttaaccac	960
acattaactg	gttatcaatt	ggcaactgtc	tcccatgtct	ataacagact	ctttgaagaa	1020
aatcttatcc	caactacaaa	atcaggagaa	agatatttta	ttcaaaatat	gaaaaaaaca	1080
gctgaacaag	aatatactgt	ttacctttca	gaaacacctt	attctaaaga	gaacgctccc	1140
gtaatttctt	atgatgcaag	acctgttgat	tgggattatc	actcaggcgc	ttcaggatca	1200
cttgaaaatc	agcctaacat	ctatactgaa	gaagattcaa	ctgaattttt	gggtaataaa	1260
ccacaagcag	cttgttatcc	aaacaaacaa	tttgcttgcg	aaaatactga	ctctaaatac	1320
aactatagct	atttagaaaa	atag				1344

<210> 81

<211> 2280

<212> DNA

<213> Streptococcus agalactiae

<400> 81

atgaatcctt	taataattgg	aatgaatgat	aaacaagcag	aagcgggtaca	aacgacagac	60
ggaccgcttt	tgattatggc	aggagctggc	tctggaaaaa	cacgtgttct	gactcatcgt	120
attgcttatt	taatagatga	aaaatatggt	aatccttgga	atatttttagc	gattactttt	180
actaataaag	cagcgcgtga	aatgcgtgaa	cggtgtatcg	ccttgaatcc	agctacccaa	240
gatactttga	ttgcaacttt	tcatagtatg	tgtgttcgta	ttttacgtcg	tgaagctgat	300
tatattggat	ataatcgtaa	ctttacaatc	gttgatccag	gtgagcagcg	tactttaatg	360

GBS patentin.ST25

aagcgaatca ttaagcaatt aaatttggac acaaaaaagt ggaatgaacg ttcaatttta	420
ggtacaatct ctaatgctaa aaatgacctt cttgatgaaa ttgcatatga gaagcaagcc	480
ggagatatgt atacacaggt aattgctaaa tgctataaag cttatcaaga ggaattacgt	540
agaagtgagg ccatggattt cgatgacttg attatgatga cacttcgatt atttgatcag	600
aataaagatg ttttggccta ttaccaacag aggtatcaat atatccatgt agacgagtat	660
caagatacta accacgctca ataccaatta gttaagttat tagcttcgcg tttcaaaaat	720
atttgtgttg ttggtgatgc cgatcaatcc atttacggat ggcgtggagc tgatatgcaa	780
aatattcttg attttgaaaa ggactatccg caagccaaag ttgtattatt agaagaaaat	840
tatcgatcga ctaagaaaat acttcaagct gctaataatg tgattaatca taataaaaat	900
cgccgtccca aaaaattatg gactcaaaaat gatgaagggt agcaaattgt atatcataga	960
gctaacaatg agcaagaaga agccgttttt gtagcatcaa ctattgataa catcgttcga	1020
gaacaaggaa aaaatttcaa agattttgcc gttctttatc gtacgaatgc gcaatctcgt	1080
actattgagg aagcactttt aaaatccaat attccatata caatggtttg tggaacaaaa	1140
ttctatagtc gtaaagaaat tcgagatggt attgcttatt tcaatatcct tgcaaatact	1200
tctgataata tttcttttga gcggattgta aatgaaccta aaagaggggt tgggccaggc	1260
acttttagaaa aaatacggtc atttgcctat gaacagaaca tgtctcttct tgatgcctct	1320
tcaaatgtca tgatgtcgcc cttaaaagggt aaggctgctc aagctgtttg ggatttagct	1380
aatctgattt tgactctacg tagtaagcta gatagttaa ctgtaacgga gattacagaa	1440
aacctactgg ataagacagg atatctagaa gcacttcaag ttcaaaatac attagaaagt	1500
caagcgcgta ttgaaaatat tgaagaattc ttgtcagtga ctaaaaattt tgacgataac	1560
cctgagatta cagtagaggg tgaaactgggt ttagatcgct tatcgcgttt tttaaatgat	1620
ttagctttaa tagcagatac tgatgatagc gccactgaaa cggctgaggt cactttaatg	1680
acattacatg ctgccaaggg tctagaattt ccagttgttt tcttaatcgg tatggaagaa	1740
ggagtatttc ctttatcgcg tgcaatagag gatgctgatg aattagaaga agagcgtcgt	1800
ttagcttatg tcgggattac gagagcagaa caaatacttt tccttaccac tgctaatacc	1860
cgtactttat ttggtaaaac tagttataat agaccaaccc gttttatacg tgagattgat	1920
gatgagctga tacaacatca agggttggct cgaccagtta attcttcatt tgggtgtgaaa	1980
tattcaaaaag aacagcctac acaatttggt caaggaatga gtcttcaaca agcgcttcag	2040
gcacgtaaaa gtaattcaca acctcaagta actgcccac tccaggctct taacgcgaac	2100
aatagccatg agacatcatg ggagattgggt gatgttgcaa ctcataaaaa atggggggac	2160
ggtacgggtc ttgaagtttc aggtagcgga aagactcaag agttaaaaaat aaattttcca	2220
ggtattgggt taaagaaatt attagcgagt gtcgctccta ttagtaaaaa ggaaaactaa	2280

<211> 393

<212> DNA

<213> Streptococcus agalactiae

<400> 82

```

atgaaattat acgttcaatt aatggttatt ttaacctttt cattcgctgg tgaggttcta      60
tctactatat tcaacttacc tgtaccagggt agtattattg gattaatatt actattccta      120
gcgttaaaat acaaaatcat caggctcagg catattgatg ccgtggggaa ttttctatta      180
gcaaatatga ccattttatt ttaccacca gcagttggac tgatggagca ctttcaagac      240
ataaaaccct atctttttgg gatagctatc attatcttag gagcgctatt tctcaatatt      300
ctaactattg gactgggtatc ccaatggatc aaaaagagat atgaaggaga ttatccagaa      360
attggaggta aaaatggcaa ctttaacgaa taa                                     393

```

<210> 83

<211> 474

<212> DNA

<213> Streptococcus agalactiae

<400> 83

```

atgatttttg tcacagtggg gacacatgaa cagcagttca accgtcttat taaagaagtt      60
gatagattaa aaggacagg tgctattgat caagaagtgt tcattcaaac gggttactca      120
gactttgaac ctcagaattg tcagtgggtca aaatttctct catatgatga tatgaactct      180
tacatgaaag aagctgagat tgttatcaca catggcggtc cagcgacgtt tatgtcagtt      240
atctctttag ggaaattacc agtcgttggt cctaggagaa agcagtttgg tgaacatatc      300
aatgatcatc aaatacaatt ttttaaaaaa attgcccacc tgtatccctt ggcttggatt      360
gaagatgtag atggacttgc ggaagtgttg aaaaggaata tagctacaga aaaatatcag      420
ggaaataatg atatgttttg tcataaatta gaaaaaatta taggtgaaat atga          474

```

<210> 84

<211> 762

<212> DNA

<213> Streptococcus agalactiae

<400> 84

```

atgggtgatga aaatcataga gttaaagaa gcaaccgtac aagtcagtaa tggtttagca      60
gaaatgaaaa cgatattaga ccatgttaat ttgagtattt atgaacatga cttcattaca      120
atattgggtg gaaatggagc tggaaaatca acgcttttta atgtaattgc aggtaccttg      180

```

GBS patentin.ST25

atgttaagcg gtggaaatat ttacatcatg ggacaagatg ttactaattt accagcagaa	240
aaacgagcta aatattttatc acgggtattt caagatccga aaatgggaac agcacctagg	300
atgacagttg ctgaaaattt attagttgct aaatttcgag gtgaaaagag accgttagtt	360
cctagaaaaga ttactaacta taccgaagaa tttcaaaaat tgattgctag aactggtaat	420
ggacttgatc gccattttaga gacacctaca ggtttattat cagggtggaca aagacaagca	480
cttagtttat taatggcaac tttgaaaaaa ccaaattctgt tattattgga cgaacacaca	540
gcagcgcttg atcctagaac aagtgtttcg cttatgggct tgactgatga gtttatcaaa	600
caagattcgt tgactgcctt aatgattaca catcatatgg aagatgctct caaatatgga	660
aatcgtatat tagtaatgaa agatggcaag attgtcagag atttaaataca ggcacaaaaa	720
aacaagatgg ctatagctga ctattatcaa ttatttgatt aa	762

<210> 85

<211> 3219

<212> DNA

<213> Streptococcus agalactiae

<400> 85

atggaaatca aaaagaaaca tcgtattatg ctttattcag cccttatttt aggaacaata	60
ttggttaaca atagttacca agctaaagct gaagagctta caaaactac ctcaacgtcc	120
caaataagag atactcaaac taataatatt gaagttctcc agactgaaag taccactgtc	180
aaagagacta gcaccacaac cacacaacaa gatctgtcta accccacagc ttcaaccgca	240
actgcaacag ccactcatag cacaatgaaa caagtagtag ataatcaaac tcaaaataag	300
gagctgggtga aaaacggaga ttttaataca actaaccctg tatctggaag ctgggtcacat	360
acaagcgcta ggggaatggtc tgcttggatt gataaagaaa atactgctga taaatcacct	420
attatccaac gtaccgaaca aggccaagta agcctatcca gcgacaaagg ctttagaggt	480
gctgtaacac aaaaagtga cattgatccc actaaaaaat atgaggtcaa gtttgatatt	540
gaaacaagta acaaggctgg acaagctttc cttcgtatta tggagaaaaa agacaacaat	600
acgcgacttt ggctttctga gatgaccagc ggtactacta acaaacatac ctttaacaaag	660
atatataacc caaagttaaa tgtctccgag gtgacacttg aactttatta tgaaaaagga	720
actggttctg ctacttttga taatatatca atgaaagcaa aaggccctaa agactcagag	780
catccacaac ccgtcacaac acaaattgaa gaaagcgta atacggcttt aaacaaaaat	840
tacgttttta ataaagctga ctaccaatac actctaacca atccgtctct cgggaaaatt	900
gttgggtggaa tattgtatcc aaacgctact ggttcaacaa ctgttaaaat atctgataaa	960
tctggtaaaa taattaaaga agtaccgtta tcagttacag cttcaacaga agataagttt	1020
acaaaactcc tcgacaaatg gaacgacgtg actattggta atcatgttta cgataactaat	1080

GBS patentin.ST25

gattcgaaca tgcaaaagat taatcagaaa ttagatgaaa ctaacgccaa aaacatcaaa	1140
actatcaaac tggattctaa tcacactttc ctttggaaag atttagataa tctcaataat	1200
tcagcacagt taaccgctac ttatcgtcgt ttggaagatt tagctaaaca aatcaccaat	1260
ccccactcta ctatttacia aaatgaaaaa gctattcgta ctgtaaaaga gagtctggct	1320
tggcttcac aaactttcta caatgttaat aaagatatag aaggctctgc caattggtgg	1380
gattttgaaa tcggtgtccc tcgctcaatt acagctacc tagctctcat gaataactac	1440
ttcactgacg ctgaaataaa aacttatacc gacccaattg aacactttgt tcctgatgca	1500
ggatatttcc gtaaaacgct tgacaatcca tttaaagccc ttggtggtaa tctagtcgat	1560
atggggcgcg ttaaaatcat tgaagggtta cttcgtaaag acaatactat tatcgaaaaa	1620
acttctcatt ctctaaaaaa tctttttact actgctacta aagctgaagg tttctatgct	1680
gacggttctt acatcgacca tacaatgtt gcttatactg gcgcttatgg taatgttctg	1740
atagatgggt tgacacaatt gctgcctatc attcaagaaa ctgactataa aatctcta	1800
caagaacttg atatgggtta taaatggatt aatcaatcat ttttacctt aattgtaaaa	1860
ggtgagttaa tggatatgag tcgtggacgc tcaattagta gagaggcagc ttcttcgc	1920
gcggctgcag ttgaagttct cagagggttc ctcagattgg ctaacatgtc taatgaagag	1980
cgaaacttag acctcaaacc aactattaaa acgattatca cttcaaataa attctaca	2040
gtcttcaata acctcaaacc gtattccgat attgccaaca tgaataagat gcttaatgac	2100
agtacagtcg ctactaaacc tttaaaaagt aatttatcaa ctttaataag catggaccgc	2160
ttagcttatt ataatgccga gaaagacttt gggttcgcgc tttcattaca ttctaaacgt	2220
acctcaact atgaaggaat gaatgatgaa aatacacgtg attggtatac cggagatgg	2280
atgttctatc tttataatag tgatcaatct cattatagta atcatttttg gccaacctgc	2340
aatccttata aaatggctgg aacaactgaa aaagatgcta agcgtgaaga taccactaag	2400
gaattcatga gcaaacatag caaagacgct aaagaaaaaa ccggtcaagt tacaggaaca	2460
tctgactttg ttggttcgt caaacttaat gatcactttg ctcttgccgc tatggatttt	2520
actaactggg atcgcacctt aacagcacia aaagggtggg ttatcttaaa tgataagatt	2580
gtctttttag gtagcaacat caagaatact aacggcattg gaaatgtttc tacaacaatt	2640
gatcaacgaa aagacgattc taaaacacct tatactacat acgtcaatgg aaaaactatt	2700
gatttaaaac aagcaagttc tcaacaattt acagatacaa aaagtgtctt tttagaatca	2760
aaagaacctg gtcgcaatat tgggttatatc ttttttaaaa atagcactat tgatattgaa	2820
cgcaaagagc aaacaggtac ttggaacagc attaatcgta cttctaaaaa tacctcaatc	2880
gttagcaatc cttttatcac tataagccaa aagcatgaca acaaagggtga tagctatgg	2940
tacatgatgg ttccaaacat tgatcgaca agttttgata aattagccaa cagcaaagaa	3000
gtagaattac tagaaaatag ttcaaaacaa caagttatct atgataaaaa cagtcaaact	3060
tgggctgtta tcaaacacga taatcaagag agtctcatta acaatcaatt caaaatgaat	3120

GBS patentin.ST25

aaagcgggac ttacctagt acaaaaagtt ggtaatgact atcaaatgt ctattaccaa 3180
 cctcaaacca tgacaaaaac agaccaatta gctatctaa 3219

<210> 86

<211> 234

<212> DNA

<213> Streptococcus agalactiae

<400> 86
 atgcattctt tttctaattc tggatattct tatgataatg ccgtaactga agcatttttc 60
 aagtatttaa agcatagaca aatcaaccga aacattatc aaaatatcaa acaggttcaa 120
 ttagactgct ttgaatacat tgagaatttt tataacaatt acaaccaca tacggctaata 180
 ctaggactaa cccctaata gaaagaagaa aattatttta acgcaataaa ataa 234

<210> 87

<211> 2469

<212> DNA

<213> Streptococcus agalactiae

<400> 87
 gtgaagaaaa catatgggta tatcggtcga gttgctgcc tttactagc tactcatatt 60
 ggaagttacc aacttggtta gcatcatatg ggtctagcaa caaaggacaa tcagattgcc 120
 tatattgatg acagcaaagg taaggcaaaa gccctaataa caaacaacac gatggatcaa 180
 atcagtgtg aagaaggcat ctctgtgtaa cagatcgtag tcaaaattac tgaccaaggc 240
 tatgtgacct cacatgggta ccattatcat tttacaatg ggaaagttcc ttatgatgcg 300
 attattagt aagagttggt gatgacggat cctaattacc gttttaaaca atcagacgtt 360
 atcaatgaaa tcttagacgg ttacgttatt aaagtcaatg gcaactatta tgtttacctc 420
 aagccaggta gtaagcgcaa aaacattcga accaaacaac aaattgctga gcaagtagcc 480
 aaaggaacta aagaagctaa agaaaaaggt ttagctcaag tggcccatct cagtaaagaa 540
 gaagttgcgg cagtcaatga agcaaaaaga caaggacgct atactacaga cgatggctat 600
 attttttagtc cgacagatat cattgatgat ttaggagatg cttatttagt acctcatggt 660
 aatcactatc attatattcc taaaaaggat ttgtctccaa gtgagctagc tgctgcacaa 720
 gcctactgga gtcaaaaaca aggtcgaggt gctagaccgt ctgattaccg cccgacacca 780
 gccccaggtc gtaggaaagc cccaattcct gatgtgacgc ctaaccctgg acaaggatcat 840
 cagccagata acggtggcta tcatccagcg cctcctaggc caaatgatgc gtcacaaaac 900
 aaacacaaaa gagatgagtt taaaggaaaa acctttaagg aactttttaga tcaactacac 960

GBS patentin.ST25

cgtcttgatt tgaaataccg tcatgtggaa gaagatgggt tgatttttga accgactcaa 1020
 gtgatcaaat caaacgcttt tgggtatgtg gtgcctcatg gagatcatta tcatattatc 1080
 ccaagaagtc agttatcacc tcttgaaatg gaattagcag atcgatactt agctggccaa 1140
 actgaggaca atgactcagg ttcagagcac tcaaaacat cagataaaga agtgacacat 1200
 acctttcttg gtcatcgcat caaagcttac ggaaaaggct tagatggtaa accatatgat 1260
 acgagtgatg cttatgtttt tagtaaagaa tccattcatt cagtggataa atcaggagtt 1320
 acagctaaac acggagatca ttccactat ataggatttg gagaacttga acaatatgag 1380
 ttggatgagg tcgctaactg ggtgaaagca aaaggccaag ctgatgagct tgctgctgct 1440
 ttggatcagg aacaaggcaa agaaaaacca ctctttgaca ctaaaaaagt gagtcgcaaa 1500
 gtaacaaaag atggttaaagt gggctatatg atgccaaaag atggttaagga ctatttctat 1560
 gctcgtgatc aacttgattt gactcagatt gcctttgccg aacaagaact aatgcttaaa 1620
 gataagaagc attaccgta tgacattgtt gacacaggta ttgagccacg acttgctgta 1680
 gatgtgtcaa gtctgccgat gcatgctggt aatgctactt acgatactgg aagttcgttt 1740
 gttatccac atattgatca tatccatgtc gttccgtatt catgggtgac gcgcgatcag 1800
 attgcaacag tcaagtatgt gatgcaacac cccgaagttc gtccggatgt atggtctaag 1860
 ccagggcatg aagagtcagg ttcggtcatt ccaaagtta cgctcttga taaacgtgct 1920
 ggtatgccaa actggcaa atccattct gctgaagaag ttcaaaaagc cctagcagaa 1980
 ggtcgttttg caacaccaga cggctatatt ttcgatccac gagatgtttt ggccaaagaa 2040
 acttttgtat ggaaagatgg ctcttttagc atcccaagag cagatggcag ttcattgaga 2100
 accattaata aatctgatct atcccaagct gagtggcaac aagctcaaga gttattggca 2160
 aagaaaaata ctggtgatgc tactgatacg gataaaccca aagaaaagca acaggcagat 2220
 aagagcaatg aaaaccaaca gccagtgaa gccagtaaag aagaaaaaga atcagatgac 2280
 tttatagaca gtttaccaga ctatggtcta gatagagcaa ccctagaaga tcatatcaat 2340
 caattagcac aaaaagctaa tatcgatcct aagtatctca tttccaacc agaagggtgc 2400
 caattttata ataaaaatgg tgaattggta acttatgata tcaagacact tcaacaaata 2460
 aacccttaa 2469

<210> 88

<211> 921

<212> DNA

<213> Streptococcus agalactiae

<400> 88

atgaaaaaag gtttttttct catggctatg gttgtgagtt tagtaatgat agcagggtgt 60
 gataagtcag caaaccccaa acagcctacg caaggcatgt cagttgtaac cagcttttac 120

GBS patentin.ST25

ccaatgtatg cgatgacaaa agaagtatct ggagacctca atgatgtgag gatgatccaa	180
tcaggtgcag gcattcattc ctttgaaccg tctgtaaatg atgtggcagc tatttatgac	240
gcggatttgt ttgtttacca ttcacatacc ttagaagctt gggcaagggg tctagaccct	300
aatttaaaaa aatcaaagggt tgatgtgttt gaagcgtcaa aacctttgac actagataga	360
gtcaaagggc tagaagatat ggaagtcaca caaggcattg accctgagac actttatgac	420
ccacatacct ggacggatcc cgttttagct ggtgaggaag ctgttaatat cgctaaagag	480
ctaggacgtt tggatcctaa acacaaagac agttacacta aaaaggctaa ggctttcaaa	540
aaagaagcag agcaactaac tgaagaatac actcaaaaat ttaaaaagggt gcgctcaaaa	600
acattcgtga cgcaacacac ggcatTTTct tatctggcta aacgattcgg cttgaaacaa	660
cttggtatct cgggtatttc tccagagcaa gagccctctc ctgcgaatt gaaagaaatt	720
caagactttg tcaaagaata caacgtcaag actatttttg cagaagacaa cgtcaatccc	780
aaaattgctc atgctattgc gaaatcaaca ggagctaaaag taaagacatt aagtccactt	840
gaagctgctc caagcggaaa caagacatat ctagaaaatc ttagagcaaa tttggaagtg	900
ctctatcaac agttgaagta a	921

<210> 89

<211> 3453

<212> DNA

<213> Streptococcus agalactiae

<400> 89	
ttgcgtaaaa aacagaaact accatttgat aaacttgcca ttgcgcttat gtctacgagc	60
atcttgctca atgcacaatc agacatcaaa gcaaatactg tgacagaaga cactcctgct	120
accgaacaaa ccgtagaaac tccacaacca acagcggttt ctgaggaagc accatcatca	180
aaggaaacta aaacccaca aactcctagt gatgcaggag aaacagtagc agatgacgct	240
aatgatctag cccctcaagc tcttgctaaa actgctgata caccagcaac ctcaaaagcg	300
actattaggg atttgaacga cccttctcag gtcaaaaccc tgcaggaaaa agcaggcaag	360
ggagctggga ctgttggtgc agtgattgat gctggTTTTg ataaaaatca tgaagcgtgg	420
cgcttaacag acaaagccaa agcacgttac caatcaaaag aagatcttga aaaagctaaa	480
aaagagcacg gtattaccta tggcgagtgg gtcaatgata aggttgctta ctaccatgac	540
tatagtaaaag atggtaaaac cgctgtcgat caagagcacg gcacacacgt gtcaggaatc	600
ttgtcaggaa atgctccatc tgaaacgaaa gaaccttacc gcctagaagg tgcgatgcct	660
gaggctcaat tgcttttgat gcgtgtcgaa attgtaaatg gactagcaga ctatgctcgt	720
aactacgctc aagctatcag agatgctatc aacttgggag ctaagggtgat taatatgagc	780
tttggtaatg ctgcactagc ttacgccaac cttccagacg aaaccaaaaa agcctttgac	840

GBS patentin.ST25

tatgccaaat	caaaaggtgt	tagcattgtg	acctcagctg	gtaatgatag	tagctttggg	900
ggcaagaccc	gtctacctct	agcagatcat	cctgattatg	gggtggttgg	gacacctgca	960
gcggcagact	caacattgac	agttgcttct	tacagcccag	ataaacagct	cactgaaact	1020
gctacggtca	aaacagccga	tcagcaagat	aaagaaatgc	ctgttctttc	aacaaaccgt	1080
tttgagccaa	acaaggctta	cgactatgct	tatgctaatc	gagggacgaa	agaggatgat	1140
tttaaggatg	tcaaaggtaa	gattgccctt	attgaacgtg	gcgatattga	tttcaaagat	1200
aagattgcaa	aagctaaaaa	agctggtgct	gtaggagtct	tgatctatga	caatcaggac	1260
aagggcttcc	cgattgaatt	gccaaatggt	gatcagatgc	ctgcggcctt	tatcagtcga	1320
aaagatggtc	tcttattaaa	agacaatccc	caaaaaacca	tcaccttcaa	tgcgacacct	1380
aagggtattgc	caacagcaag	tggcaccaaa	ctaagccgct	tctcaagctg	gggtctgaca	1440
gctgacggtg	atattaagcc	agatattgca	gcacccggcc	aagatatattt	gtcatcagtg	1500
gctaacaaca	agtatgccaa	actttctgga	actagtatgt	ctgcgccatt	agtagcgggt	1560
atcatgggac	tgttgcaaaa	gcagtatgag	acacagtatc	ctgatatgac	accatcagag	1620
cgtcttgatt	tagctaaaaa	agtattgatg	agctcagcaa	ctgccttata	tgatgaagat	1680
gaaaaagctt	atttttctcc	tcgccaacaa	ggagcaggag	cagtcgatgc	taaaaaagct	1740
tcagcagcaa	cgatgtatgt	gacagataag	gataatacct	caagcaaggt	tcacctgaac	1800
aatgtttctg	ataaatttga	agtaacagta	acagttcaca	acaaatctga	taaacctcaa	1860
gagttgtatt	accaagcaac	tgttcaaaca	gataaagtag	atggaaaaca	ctttgccttg	1920
gctcctaaag	cattgtatga	gacatcatgg	caaaaaatca	caattccagc	caatagcagc	1980
aaacaagtca	ccgttccaat	cgatgctagt	cgatttagca	aggacttgct	tgcccaaatg	2040
aaaaatggct	atttcttaga	aggttttggt	cgtttcaaac	aagatcctaa	aaaagaagag	2100
cttatgagca	ttccatatat	tggtttccga	ggtgattttg	gcaatctgtc	agccttagaa	2160
aaaccaatct	atgatagcaa	agacggtagc	agctactatc	atgaagcaaa	tagtgatgcc	2220
aaagaccaat	tagatggtga	tggattacag	ttttacgctc	tgaaaaataa	ctttacagca	2280
cttaccacag	agtctaacc	gtggacgatt	attaaagctg	tcaaagaagg	ggttgaaaac	2340
atagaggata	tcgaatcttc	agagatcaca	gaaaccattt	ttgcaggtag	ttttgcaaaa	2400
caagacgatg	atagccacta	ctatatccac	cgtcacgcta	atggcaagcc	atatgctgcg	2460
atctctccaa	atggggacgg	taacagagat	tatgtccaat	tccaaggtag	tttcttgctg	2520
aatgctaaaa	accttggtgc	tgaagtcttg	gacaaagaag	gaaatgttgt	ttggacaagt	2580
gaggtaaccc	agcaagttgt	taaaaactac	aacaatgact	tggcaagcac	acttggttca	2640
acccgttttg	aaaaaacgcg	ttgggacggt	aaagataaag	acggcaaagt	tggtgctaac	2700
ggaacctaca	cctatcgtgt	ccgtacact	ccgattagct	caggtgcaaa	agaacaacac	2760
actgattttg	atgtgattgt	agacaatacg	acacctgaag	tcgcaacatc	ggcaacattc	2820
tcaacagaag	atcgtcgttt	gacacttgca	tctaaaccaa	aaaccagcca	accggtttac	2880

GBS patentin.ST25

cgtagcgta ttgcttatac ttacatggat gaggatctgc caacaacaga gtatatttct	2940
ccaaatgaag atggtacctt tactcttcct gaagaggctg aaacaatgga aggcgctact	3000
gttcattga aaatgtcaga ctttacttat gttgttgaag atatggctgg taacatcact	3060
tataaccag tgactaagct attggagggc cactctaata agccagaaca agacggttca	3120
gatcaagcac cagacaaaaa accagaagct aaaccagaac aagacgggtc aggtcaaaca	3180
ccagataaaa aaacagaaac taaaccagaa aaagatagtt cagggtcaaacc accaggtaaa	3240
actcctcaa aaggtcaacc ttctcgtagt ctagagaaac gatcttctaa gcgtgcttta	3300
gctacaaaag catcaacaag agatcagtt ccaacgacta atgacaagga tacaatcgt	3360
ttacatctcc ttaagttagt tatgaccact ttcttcttgg gattagtagc tcatatattt	3420
aaaacaaaac gccaaaaaga aactaaaaaa tag	3453

<210> 90

<211> 1212

<212> DNA

<213> Streptococcus agalactiae

<400> 90	
tttagtgtaa cctattcaca gtctgaacgt acggttggtt tctcttttgg agaaataaca	60
tttagtagga gtcgctggac aaatggcttt gaaactagaa taccagtaga tgagtggta	120
ggctcttgaaa aatataagag atattcaata gaattcttat atcatgttgc aaaattggct	180
acaatgatgc cttatcgtca agtttgcaaa gtaatagata gcactttgca aacaatcata	240
acaaaagact gtgttttaaa agcagtaaaa tttgtagaaa aattgttaaa agaaaaagaa	300
cgctatcgtt tttattttgga agagccaccc gaacgtaaaa aagtgaaaaa actgtatgtt	360
gagggtagtg gagtcatgat taaaagcaca gattctagag aggaaagaag gtatttagat	420
ttaacacatt ttgttattca tacaggctca aaaaaagttt ctactaaaag atatgaattg	480
caggacaagc acgaaatatt acagcttaat tatgataaag ctaaataata tcttttagat	540
tatattttata ataactatga agtagatgac gatactattt taatcactaa ctctgatatg	600
ggtaaaggct atactagtag agtttttaag gaattaggaa aagcacttaa ggtaaagaaa	660
catgagcatt tttgggatat ctatcatgtt aaagaaaagt taagttcata ctttagaaaa	720
tatccaattg aattaaccga ttttgcttta gatgcggtaa aaaaataata ttctgataag	780
cttgaattag tttttgatac tgttgaatca ctgatttgtg atgaacttga agatcaagaa	840
tttcagaagt ttaagaaaaa agtattaaat aatttcfaat atataaaacc agctcatctt	900
agaaatcttt caaatcgtgg tattggatc atggaatcac aacacagaaa gataacgtat	960
agaatgaagc gacgtggcat gtattgggtca aagtggggaa tctccacaat ggcaaatatg	1020
attatacttg aaagagctaa cggtttacga gaattatttt tcggttcttg gagaaaggta	1080

GBS patentin.ST25

tacagtgagt ataaagaagg ttcatttagt gcagggcgac tttttaaaaa gacagatgaa	1140
ttagataaat tttctaagcc ctttctaaaa aatggcagaa aatggagtat aacaggaatc	1200
aaaacaaaat ag	1212

<210> 91

<211> 837

<212> DNA

<213> Streptococcus agalactiae

<400> 91

aaagcaagca gcggtgatta tggcacaaaa agggaaataa tcaactgctaa taaggataaa	60
tacagcattt caaagatgtg tcgctggctg aatatgccac gctcaagtta ttactatcaa	120
gccgtggagt cagtatctaa aacggagttt gaagaaacta ttaaaagaat ttttctcgat	180
agcgagtcta gatacggatc cagaaaaatc aaaatatgct tgaataacga aggtatcaca	240
ctttcacgtc gtcggattcg acgcattatg aagcgactca atttggtttc tgtttatcag	300
aaagccacct tcaaaccaca ttctagaggc aagaatgaag cccctattcc caaccactta	360
gacaggcaat ttaagcaaga aagaccacta caagccttag tcaactgactt aacctatggt	420
cgtgtaggca atcgttgggc ttatgtttgc ctcatcattg acctatacaa ccgtgaaatc	480
atcggcctgt ctcttggttg gcacaagacc gctgaactcg ttaagcaagc catacaaagc	540
atcccttacg ccctgaccaa agtcaagatg ttccattcag atcgtggcaa agagtttgat	600
aatcagttaa ttgatgaaat attggaagcc tttggaatca cacgttcgct tagtcaggct	660
ggttgtcctt atgacaatgc cgtagctgaa agtacgtatc gtgctttcaa aattgaattt	720
gtttatcaag aaacctttca atcgttgga gaactagctc ttaagactga aaaggcaaca	780
cttttctgta caacatttat aaagtgttgc cttttcaggt ttttaccat gctataa	837

<210> 92

<211> 315

<212> DNA

<213> Streptococcus agalactiae

<400> 92

atgaagacaa gaaatcgtaa aggtggttat ttagcgaata ctgcaaata gtacatcgac	60
tctaaacagg caattcattg cttgagtgtga gaacttgaac cgcaaattag gtttgaagag	120
ggtcagccta ctggggagat tatcgcttat aaggcttggt tctctcaaaa agggcttccg	180
ccttttatgg tgaagtttga aaatgaagtg acactaccag catatatggt aatgggtgcaa	240
tttgagaatc ttcaagcttg tgaggttggg ttcaatgttt atttcaaggc agacaatctc	300

GBS patentin.ST25

aaggaggtca aataa

315

<210> 93

<211> 6201

<212> DNA

<213> streptococcus agalactiae

<400> 93

ttgtccactt ttgattcagt tacaggaagg accaatcact tggaagctta tgaagggctg	60
aaccttttctg aaaaatttgc cattttaagt cactttgaca aacttagaaa tgagctgcag	120
acaccatcta ttcagctagg ggagtttgat agggaaatgg aagctttttc aatcactttg	180
ggaaatgaac tgttgggtta tttagaggca aatggcagcc cctatgagtt gaagcgagaa	240
ttgaatcagg ccgaaatgat ggcagtcctt gagcttagcc gtcaactggg tgcaaaattt	300
tctacaaaac tagaggagct gggaattgat ttgggttcat ttcaaccaga ccaagtcaac	360
atcttattgg atgccgttgg tcgttttcgc ttgaaaaatg cggacattgc tttattaggc	420
ggttatccaa aagcgagtgt ttcccagcta gctcttgcca cagaactcct ccagatggga	480
ctaagtcatg ataaggtaga atttttctta accagtcagc ttcagttaga ggatatgcga	540
caggtcgctt ttgctttcct acatgaaagc ttgaccagag aagaagcaga gcaatttgaa	600
acagaccgct ttcgtcatat aagcttaaac tttcgagaat ggcgagaact tctagaaaag	660
caagagccag aaatggtgga gatgtcagac gtcagcccgc ttgttcggga agtcttgcag	720
cattatccac ttggttcaag ggtcacttat aaaggacagg agtttgagat cttgtctatt	780
gaagctgcgg acatggataa tctgattcga atagagcttc aaaatgattt ttcatatctc	840
attgaacaaa atcccgttct ctattttcaa aacttggcag aaatcaggca agttcttcat	900
ttgtctcggt cggaatttgt agaaagagag gaacaacctg aggaagaatg gactctcttt	960
tcgtttatgg atgaggggac agaggataac gaaaaggaac ctgagattgt ttttgaatct	1020
accgataaag ttgttacatt agatagtcag ccagcacaag taagtgagac tatatccgaa	1080
tcagttcctg aaaccaaaga ggtgattgaa gcagaacaag caatagcagt tgattttagc	1140
tttcctgaag atttgactaa tttttacccc aaaacagcta gggataaagt agtggcgaat	1200
ctcgtagcta ttcgtcttgt aaaagaatta gaaagtgcta atcaatcagc aacacctaatt	1260
gaacaagaaa ttcttgccaa atatgtgggt tgggggtggc ttgccaatga attctttgat	1320
gagtacaatc cgaagttttc taaggaaaga gaggagtga aaactctcgt ttctgataaa	1380
gagtattccg atatgaaaca atcatctcta acggcctact atacggatcc gcttttaatt	1440
cgtcagatgt ggtctaagtt agaacaagac ggcttttagtg gtggaaaaat attagaccca	1500
tcaatgggaa cagggaaattt ctttgcggct atgccagctc atttgagggg aaagagtgag	1560
ctgtgtgggg ttgagttaga tactatcaca ggagcgatag ctaagcagct tcattcaaat	1620

GBS patentin.ST25

gtccatattg	aagtaaaggg	atttgagacg	gttgctttta	atgataatag	ttttgatttg	1680
gttattttcaa	atgttccctt	tgccaatatc	cgtatccgcg	ataatcagta	cgataagccc	1740
tatatgattc	atgactactt	tgtcaagaaa	tctcttgatt	tggtacatga	tggtgggcaa	1800
gtagccatta	tttctccac	aggaaccatg	gacaaacgga	cagaaaatat	tctccaagat	1860
attcgtgaga	cgacggattt	tcttggtggc	gtgcgtttgc	cagatacggc	ttttaaggcc	1920
attgcaggta	caagtgtgac	aacggatatg	cttttctttc	agaaacatct	gaacaaaggc	1980
tatcaagcag	atgacattgc	cttttcaggt	tctgttcgtt	atgacaagga	cgagcgtatt	2040
tggctcaatc	cctactttga	tggggagtat	aatgcccagg	ttcttggaag	gtatgagatt	2100
aaaaacttta	acggtggaac	actttcgggt	aaggaaacga	ctgataacct	gattgcbgagt	2160
gttcgagaag	ccttgcaaca	tgtaaaagca	ccaaggggta	ttgataaaac	agaagtcagt	2220
attaactcgg	atgtgattgc	aagacaggtc	atagatacca	ccattccacc	tgaaattaga	2280
gaaaaccttg	aacaatatag	ctatgggttac	aaagggttcta	ccatttatta	tcgtgataat	2340
aaggggattc	gtgttgggac	aaaaacggag	gaaattagct	attatgtgga	tgatgaggga	2400
aactttcagg	cttgggagtc	caagcattca	caaaaacaga	ttgaccgttt	taataactta	2460
gaagtcacag	atagcacagc	tcttgatggt	tatgtgactg	aagaacctgc	gaaacgtggg	2520
caatttaaag	gatattttcaa	aaaggcggtt	ttttatgaag	ctcctttgtc	tgaaaaagaa	2580
gtggcacgga	ttaaaggaat	ggtagatatt	cgcaatgcct	atcaagaggt	cattgctatt	2640
caacgcaatt	atgattacga	taagaatgag	tttaaccgct	tgttaggaaa	cctcaatcgc	2700
acctatgata	gctttgtcaa	acgctatggc	tttttgaaca	gtccagttaa	ccgaaattta	2760
tttgatagtg	atgataagta	ttcgctttta	gctagtctcg	aagatgaaag	tcttgaccca	2820
agtgggaaga	cggtcattta	tacgaagtca	ctggcctttg	aaaaagcctt	gggtccgtcct	2880
gaaaaaatgg	ttaaagaggt	gtcaaccgct	cttgatgcac	tcaactccag	tcttgcggtt	2940
ggtcgtggag	ttgactttga	ttacatggct	tccatctatc	aaacagcatc	taaggcagct	3000
ttgattgagg	agctgggaga	tcagattata	ccagatccag	aaagttattt	aaaaggacag	3060
ctgacctatg	tatctcgcca	ggagttttta	tcaggagata	ttgtgacaaa	attagaagtt	3120
atggacttac	tgttaaagca	agacaatcat	gatttttaact	gggcgcatta	tggtaatattg	3180
ttagaaagtg	ttcgtccagc	acgagtgatg	ttggcagata	ttgattatcg	aattggttca	3240
cgttggattc	cttttagctgt	ttatggaaaa	tttgtccaag	aagcctttat	ggggaagaat	3300
tatgacttaa	cggctacaga	agtggaagag	gtcctctctg	tcagcccgat	tgatgggacg	3360
atggaatttc	ggacacgggt	tgcctatacc	tactcaacag	cgacggatag	aagcctgggt	3420
gtagcaggct	cacgctatga	tagtggtcgg	aaaatctttg	agaatctgct	taactccaat	3480
cagccaacca	tcacgaagca	gattcaagag	ggagataaga	aaaagaatgt	gacagatgtg	3540
gagaagacaa	ccgttctgcg	tgctaaagaa	gcacaaatcc	aagacctctt	tcaagatttt	3600
gtcgcaagct	atcctgaagc	ccaacagatg	attgaggata	cctataatag	tctctataat	3660

GBS patentin.ST25

cgtaccgtct	ctaaagttta	tgátggcagc	cgtttggaga	ttgatggttt	ggctcaaaat	3720
atttcgcttc	gtcctcatca	aaaaaatgcc	attcagcgaa	tcgtggagga	aaaacgggct	3780
cttttagctc	atgaagtggg	ttcaggcaaa	actttaacca	ttcttggagc	aggctttaaa	3840
ctgaaagagt	taggtatggg	acataaaccg	ctttatgtgg	taccttctag	cttgaccgct	3900
cagtttggtc	aagaaatcat	gaagtcttc	ccaacgaaga	aagtctacgt	gacgacaaag	3960
aaagattttg	ccaaagctcg	gcgcaagcag	tttgtctcac	gtattattac	aggggattac	4020
gatgccattg	tcatcgggga	ctcccagttt	gaaaaaatcc	ccatgagtca	ggaaaaacag	4080
gtgacttata	ttcaagataa	gttgaacaa	ttacgggaga	taaagcaagg	aagcgatagt	4140
gactacacag	tcaaagaagc	ggagcgttcg	attaaagggt	tggaaaacca	attggaagaa	4200
ctccagaaac	tagatcgaga	tacctttatt	gaatttgaaa	atcttggcat	tgattttctc	4260
tttgtggacg	aagcccatca	tttcaaaaat	attaggccga	ttactgggtct	gggaaatgta	4320
gcgggaatta	ccaacacgac	ttctaaaaag	aacgtggata	tggaaatgaa	agtgagacag	4380
attcaggcag	agtatggaga	tagaaatgtc	gtttttgcca	caggaacgcc	ggtgtctaata	4440
tccattagtg	aactctatac	tatgatgaac	tatattcagc	cagatgtcct	agaacgctac	4500
caagtttcta	actttgactc	ctgggttgga	gcttttggca	atatcgaaaa	ttcgtatggag	4560
ctagcgccaa	caggagataa	gtatcaacc	aagaaacggt	ttaaaaagtt	tgtgaatcta	4620
cctgaactca	tgcggattta	taaagaaacc	gctgatattc	aaacgtcaga	tatgttggat	4680
ttacctgtac	ctgaagccac	agtcattgcg	gtggaaagtg	aactcacaga	agctcagaaa	4740
aactaccttg	aagaattggg	ggaccgttca	gatgcgatta	aatcaggaag	cgttgaccct	4800
agtgtcgata	acatgttaaa	ggtgataggc	gaagccagaa	agctagccat	tgatatgcgt	4860
ttgattgacc	ctgcctatac	cttatctgac	aatcagaaga	ttatgcaagt	agtggaatac	4920
gtggaacgga	tttaccgtga	gggcaaagga	gataaggcta	cacagatgat	tttctctgac	4980
attggcacgc	ctaaaagtaa	agaagaagga	tttgatgtct	ataatgaatt	gaaagccctc	5040
ttagttgacc	gaggaattcc	aaaagaagaa	attgcctttg	tccatgacgc	taatacggat	5100
gagaagaaaa	attctttgtc	acgaaagggtc	aatagtgggg	aagtaaggat	tctcatggct	5160
tcaactgaaa	aaggaggaac	aggattaaac	gtgcaagcac	gcatgaaagc	tgttcaccat	5220
ttagacgttc	cttggcgctc	ctcagacatt	cagcaacgca	atggacgttt	gattagacaa	5280
ggaaatcaac	atcagaatgt	agagatttat	cattatatta	ccaaaggttc	atttgataac	5340
tatttgtggg	ctacacaaga	gaataagttg	cgttatatta	aacaaattat	gacttcaaaa	5400
gatcctgttc	ggtcagcaga	agatattgac	gagcaaacca	tgaccgcttc	agatttcaaa	5460
gcgttagcta	ctggcaatcc	ctatctcaaa	ctcaaaatgg	agttagagaa	tgaattgacc	5520
gtcttagaaa	atcagaaacg	tgctttcaat	cgctccaaag	atgaatacag	gcacactatt	5580
tcctattgcg	agaaaaactt	acctgttatg	gaaaaacgat	taaggcagta	tgacagagat	5640
attgagaaat	cacaagcaac	gaagaatcaa	gagtttatca	tgcggtttga	taaccagaca	5700

GBS patentin.ST25

attgacaatc gcagcgaagc tggggattat ttacgaaaac tcatcaccta taatcgttcc	5760
gaaaccaaag aagtcagaac cttagcgacc tttagaggct ttgagcttaa aatggctaca	5820
cgaagtcctg gtgaaccctt gtctgacatg gtgtctctaa ctatttcagg ggataaccag	5880
tattcagttt cccttgattt aaaatcagac gtgggaacga ttcaacggat taacaacgcc	5940
attgaccata tcctagagga taaggaaaag acagaagaga tgacaaacaa cctcaaagat	6000
aagctagcag tcgcaagagt tgaagttgag aaagtctttg caaaggaaga ggaatatcag	6060
ttggtaaagg ccaagtatga tgtacttgcc ccattagtgg aaagagaagc agacttagaa	6120
gaaattgacg tagcactttc ccaatttagt agctctgacc catgcttgaa aaaagatcaa	6180
cagttagtcc ttgacattta a	6201

<210> 94

<211> 4905

<212> DNA

<213> Streptococcus agalactiae

<400> 94

atgaccacaa aatgcaatca tcattttctc atcaatcagg agaaaggcga aaagtatgtt	60
tttcgtaaaa gtaagcaata tcgcacgctg tgttcggttg ctttaggaac agttgtgatg	120
gcattcgtag ctttggccgg accgatggtg caggcggatg aagtagggag aactgttgcg	180
acaagtgtac agacggaaac gaatcctgca acaaatttaa aagaaaatca gccaaagtcg	240
attgcggaac aaaaagatag tcttgacgca accggtcaat caactggaac ggtgacagtc	300
actgttccac atgataaggt gacacaagct gtcgataagg caaagaccga aggaataaaa	360
gcagtacaag acaagccgat ggacttaggc aatacagtat ccgcagctga aaccagccaa	420
caactcaaaa aggagaaga agatgccaca aaccaaacaa caactatttc taaaactggt	480
gaaatctaca agtctgataa agcaacttat gaagctgaaa agaagtgggt agagaagcgt	540
aatgaagagt taactgctgc ttatgataag gcagaacaaa cagggactgg cttaaaccat	600
tcggttgata cgactgtttc agaattgaag tcgcaagacc aaaacgctca tgtgaccgtg	660
aacacacaaa cagtaaaatc aggagatggg acgagtgttt caggctatca ggagtacgtc	720
aagtctgttg cggccattga taagaagaat aaagcgaact tagctgatta tcggactaag	780
aaacaagccg cagacgctgt tgtggctaag aatcaactca ttcaaaaaga gaatgaagct	840
gggcttgcta aggcaaaagc agaaaatgaa gcgattgaca gacggaataa agaagggcaa	900
aaagctgttg atgaagcaaa taaggctggg caagccgcag tagagcaagc gaaccaagaa	960
aaacaaaaac aggccgcaaa ccgtgctttt gaaattgcga caattaccaa acggaataaa	1020
gaaagagaag aagtcgcaaa gaaagaaaat gcagcgattg atgcttataa tgcgaaagaa	1080
tggatccgct ataagcggga tttagcaaac atctcaaaag gggaggaagg ctacatttca	1140

GBS patentin.ST25

gaagcccttg	cgcaggctct	agatttaa	at	catggcgaac	cgcagggtcaa	acatggtgca	1200
ggtactcgaa	atccagatcg	aatcatttca	aagggagatg	ccatggtggg	tggtatttct		1260
aacattcttg	attcaacggg	tttctttgtc	tacaatcact	ttaaaacagg	tgaaacgctg		1320
aactttacct	atcaaaaatct	gaagcatgca	cgttttgatg	ggaagaaaat	tacagccata		1380
acttatgata	ttaccaatct	ggtttcacca	actggaacca	atgcgggtgca	gttagttggt		1440
ccaaacgacc	caacagaagg	ctttattgct	tatcgcaatg	atggcgctgg	aaattggcgg		1500
acagataaga	tggaagtccg	tgtcaaagct	cggtatttct	tagaagacgg	ttcacaagtg		1560
acctttacta	aagaaaaacc	aggtgtcttt	accactcgt	cactcaatca	taatgatatt		1620
gggcttgaat	atgttaaaga	ctcatcaggt	aaatttggtc	ctattcatgg	ttcaagtgtg		1680
caagtaacca	atgagggtct	agcccgttcg	ttagggtcaa	accgagcgag	tgacttgaag		1740
ttgccagaag	aatgggatac	gacttctagt	cgctatgctt	ataaaggagc	gattgtatca		1800
acagtcacat	cggggaatat	ttataccgta	acctttggcc	aaggagatat	gccaaaccaa		1860
gtgggaggga	agacctattg	gtttgcttta	aatactttgc	cagtcgcaaa	aacagtgact		1920
ccctacaatc	caaagactca	tgtaagacca	cagctggatc	cagttcctga	accgataaaa		1980
gttacaccag	aaacttatac	tcctaaaatc	tttactcctg	aaaaaccagt	aacctttact		2040
ccaaaatcag	tagaaaaagt	gccccaacct	agtttgacct	taacaaaagt	cacactacca		2100
acaaatctga	agctagaacc	attacccaaa	gctccacaaa	agccaaccgt	tcattaccac		2160
gattacctct	taaccacaac	acccgctatc	gcaaaagaag	tgatgaatgt	tgacaaaagt		2220
aatcttcatg	gtaaacagggt	ggctaaggat	tccactgtta	tttatccctt	gacagtagat		2280
gttttatctc	caaatcgttc	caagataacc	agtcttatct	ttgaagatta	tctgcctgct		2340
ggttatgcgt	ttgatatgac	gaagacacaa	gcggagaata	gcgactatga	cttaaccttt		2400
gataaaaata	agaactttgt	gaccttgaaa	gcgaaagata	gcttacttca	aacgttgaat		2460
aaagagttaa	acaagtctta	tcaactgtct	gctccaaaac	tttatgggtc	agttcaaaat		2520
gatggggcga	cttattctaa	tagctataaa	ctccttatta	acaaggacac	cccaaaccac		2580
tatacggtta	tttcaaacgt	agttagaatt	cggactccag	gagacgggtga	aacgaccagc		2640
cgaatccggc	ctaaaaagga	caatgaaaat	gcggacgggtg	tgttgataaa	tgatacgggt		2700
gttgctctta	gtacaaccaa	tcattaccgt	ttgacctggg	atttggatca	gtacaagggg		2760
gatacttctt	caaaagatac	cattgcacga	ggattccttt	ttgtagatga	ctaccagaa		2820
gaagcacttg	acttggtaga	taaagggaca	gttatcacca	cccttgatgg	taaagctggt		2880
tcagggtattt	ctgtatacag	ctatacatcc	cttgataaag	caccaaagaa	gctacaagat		2940
aaattagctc	gtgcgaacat	ttcgccaaaa	ggagcggtcc	aggtctttga	accggacaat		3000
catcaagcgt	tttacgatac	ttacgttaag	actgggcagt	ctttagccct	tctcacaaaa		3060
atgaaggtaa	aagatagttt	gtacggtcag	actgtcagat	acaaaaataa	agcctaccaa		3120
gttgattttg	gcaatggcta	tgaaactaag	gaagtcgtca	atacagtcgt	tcatccagag		3180

GBS patentin.ST25

cctaagaaac aaaatctcaa taaggacaag gtggacatca atggcaaagc gatgcttgtc	3240
ggctcccaaa acttctatac gctttcttgg gatttagatc agtatcgtgg cctacaagcg	3300
gataagagtc agattgctca aggcttttac tttgtggacg attatcccga agatgttctt	3360
cttcctgaca caaaagccat tcaaattatg acgaaagacg ggaaagctgt taaaggaatg	3420
gagataaaaa cctatcatca actctcagat gctccaaagg aattgcaggc agctcttgcc	3480
aaacgtaata tcacgccccaa aggcgctttt caagtcttta tgccaaaaga tccacaagct	3540
ttttataaag cttatgtgac aactgggtcaa aacttgacta ttgtgaatcc gatgacgggt	3600
cgtgaagcag tatacaactc aggggaagtct tatgataatg tggcctatca agtggacttt	3660
ggacaggcct atgaaacgaa tatagtgacc aatcacgtgc caacagtaaa cccgcataag	3720
tccaatacca ataaagaagg tgtgtcaata gaaggtaaga cagtccttcc gaatacgggtc	3780
aactactata aaattgttct agattatagt cagtacaaga atatgattgt gacagatgat	3840
gtcctcgtca aaggttttta tatggtggat gattaccagc aagaagcact tactcctcat	3900
ccagatggga ctcaagtgat ggatcagaac gggaaatttg tcagaggcct gtctgttcga	3960
acttacgcaa gtttggcaga tgcaccgaaa gcagtacaag aagcaatgaa atctcgaaat	4020
ttcattccta aaggagctat tcaggctctt caggcagatg acccaaaaac tttctttgaa	4080
acttatgtga aaacaggaca aaaattgggt gtgacaacac cgatgacagt gaagaatgaa	4140
cggattcaaa caggcggtca gtatgagaat acagcttatc agattgattt tggcatcgct	4200
tatgtaacgg aaacagttgt gaataatgta ccaaaattag aacctcaaaa agatgtggtc	4260
attgacttat ctcaaaaaga taagagtta aacggaaaag caatcgcttt ggatcagggtc	4320
tttaactacc gcttggtagg ttcacttatc ccacgcaatc gtgcgacagc cttggtggaa	4380
tacagtttta aagatgacta cgatgaaaag cacgatgaat ataagggtgt ttataaagcc	4440
tatactttgc gtgatgtaac cttaaaagat ggcacagtat taaagcaggg gacagaagtg	4500
acgaaataca ccttacaag tgttgataag gcaaaaggaa cgattgcatc tcgttttgat	4560
acagcttttt tggaaaatat agctgatgaa tcagagtttc aggctgagct ttatcttcag	4620
atgaaacgca ttgcttcagg tgatgttgaa aatacagtta ttcatagtgt caatggttat	4680
aatattcgct ctaacacggg taagaccaca accccacaac cagagtcacc gactcctgat	4740
aaccaccgt caccccaacc gccagttcca accacagaat cccagttca agctagtgtc	4800
ctaccaagta caggggaaag tcaatccctt ttggcgctca ttggaggagg tctcctgctt	4860
ggcctcgctt acggactttc taaacgaaaa aaggagaaaa actaa	4905

<210> 95

<211> 2109

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 95
 atggcaaata ataattttta taatcgtgac ctttttgaa atatggatga tatttttaat 60
 tctctaattg gaaatatggg gggctataat agtgagaata aacgatactt aatcaatgga 120
 cggaagtta ctctgaaga attcagtcaa tatcgtcaaa ctggaaaact ccccggtcaa 180
 gagctaaata accaaaatac tcctacaaac caagtctctg cagatagtgt ttgactaaa 240
 ttaggaacta atttaaccga tcaagcacgt cagcatttgc tagatccagt tattggacga 300
 aacaaagaaa ttcaggaaac tgcagaaatt ctagctcgtc gtactaaaaa taatcctggt 360
 ctagttggtg atgcagggtg tggtaaaaca gctgttattg aaggtttggc acaagcaatt 420
 ataaatggtg atgtccctgc tgctatcaaa aataaagaaa tcatttcgat agatatctct 480
 agccttgaag ctggcaccca atataggggt agttttgaag aaaatattca aaatatcata 540
 aaagaagtta aggaaacagg aaatattatt ctcttctttg atgaaataca ccaaattata 600
 ggagccggtt caactggtgg tgatagtggc tctaaggggc tcgcagatat acttaagcct 660
 gcactttcac gtggtgaatt aacggttata ggtgcaacta ctcaagatga atatcgtaac 720
 accattctca agaatgctgc cttagcacgc cgctttaacg aagttaaagt caatgcacct 780
 tctgcacaag atactttcaa tatecttatg gggataagaa acctctatga gcaacatcat 840
 aatgttggtt tacctgactc tgttttgaaa gcagctgtag atttatctat tcaatacata 900
 ccacaaagaa gtctccctga taaagcaatt gacctattg atatgactgc tgcacaccta 960
 gctgcgcaac atcccgtaac tgaccttaaa tccttagaaa aagaaatcgc tgcgcaaaga 1020
 gacaagcaag aaaaagctgt caatactgaa gattttgaag aagctcttaa ggtcaagaca 1080
 cgcattgaag agttacaaaa ccagattgat aatcataccg aaggacaaaa agtcactgca 1140
 actatcaatg atatcgctat gtcaattgag cgtctaactg gagttcctgt atcaaatatg 1200
 ggtgctagtg atattgaacg cttaaaagaa cttggcaatc gtctaaaagg taaagtcatt 1260
 ggtcaaaatg atgctgttga ggcagttgca agagctattc gccgaaatcg tgctggtttc 1320
 gatgatggtg atcgtccgat tggtagcttt ctatttggtg gaccaactgg agttggttaa 1380
 actgagctag caaagcaatt agcttttgat atgttcggat caaaggatgc tatcgttaga 1440
 cttgatatgt ctgaatataa tgatcgtact gcagtttcta agctaattgg agcgactgct 1500
 ggttacgttg gttatgacga caatagtaat acactaacag aacgtatccg tcgaaatcct 1560
 tattctattg ttcttcttga tgaaatcgaa aaagctgacc cgcaagttat cacgcttctc 1620
 cttaagttc tagatgatgg tcgtttaact gatgggtcaag gaaacactat taactttaaa 1680
 aatactgtta tcattgcaac ctcaaagca ggttttgaa acgaagcatt tacagggtgac 1740
 agcgataaag acttgaaaat tatggaacga atttctccat atttccgtcc agaatttcta 1800
 aatcgtttca atggtgttat tgaattctct cacctaagca aagatgactt aaacgaaatt 1860
 gtagatttga tgcttgatga agttaaccaa acaattggca aaaaaggaat tgaccttggt 1920
 gtagatgaaa atgttaaatac acacttaatt gacctgggtt atgacgaagc aatgggagta 1980

GBS patentin.ST25

cgtccattgc gccgtgtcat cgagcaagaa attcgagatc gcatcacaga ctactatctc	2040
gatcatacag atgttaaaca cctaaaagct aatttgcaag atggccaaat cgtcatttct	2100
gaaagataa	2109

<210> 96

<211> 945

<212> DNA

<213> Streptococcus agalactiae

<400> 96	
atgggaagat ttaaagaact tttagagagt aaaaaagctc tcatcctaca cggtgccttg	60
gggaccgagc ttgagagtag aggtttgtgat gtttctggta aactttggtc agacaaatat	120
ctgattgagg atccagcagc tattcagacc attcatgaag attatatctg tgctggcgct	180
gatattgtga cgacatcaac ttatcaggcg actttacaag ggctagctca agttggtgtc	240
tctgaaagtc aggcagaaga cttgattcgc ttgactgttc agttggcaaa agctgtgcgt	300
gagcaagttt ggaaaagt ttt gacaaaagaa gaaaaatcag aaagaatcta tcctttgatt	360
tctggggatg ttgggtcccta cgctgccttt ttggcggacg gttctgagta cacagggtc	420
tacgatattt ataaggaagg tctcaaaaat ttccatcgcc atcgtattga gcttctttta	480
gatgaggggtg ttgaccttct ggcaattgaa accattccaa atgctcagga ggctgaggct	540
cttattgagc tacttgtcga ggatttcctt cagggttgagg cttatatgtc attcacctct	600
caagatggta agaccatctc agatggtagt gctgttgagc gcttggcgaa agctattgat	660
gttagccac aggtcgtggc gctgggcatt aactgttcaa gtccatcggt agttgctgat	720
ttcttgcaag caatagcaga gcagacggac aagcctcttg tgacctatcc aaactctgga	780
gagatttatg atggggcaag ccaatcttgg caatctagcc gagatcattc acacacccta	840
cttgaaaata caagtgactg gcaaaaactt ggcgccaag ttgtcggagg ttgttgccga	900
actagaccag ctgatattgc tgacctctca gaacatttga cataa	945

<210> 97

<211> 1173

<212> DNA

<213> Streptococcus agalactiae

<400> 97	
atgaaaatag gaattgataa gattggtttt gcaaccagtc aatatgtcct tgaaatgact	60
gatttggtta ttgctcgcca agttgaccct gaaaaattca gcaagggatt attgttagat	120
tcacttagta ttacgccagt tacagaagat atcgttacac ttgcagcctc tgcagcta	180

GBS patentin.ST25

gatattttat ctgatgagga caaagaaact attgatatgg tgattgtcgc tacagaatca	240
agtatcgatc agagtaaggc ggcttctgtc tatgtacatc aactttttaga gattcaacct	300
ttcgcaaggt cattcgagat gaaagaagca tgctatagcg caactgctgc tcttgattac	360
gctaaattac atgtagaaaa acatccagat tctaaagtat tagtgatagc ttcagatatt	420
gctaaatatg gcattaaatc tactggagaa tccactcaag gtgcaggcag tatcgctatg	480
cttattagtc aaaacccatc cattctagag ctaaaagagg accgtctagc gcaaaccctg	540
gatattatgg acttttggcg accaaattat tctgatgttc cttatgttaa tggcatgttt	600
tcaacaaaac aatatctaga tatgctaaaa actacttggg aagaatatca aaaacgtttt	660
aatactagtc taagtgacta tgctgctttt tgtttccata tcccttttcc aaaattagct	720
ttaaagggct ttaataaaat tctagataat aacctagatg aacaaaagaa agctgaacta	780
caagaaaatt ttgagcactc tattacttat agtaagaaaa ttggaaattg ctatactggc	840
tcattgtatc taggacttct atcgttacta gaaaatagtc aaaattttaa agcagggtgat	900
caaattgcct tcttttcata cggtagcgga gctgttgctg aaatttttac cggtcagtta	960
gtagacggct accaaaataa acttcagagc gatcgatgg atcaactcaa taaacgtcaa	1020
aaaattacag taactgagta tgagaaaactc ttctttgaaa aaacaatcct agacgaaaat	1080
ggaaatgcca acttcaacac ctaccgtact ggcacttttt ctctagactc tatttgcgaa	1140
catcaacgta tctacaagaa aattaataat taa	1173

<210> 98

<211> 915

<212> DNA

<213> Streptococcus agalactiae

<400> 98	
atgaaaagtg cttatatctt ttttaatcca aaatctggta aagatgaaca agcattggca	60
caagaagtaa aatcttattt aatagaacat gattttcaag acgattatgt tcgtatcatt	120
acaccttcat ctgttgagga agctgtcgcc ttagcaaaaa aagcatcaga agaccatatt	180
gacttgggta ttccttttagg gggagatggc actattaata aaatctgtgg tgggtgtctac	240
gctgggtggg cttatcctac tatcggacta gtacctgccg ggaccgtcaa taacttttca	300
aaagctttga acatcccaca agagaggaat ctcgctcttg aaaaccttct aaacgggtcat	360
gtaaagtccg tagatatctg taaagttaac gacgattaca tgattagcag tttaacactt	420
gggctccttg ctgatattgc tgctaattgtc acttctgaaa tgaagcgtaa attaggacct	480
tttgctttcg taggtgatgc ctaccgtata ttaaagcgta atcgatcata ttctattact	540
cttgcttacg ataataatgt acggctcttta cgacgcgggt tactacttat taccatgacc	600
aattcgattg ccggtatgcc agccttctct ccagaagcaa caattgatga tggacttttt	660

GBS patentin.ST25

agagtctaca ctatggaaca tattcacttc ttcaaattat tgttgcattc aagacaattt	720
cgtaagggag attttagtca agcaaaggag ataaaacatt ttcataccaa taatctgact	780
atttcaactt ttaaacgtaa aaaatcagct atccctaaag ttcgtattga tggcgatcca	840
ggtgaccaat tgcctgtaaa agttgaagtc atccctaaag ccttaaagtt tatcattcct	900
aactcattac cataa	915

<210> 99

<211> 855

<212> DNA

<213> Streptococcus agalactiae

<400> 99	
atgacaacat ttactgctaa atttattgac caagagtggg aagtcccagt agaatcaggt	60
cgctaccata tgattgttgg ggaattttgt ctttatgcac aacgtccgca gattgcacgc	120
caactgcttg gtttggataa acatatttct atcagttttg tggatgatgt tccaagtgat	180
ataggactta ttttagcca accagaacag gttactggtg ctaagtcgct tcgtgatatt	240
tatcatttga ctgacccgac ctacaaaggt ctttatacta tcccaatttt aattgacaag	300
actgataatc gtattgtctg taaggaatct gcagatatgc ttcgactttt tactacagat	360
ttctctgatt tgcataaga ggatgctcct gtccttttca gccaaagaaac tgcttcactt	420
attgataatg atattaaaga cattaataat aacttccaaa gcttaatgta taagttagct	480
tttcttgata aacaagcaga ttatgatact tatagtaagg aattcttcac ttttctagat	540
caaaaagaac acttactagg acaacgctct ttcttgctcg gagataatct aagtgaggtt	600
gatattcatt tctttacacc attagtccgc tgggatattg ctgggcgtga tcttctacta	660
cttaatcaga aagcgctaga agactaccca aatatttttt cttgggctaa aactttatac	720
aatgacttta atttaaaaac attaaccaat ccacaatcca taaaaaataa ctattactta	780
ggcaaatttg gaagagctgt tcgtcatcat accatcgtac caacagggtcc aaatatggta	840
aaatgggaaa aataa	855

<210> 100

<211> 2073

<212> DNA

<213> Streptococcus agalactiae

<400> 100	
atgaaaaaga aaattatttt gaaaagtagt gtccttggtt tagtcgctgg gacttctatt	60
atgttctcaa ggcgattcgc tgaccaagtc ggcgtccaag ttataggcgt caatgacttt	120

GBS patentin.ST25

catggtgcac ttgacaatac tggaacagca aatatgcctg acggaaaagt tactaatgct	180
ggcactgctg ctcaattaga tgcttatata gatgatgctc aaaaagattt caaacaact	240
aaccctaattg gtgaaagcat tagagttcaa gctggtgata tggttggagc aagtccagct	300
aactcagggc ttcttcaaga tgaaccaacc gttaaaacat ttaatgcaat gaatgttgag	360
tatggcacat taggtaacca tgaatttgat gaaggtttgg cagaatacaa tcgtatcgtt	420
actggaaagg cccctgctcc agattctaata ataaataata ttacgaaatc ataccacac	480
gaagctgcaa aacaagaaat tgtagtggca aacgttattg ataaagttaa caaacaatc	540
ccttacaatt ggaaacctta cgctattaaa aatattcctg taaataacaa aagtgtgaac	600
gttggtttta tcggaatcgt taccaaagac atcccaaacc ttgtcttacg taaaaattat	660
gaacaatatg aatttttaga tgaagctgaa acaatcgta aatacgcaa agaattacaa	720
gctaaaaatg tcaaggctat tgtatgcctt gctcatgtac ctgcaacaag caaggatgat	780
attgctgaag gtgaagcagc agaaatgatg aaaaaagtca atcaactctt ccctgaaaat	840
agcgtagata ttgtctttgc tggacacaat catcaatata caaatggtct tgttggtaaa	900
actcgcatg tacaagcgct ctctcaagga aaagcctatg ctgacgtacg tgggtgccta	960
gatactgata cacaagattt cattgaaacc ccttcagcta aagtagttgc agttgctcct	1020
ggtaaaaaaa caggtagtgc cgatattcaa gccattgttg accaagctaa tactatcgtt	1080
aaacaagtaa cagaagctaa aattggtact gccgaggtaa gtggcatgat tacgcgttct	1140
gttgatcaag ataatgttag tccagtaggc agcctcatca cagaggctca actagcaatt	1200
gctcgaaaaa gctggccaga tatcgatttt gccatgacaa ataatggtgg cattcggtct	1260
gacttactca tcaaaccaga tggaacaatc acctggggag ctgcacaagc agttcaacct	1320
tttggttaata tcttacaagt cgtcgaaatt actggtagag atctttataa agcactcaac	1380
gaacaatacg accaaaaaca aaatttcttc cttcaaatac ctggtctgcg atacacttac	1440
acagataata aagagggcgg agaagaaaca ccatttaaag ttgtaaaagc ttataaatca	1500
aatggtgaag aaatcaatcc tgatgcaaaa tacaattag ttatcaatga ctttttattc	1560
gggtggtggtg atggctttgc aagcttcaga aatgccaaac ttctaggagc cattaatccc	1620
gatacagagg tattttatggc ctatatcact gatttagaaa aagctggtaa aaaagtgagc	1680
gttccaaata ataaacctaa aatctatgtc actatgaaga tggttaatga aactattaca	1740
caaatgatg gtacacatag cattattaag aaactttatt tagatcgaca aggaaatatt	1800
gtagcacaag agattgtatc agacacttta aaccaacaa aatcaaaatc tacaaaaatc	1860
aaccctgtaa ctacaattca caaaaaacaa ttacaccaat ttacagctat taaccctatg	1920
agaaattatg gcaaacatc aaactccact actgtaaaat caaaacaatt accaaaaaca	1980
aactctgaat atggacaatc attccttatg tctgtctttg gtgttggtgact tataggaatt	2040
gctttaaata caaagaaaaa acatatgaaa taa	2073

GBS patentin.ST25

<210> 101

<211> 1740

<212> DNA

<213> Streptococcus agalactiae

<400> 101

atggcatata tttggtctta tttgaaaagg taccccaatt gggttatggct tgatttacta	60
ggagctatgc tttttgtgac gggtatccta ggaatgccca cagccttagc gggatgatt	120
gataatggcg ttacaaaagg tgatcggact ggagtttatc tgtggacgtt catcatgttt	180
atatttggtg tactaggtat tattggggtt attacgatgg cttacgcata tagtcgctta	240
acgacaacaa tgattagaga tatgcgtaat gatatgtatg ctaagcttca agaatactcc	300
catcatgaat atgaacagat aggtgtatct tcaactagta cacgtatgac aagcgatact	360
tttgttttga tgcaatttgc tgaaatgtct ttacgttttag gcctagtaac tcctatggta	420
atgattttta gcgtgggttat gatactaatt acgagtcctat ctttggcttg gcttgtagcg	480
gttgcgatgc ctcttttggg aggagtcgtt ttatatgtag ctataaaaac aaaaccttta	540
tctgaaagac aacagactat gcttgataaa atcaatcaat atgttcgtga aaatttaaca	600
gggttacgag ttgttagagc ctttgcaaga gagaattttc aatcacaaaa atttcaagtc	660
gctaaccaac gttacacaga tacttcaact ggtcttttta aattaacagg gctaacagaa	720
ccacttttcg ttcaaattat tattgcaatg attgtggcta tcgtttgggt tgctttggat	780
cccttacaaa gaggtgctat taaaataggg gatttagttg cttttatcga atatagcttc	840
catgctctct tttcattttt gctatttgcc aatcttttta ctatgtatcc tcgtatgggtg	900
gtatcaagcc atcgtattag agaggtgatg gatatgccaa tctctatcaa tcctaagcc	960
gaaggtgtta cggatacgaa acttaaaggg catttagaat ttgataatgt aacattcgct	1020
tatccaggag aaacagagag tcccgttttg catgatattt cttttaaagc taagcctgga	1080
gaaacaattg cttttatttg ttcaacaggt tcaggaaaat cttctcttgt taatttgatt	1140
ccacgttttt atgatgtgac acttggaata atcttagtag atggagttga tgtaagagat	1200
tataacctta aatcacttcg ccaaaagatt ggatttatcc cccaaaaagc tcttttattt	1260
acagggacaa taggagagaa tttaaaatat ggaaaagctg atgctactat tgatgatctt	1320
agacaagcgg ttgatatttc tcaagctaaa gagtttattg agagtcacca agaagccttt	1380
gaaacgcatt tagctgaagg tgggagcaat ctttctgggg gtcaaaaaca acggttatct	1440
attgctaggg ctgttggtta agatccagat ttatatattt ttgatgattc attttctgct	1500
ctcgattata agacagacgc tactttaaga gcgcgtctaa aagaagtaac cggtgattct	1560
acagttttga tagttgctca aagggtgggt acgattatgg atgctgatca gattattgtc	1620
cttgatgaag gcgaaattgt cggtcgtggg acccagctc aattaataga aaataatgct	1680
atttatcgtg aaatcgtga gtcacaactg aagaaccaa acttatcaga aggagagtga	1740

GBS patentin.ST25

<210> 102

<211> 1632

<212> DNA

<213> Streptococcus agalactiae

<400> 102

atgaaaaaag gacaagtaaa tgataactaag caatcttact ctctacgtaa atataaattt	60
ggtttagcat cagtaatttt agggccattc ataatgggtca caagtcctgt ttttgcgat	120
caaactacat cggttcaagt taataatcag acaggcacta gtgtggatgc taataattct	180
tccaatgaga caagtgcgtc aagtgtgatt acttccaata atgatagtgt tcaagcgtct	240
gataaagttg taaatagtca aaatacggca acaaaggaca ttactactcc tttagtagag	300
acaaagccaa tgggtggaaaa aacattacct gaacaaggga attatgttta tagcaaagaa	360
accgaggtga aaaatacacc ttcaaaatca gccccagtag ctttctatgc aaagaaaggt	420
gataaagttt tctatgacca agtatttaat aaagataatg tgaaatggat ttcataataag	480
tctttttgtg gcgtacgtcg atacgcagct attgagtcac tagatccatc aggaggttca	540
gagactaaag cacctactcc tgtaacaaat tcaggaagca ataataaga gaaaatagca	600
acgcaaggaa attatacatt ttacataaaa gtagaagtaa aaaatgaagc taaggtagcg	660
agtccaactc aatttacatt ggacaaagga gacagaattt tttacgacca aatactaact	720
attgaaggaa atcagtgggt atcttataaa tcattcaatg gtgttcgtcg ttttgttttg	780
ctaggtaaag catcttcagt agaaaaaact gaagataaag aaaaagtgtc tcctcaacca	840
caagcccgtg ttactaaaac tggtagactg actattttcta acgaaacaac tacaggtttt	900
gatattttta ttacgaatat taaagatgat aacgggtatcg ctgctgttaa ggtaccgggt	960
tggactgaac aaggagggca agatgatatt aaatgggtata cagctgtaac tactggggat	1020
ggcaactaca aagtagctgt atcatttgct gaccataaga atgagaaggg tctttataat	1080
attcatttat actaccaaga agctagtggt acacttgtag gtgtaacagg aactaaagt	1140
acagtagctg gaactaattc ttctcaagaa cctattgaaa atggtttagc aaagactggt	1200
gtttataata ttatcgggaag tactgaagta aaaaatgaag ctaaaatatc aagtcagacc	1260
caatttactt tagaaaaagg tgacaaaata aattatgatc aagtattgac agcagatggt	1320
taccagtgga tttcttacia atcttatagt ggtgttcgtc gctatattcc tgtgaaaaag	1380
ctaactacaa gtagtgaaaa agcgaaagat gaggcgacta aaccgactag ttatcccaac	1440
ttacctaaaa cagggtacct tacatttact aaaactgtag atgtgaagag tcaacctaaa	1500
gtatcaagtc cagtgggaatt taattttcaa aagggtgaaa aaatacatta tgatcaagtg	1560
ttagtagtag atgggtcatca gtggatttca tacaagagtt attccggtat tcgtcgctat	1620
attgaaattt aa	1632

GBS patentin.ST25

<210> 103
 <211> 1248
 <212> DNA
 <213> Streptococcus agalactiae

<400> 103
 atggaaaatt ggaagtttgc cctatcatcg attctagggc acaagatgcg tgcttttctg 60
 accatgttag ggatcatcat tgggggttgc tcagtttgtt taattatggc cttaggtaag 120
 ggcataaag attcgggttac aaatgagatt acaaagtctc agaagaacct tcagatttat 180
 tataaaacaa aagaagacca aaaaaatgag gataactttg gagctcaagg ggctttcatg 240
 caaggtagtg ataccaaccg taaggaacca attattcaag aatcatgggt aaaaaagatt 300
 gctaaggaag tagatggtgt tagtggctac tatgtaacca atcaaacaaa tgctccagta 360
 gcttaccttg aaaaaaaggc aaagacgggt aatataacag gagttaaccg cacttacctt 420
 ggtatcaaaa agttcaaaat taaaagtggc cgtcaattcc aagaggagga ttataaccaa 480
 ttctcgagag ttattttact agaagaaaaa ttagctcaga gattattcca gacaaatgaa 540
 gcagcgtaa ataaggtggt gactgtaaaa aataaatctt acttagtagt ggggggtttat 600
 tcggatccag aagctgggtc aggcttatat ggaagtaatt ctgatgggaa tgctatttta 660
 accaatacac agttagcttc ggagtttggt gctaaagaag cagaaaacat atattttcat 720
 cttaatgatg tatcgcaatc caatcgcat ggtaaagaaa taggcaaacg ttaacagac 780
 attagtcatg ctaaggatgg gtactatgat aattttgaca tgacatctat agttaaatct 840
 atcaataccc aagttggtat tatgacaggt gttattggag cgattgcagc aatttctctc 900
 ctagttggtg gtatcggagt gatgaatatt atgttagtct ctgtaactga gcgcacgaga 960
 gaaattggcc ttcgtaaagc ccttggggca actcgacgta aaattttagc tcaattttta 1020
 attgaatcaa tggctttaac gattttgggt ggattaattg gggtattact agcctatgga 1080
 ggtacgatgt taattgctaa tgcgcaagat aagattactc cttctgtgtc acttaacgtg 1140
 gctataggca gtttaatttt ctcagcattt attggaatta tatttggttt attacctgct 1200
 aataaagcca gcaaattaaa cccaattgat gctttacgat atgaataa 1248

<210> 104
 <211> 1215
 <212> DNA
 <213> Streptococcus agalactiae

<400> 104
 atgcagtatt cagaaattat gattcgttat ggagaactct ctactaagaa gaaaaaccgt 60

GBS patentin.ST25

atgcgcttca tcaataagtt aaaaaataat atggagcatg tactctccat ttatccagat	120
gtttcagtaa aaacagatcg tgatagagga catgtatadc tcaatggtac agattatcat	180
gaagttgcag agtccttaaa agagatTTTT ggtatccaag ctttttctcc atcttttaaa	240
gtagaaaaaa atgttgatac attggtaaaa gctgtccagg aaattatgac ttccgtttat	300
aaagatggga tgacttttaa aattaccgca aaacgtagtg accactcatt tgaattggat	360
agccgtgctc taaatcatac tttaggagat gccgtTTTT cagtcttgcc aaatattaag	420
gctcagatga agcaaccaga tatcaatctt aaagtcgaga tacgagatga ggctgcttat	480
atttcatatg agaataattag ggggtgcagga ggattaccgg taggaacatc tggaaaaggg	540
atgctgatgt tgtctggtgg gattgattct ccggtggcag gttacctagc gttaaaacgt	600
gggtgtagata tagaagcagt tcattttgca agtcctcctt atactagccc aggtgcattg	660
aaaaaagcac atgatttaac acgtaaattg acaaaatttg gtggtaatat tcaatttatt	720
gaagttccat tcacagaaat tcaagaggaa attaaggaaa aagctcctga agcctacttg	780
atgacgttaa cacgtaggtt tatgatgcgt attacagatc gtattcgtga gaaccgaaat	840
ggctttgtta ttattaacgg tgaaagttta gggcaggtgg caagccaaac gctagaaagt	900
atgcaagcca ttaatgctgt cactgcaaca ccgattattc gtcctgtggt cacgatggat	960
aagctagaaa ttattgatat tgctcaaaaa atagatactt ttgatatttc aattcaacca	1020
tttgaggatt gctgtacgat ttttgcacca gatcgcccaa aaactaacc taaaattaag	1080
aatacagaac agtatgagaa acgtatggat gtagaaggtc tggtagagag ggcagttgca	1140
gggattatgg taactactat tcaacctcaa gcagatagtg atgatgttga tgacttgatt	1200
gacgatttat tataa	1215

<210> 105

<211> 360

<212> DNA

<213> Streptococcus agalactiae

<400> 105	
atggctcgtg ttaaagggtg agttgtttca cgtaaacgtc gtaaacgcgt acttaaatta	60
gctaaagggt actatggtgc aaacatatac ttgttccgta ctgcaaaaga acaagtaatg	120
aattcttact actatgcata ccgtgaccgt cgtcagaaaa aacgtgactt ccgtaaatta	180
tggtactctc gtatcaatgc ggctgctcgt atgaatgggt tatcatattc gcaattgatg	240
cacggtttga aattagctga aatcgaagtt aaccgtaaaa tgcttgctga tttagcagtt	300
aacgatgcag cagctttcac agctcttgca gatgcagcta aagctaaact tggtaaataa	360

<210> 106

GBS patentin.ST25

<211> 1026

<212> DNA

<213> Streptococcus agalactiae

<400> 106
atgttttaaag cttcaaaaaa actcgttcaa aaaaataagt caaatcattt ttggcttggt 60
tttttcataa cacttatact atttcttatt ggttggttacg ccagcttacg atttggtgct 120
atcaatttca agactagtga tttaataact gttttaaaaa atcccttaaa aaactctaata 180
gtcaggatg ttatttttga cattagacta ccacgcataa ttgcagctat cttagtaggt 240
gcagctatgt cacaagcagg tgctattatg cagggagtc ctcgaaacgc cattgctgat 300
cctggactac taggtattaa cgccggagct gggttagccc ttgttggtgc atatgctttt 360
ttagggagca tgcactatag tacgattctc attgtctgct tactagggtc tgcattttct 420
tatcttttag tcttcacact ctcttataca aagcaaaagg gttaccacca actacgactc 480
attttagctg gagcgatgat ctccacactt ttacgtctg ttggacaagt gggtacatta 540
tacttttaac tcaatcgaac tggtatcggg tggcaagcag gtggtttatc ccaaattaac 600
tggaatatgc taatcataat agcacctatc attatttttag gtttacttat ttcacaactc 660
ctagcacatc aattaactat cttgagcctt aatgaatctg tggccaaagc attgggacaa 720
aaaactcaat taatgactgc gtttctatta cttattgttt tgtttttatc ggcttcatca 780
gtcgcgttga taggaaccgt ttctttcatt ggattgatta ttccacattt tattaagctt 840
tttattccca aagattatcg tctgttatta cttttaatag gattttcagg ggctactttc 900
atgatctggg tagacttatc atctcgtatt ataaatcccc cttcagagac accaattagt 960
tctataatca gtatcgtagg gcttccatgt ttcctatggt taattagaaa agggaaaaat 1020
ctatga 1026

<210> 107

<211> 567

<212> DNA

<213> Streptococcus agalactiae

<400> 107
atgattaaaa gaccaattca tctttctcat gatttttttag cagaagttat tgataaagaa 60
gcaataacgc ttgatgcaac tatgggaaat gggaatgata ctgttttttt agcgaaaagt 120
tctaaaaaag tttatgcatt tgatattcaa gaagaagcaa tagcaaaaac gaaagcaaag 180
ctcacggagc aagggatttc taacgctgaa cttatcttgg atgggcatga aaatttgga 240
cagtatgttc atacaccttt aagagcggct atattttaatc tgggatactt accctcagcg 300
gataaaacag ttattacaaa acctcacaca actatcaagg caatcaaaaa cgtttttagac 360

GBS patentin.ST25

atTTTtagaag taggtggacg tctatcactt atgggtttatt atgggtcatga tgggtggaaaa	420
agtgagaaaag atgcggtgat agcattcgtg gaacaattac cacagaataa tttcgctaca	480
atgctttatc aaccactcaa tcaagttaat acgccccct ttttaattat ggtagaaaag	540
ttacaatcat atgaaaatga ggtgtaa	567

<210> 108

<211> 1008

<212> DNA

<213> Streptococcus agalactiae

<400> 108 atgcgagtac atattacaag tatatatggg cagtcaccgc gtagcattgc ccttatatca	60
caaaaactag ttaaggatgt cggacgtcaa cttggttatg atgaaatggg aatctacttt	120
tataatgatc atgctgaaac gcatggtgaa agaagtacta ggatggatgg tatcattgcg	180
ggattaggca gaggggatat tgttgttttt caagtaccta catggaattc aacagaattt	240
gatgaacttt ttctagataa attacaggca tacggtgcta gaattataac ttttgtacat	300
gatattgttc ccttaatggt tgagtctaatt ttttatttat tagatagagt aattgacatg	360
tataatcgtt cggatgttgt tattctacct acaaaagcga tgcattgatta tctaattgaa	420
aaagggatga ctacctctaa agttctttat caagaagtat gggatcatcc agttaatata	480
gacctccctc gtccagaatg tcaaaaagtc cttagttttg caggcgatat tcaacgcttt	540
ccctttgtca atgactggaa ggaaaatata ccgctcatct attatggaga cggaagcaga	600
ctcaattctg aggcaaagt tcatgctcag ggatggaaag atgatgtaga attgatgcta	660
agtctttcta agcggggagg atttggcctg tgttggagtg aagatagaga ggagttagtc	720
gagcgtcgtt attcgaggat gaatgcctcg tataaattat ctactttctt ggctgctgga	780
cttccaatta ttgctaacca tgatatttca agtagagact ttatcaaaca acacggatta	840
ggatttacag ttgaaacgct agaagaagct gttgaaaaaa ttaataatat ggaaaaagag	900
acttatgaca gctatgtgga aaatgttgag aagatagcaa ctctcttgcg aaatggttat	960
atcactaaaa aattgttgat agatgctgtg catatgcttt atagatag	1008

<210> 109

<211> 3933

<212> DNA

<213> Streptococcus agalactiae

<400> 109 atgtcccaa agacttttgg caagcagtta acagttgtag atactaagag tagagtcaag	60
---	----

GBS patentin.ST25

atgcataaat	caggaaaaaa	ctgggtaaga	acagtaatgt	cgcatttttaa	tctattttaaa	120
gcgattaaag	ggagagcaac	tgttgaagca	gatgtgtgta	ttcaagatgt	tgaaaaagaa	180
gaccgactat	cttcaggaaa	tttgacctat	ctcaaaggaa	tactagctgc	cggagctctg	240
gtaggtggag	cgagtttaac	cagtcgtgtt	tatgcagatg	agactccagt	tgttcaagaa	300
caatcaagtt	ctgtaccaac	actggcagaa	caaacggaag	tgactgttaa	aacaactact	360
gttcaaaatc	atcaagatgg	gacagtatcg	aaaaacatta	ttgattctaa	tagtgtatct	420
atgtcagagt	cagcctcaac	aagtactagt	gaatctgtaa	gtatgtctat	gtcaggggtca	480
actttaacaa	gtgtaagtga	atctgtaagt	acatctgctt	taacaagtgc	ttcagaatcg	540
ataagcacgt	cagcctcaga	aagtgtttca	aaatctacaa	gtattagtga	ggtttcaaat	600
attcttgaaa	ctcaagcttc	tttaactgat	aaaggaagag	agtcgttttc	ggcaaaccag	660
atagtaacag	aaagtagctt	agttactgat	gctggtaaaa	atgcttcagt	atctagccta	720
attgaaatta	caaaaccaa	atcggagtta	cagacttcca	aaatgtcaaa	tgagtcgctt	780
ataactccag	agaaatccca	agtaatgatt	gcaagcgata	aaactgggaa	tgagagtcta	840
actccgacaa	ttagattaaa	atcagttatt	cagccaagga	gtatgaactt	gatgactttg	900
agttcggaga	tggacttgat	accactagaa	gaagtgtctg	atactgaaat	gttaggtaaa	960
gatgtatcaa	gcgagttgca	gaaagttaat	attgcgttaa	aagataacac	tcttagtgag	1020
cctggaacag	ttaaattaga	tagttcagaa	aaccttgttt	tgaactttgc	cttttcaatc	1080
gcttctgtta	acgagggaga	tgtctttact	gtaaagcttt	ctgataacct	tgacacacaa	1140
gggattggta	ctatttctaaa	agttcaagat	ataatggatg	aaacggggca	gttattagcg	1200
actgggtcat	atagtccttt	aacacataat	attacataca	cctggacaag	gtatgcttct	1260
acgttgaata	atattaaagc	tagagtcaat	atgccagttt	ggcctgacca	gagaataatt	1320
tctaaaacaa	cttcagataa	gcagtgcctt	actgcaacat	tgaacaatca	agttgcttca	1380
attgaggaac	gtgttcagta	taatagtcct	tcagtgcag	aacatactaa	tgtaagaca	1440
aatgtaagat	ctcggatcat	gaagcttgat	gatgaaagac	agacagaaac	ttatattact	1500
caaattaatc	ctgaaggtaa	ggaaatgtat	ttcgcacag	gacttgggaa	tctatatact	1560
attatcgggt	cagatggaa	atcaggttca	ccagtttaatt	tattaaatgc	ggaagtaaag	1620
attctaaaaa	ctaattcaaa	aaatcttaca	gatagtatgg	atcaaaatta	tgattcgcct	1680
gagtttgaag	atgtgacttc	ccagtatagt	tatactaacy	atgggttctaa	aattaccata	1740
gatttgaaaa	caaattctat	ttcttccact	acatcttatg	ttgttttggt	caaaatacct	1800
aaacaaagtg	gtgtattgta	ttcaactgtt	tctgatataa	atcaaacata	tggttctaaa	1860
tattcttatg	ggcatacgaa	tataagtgg	gactcagatg	cgaatgccga	aattaaactt	1920
ttatcagaaa	gtgcttctac	gagtgcgctg	acgtcagcaa	gtaccagcgc	ttccatgagt	1980
gcctcgacat	cagcaagtac	cagcgcttcc	atgagtgcct	cgacatcagc	aagtaccagc	2040
gcttccatga	gtgcgtcgac	gtcagccagc	accagcgctt	caaccagcac	ctcaacgagt	2100

GBS patentin.ST25

gcctcgacat cagccagcac aagtgtttca acaagtgtca gtatgagtgc ttcaacaagt 2160
 gcaagtacga gtgcatccac gtcagcaagt actagcgctt ccacaagtgc cagcaccagc 2220
 gcctcaacga gtgcctcaac gtcagccagc actagcgctt caacgtcagc cagcaccagc 2280
 gcctcaacca gtgcttcaac cagtgtttcc acatcagcca gcactagcgc ctcaatgagt 2340
 gcgtcgatgt cagccagcac aagtgtttca atgagtgcct cgacgtcagc cagcactagc 2400
 gcctcaacca gtgcttcaac cagtgtttca accagtgcct ccacctcagc aagtatgagc 2460
 gcctcaacaa gtgcaagtac tagcgcttca acaagtgtca gtatgagcgc ctcaaccagt 2520
 gcaagtacta gtgcttcaac aagtgtccagt accagtgcct cgacgtcaac aagtactagc 2580
 gcttccacgt cagcaagtac cagtgtcatcc acatcagcaa gtatgagcgc atccacgtca 2640
 gccagcacca gcccctcaac cagtgtttca accagtgcct caaccagtgc ttcaaccagt 2700
 gcttccacat cagccagcac tagcgcttca atgagtgcct ccacgtcagc aagtactagc 2760
 gcctcaatgt cagccagtac tagcgcttca accagtgtcc gtaccagtgc ttccacctca 2820
 gcaagtatga gcgcttcaac aagtgtcaagt actagcgctt ccacaagtgc aagtatgagc 2880
 gcctcaacca gtgcaagtac tagtgccttca accagtgtcc gtaccagtgc ctcgacgtca 2940
 acaagtacta gcgcttccac gtcagcaagt accagtgcct ccacatcagc aagtatgagc 3000
 gcatccacgt cagcaagtac cagtgtcatcc acgtcagcaa gtatgagcgc ctccacaagt 3060
 gcaagtatca gtgcatccac gtcagcaagt atgagcgctt ccacaagtgc aagtaccagt 3120
 gcatcgacgt cagccagtac tagcgcttca atgagtgcct cgacgtcagc cagcaccagt 3180
 gcttccacaa gtgcaagtac tagcgcttca atgagtgcct cgacatcagc aagtaccagc 3240
 gcttccacaa gtgcaagtac gagtgccttcc acatcagcaa gtactagcgc ctcaacatcg 3300
 gcaagtacaa gttcttccac aagtgtcaagt accagtgcct cgacatcagc cagcactagc 3360
 gcctcaatga gtgcctcgac gtcagccagc acaagtgtt ccatgagtgc gtcgacgtca 3420
 gccagcacta gcgcttcaac gagtgcgtca atgtcagcca gcacaagttc ttcaacaagt 3480
 gcctcgatgt cagccagcac tagcgcttca atgagtgcct cgacgtcagc tagcactagc 3540
 gcctcaacga gtgcgtcaat gtcagccagc acaagttctt caacaagtgc ctcgatgtca 3600
 gccagcacta gcgcttcaat gagtgcgtcg acgtcagcca gcaccagcgc ttcaacgagt 3660
 gcgtcaatgt cagccagcac tagcgcttca atgagtgtcc cgacgtcagc cagcaccagc 3720
 gtctcaacga gtgcatcgac atcagcaagt accagcgctt ccacaagttc ttcaagctca 3780
 gtgacttcta attcatcaaa agagaagggtg tattctgcct taccttctac gggtgaccaa 3840
 gattattctg taactgtctac tgccttaggt ttaggtttta tgactggtgc aacccttttg 3900
 ggacgaaaaa aatctaaaaa agataaagac taa 3933

<210> 110

<211> 1992

GBS patentin.ST25

<212> DNA

<213> Streptococcus agalactiae

<400> 110

atgatagata gaaaagatac taaccgattt aaattagttt ccaaatatag cccttcggga	60
gatcaacctc aagctattga aacgttgggt gacaatattg aaggaggaga aaaagctcag	120
attttaaaag gtgctactgg tactggtaaa acctacacaa tgagccaagt tatcgcccaa	180
gttaacaagc caaccttgggt gattgcacat aataaaacct tagcagggtca actttatgga	240
gagtttaag aatTTTTTcc tgacaatgcc gtagagtact ttgtttcata ttatgattat	300
tatcaaccag aagcttatgt gccttcttcg gatacttata ttgaaaaaga tagttcagtc	360
aatgacgaaa ttgacaaatt acgtcactca gcgacttctt cgttattaga aagaaatgac	420
gttattgttg tagcatctgt ttcttgtatt tacggtttag gttctcctaa agagtatgca	480
gacagtgttg ttagccttag gccagggtcaa gaaatttcac gtgatcagtt attgaacaat	540
ctcgttgata ttcaatttga gcgtaacgat attgattttc aacgtggaaa atttcgcgtt	600
cgtggcgatg ttgtagaagt ttttcttgcg agtcgtgatg agcatgcctt tcgaattgaa	660
ttttttggtg atgaaattga tcgtataaga gaaatagaat cgtaaacagg gcgtgtgcta	720
ggagaagtgg aacattttagc tattttccca gcaacacact ttatgacaaa tgatgaacat	780
atggaagaag ctatttcaaa aatacaagct gaaatggaaa atcaagtaga actttttgaa	840
aaagaaggga aattgattga agcgcaacgt attcgacaaa ggacagaata tgatattgaa	900
atgcttcgtg aaatgggata taaaaatggt gttgagaact actcacgtca catggatggt	960
agaagtgaag gtgagccacc ttttactttg ttagatttct tcccagaaga ttttttgatt	1020
atgattgatg agagtcacat gacaatgggg caaatcaaag ggatgtataa tggagaccgt	1080
tcgcgtaaag aaatgttgggt taattacggt ttccggttac catctgcctt agataaccgt	1140
ccacttcgtc gtgaagaatt cgaaagccat gtccatcaaa ttgtctatgt atctgcaacg	1200
ccaggagact atgaaatgga gcaaacagat acagttgttg agcaaattat ccggccaaca	1260
ggacttcttg atccagaagt tgaagttaga ccaagtatgg ggcagatgga tgacttgctt	1320
ggtgaaatca atttgaggac tgaaaaagggt gagcgtaacct ttattacaac attgacaaag	1380
cgtatggcag aagacttaac agattatctc aaagaaatgg gagttaaaagt taagtatatg	1440
cacagcgata ttaaaacctt agaacgtaca gagattattc gtgatttacg acttggtgtg	1500
tttgatgttt taattggtat taatctctta cgtgaaggaa tagatgttcc tgaggtttcc	1560
cttgttgcaa tcttagatgc tgataaggaa ggtttccttc gtaatgagcg tggctttatc	1620
caaacaatcg gacgtgcagc acgtaacagt aatggtcatg ttattatgta tgctgataaa	1680
ataacagatt ctatgcaaag agctatggat gaaaccgctc gccgtcgtcg ttacaaaatg	1740
gattataatg aaaagcatgg aattgtgcca caaacaatta aaaaagaaat ccgtgattta	1800
attgctatta ctaaaagtaa tgacagcgat aagcctgaaa aagttgtcga ttacagtagt	1860

GBS patentin.ST25

ttatctaaaa aagaaaggca agctgaaatt aaagctcttc aacagcaaat gcaagaagca 1920
gctgaattat tggactttga gctagctgca caaatccgag atgttatctt agaactaaaa 1980
gcaatcgatt aa 1992

<210> 111

<211> 2184

<212> DNA

<213> Streptococcus agalactiae

<400> 111
atgaagcaca agttaaaagc ttttacgctt gctttactct caatattctt tgtgtttggt 60
ggaaagggtca gtgcagaaac tgtgaatatt gtttctgata cagcatagcg tccattcgaa 120
tttaaagatt ctgatcaaac ttataaagga atcgatgttg acatcgtaa cgaagtcgct 180
aagcgtgctg gctggaatgt taacatgacg taccaggtt ttgatgccg agttaacgct 240
gttcaatctg gacaggcaga cgcgctaag gccggaacta ctgttactga agcacgtaaa 300
aaagtcttta atttctcaga tacttattac gatacttccg ttattcttta tactaaaaat 360
aataataaag tcacaaacta caaacaacta aaaggaaaag tagtcggtgt aaaaaatgga 420
acagctgctc aaagcttctt agaggaaaat aaatctaaat acggctataa agttaaaaca 480
tttgatacaa gtgacctaat gaataacagc cttgattctg gttctattta cgccgctatg 540
gacgatcaac cagttgtgca atttgcgata aatcaaggaa aagcttacgc cattaacatg 600
gaaggcgagg cagttggtag ctttgcattt gctgtcaaaa aaggtagtgg acacgataac 660
ctaattaaag aatttaacac agcttttgca caaatgaaat cagatggcac ttataatgac 720
atcatggata aatggcttgg gaaagacgct acaaaaacaa gcggcaaagc aacaggtaat 780
gccaatgaaa aagcaactcc tgtaaagcca agttataaaa ttgtttctga ttcttcattc 840
gcaccattcg aatatcaaaa cggtaaaggg aaatatactg gttttgatat ggaattaatc 900
aagaaaattg ctaaacagca aggttttaaa cttgatatct caaatccagg ttttgatgcc 960
gctttaaatg ctgtccaatc tggacaagct gacgggtgta ttgcaggagc tacaatcaca 1020
gaagcacgcc aaaaaatctt tgatttttct gatccttatt acacatctag cgttatctta 1080
gcggttaaaa aaggaagcaa tgtcaaatca taccaagatt taaaaggaaa aacagttggt 1140
gctaaaaatg gtactgcctc atatacttgg ttatcagacc acgcagataa gtacaactat 1200
catgttaaag catttgatga agcatctaca atgtatgata gtatgaactc aggttcaatt 1260
gatgctctaa tggatgacga agcagttctt gcttacgcta ttaatcaagg tcgtaaattt 1320
gaaacaccta tcaaagggtga aaaatcaggc gatatcggat ttgcagtga aaaaggggca 1380
aatccagaat taattaaaat gtttaacaac ggtcttgctt cactcaaaaa atcgggtgag 1440
tacgataaac ttgttaaaaa atacctttcc acagccagca cctcttcaaa cgataaagct 1500

GBS patentin.ST25

gctaaacctg tagatgaatc aactatttta ggggttaattt ctaataacta caaacaattg	1560
ctatctggta ttggaactac ttttaagttta actcttatct catttgcgat tgctatgggt	1620
attgggtatta tctttgggtat gatgagcgta tcaccaagta atactctccg cacaatttca	1680
atgatttttg ttgatattgt ccgtgggtatt ccactcatga ttgtggccgc ttttattttc	1740
tgggggtattc ctaatttaat cgaaagcatc acaggtcacc aaagtccaat taatgacttc	1800
gttgctgcta ctatcgctct ttcttttaaat ggtgggtgcgt acattgctga aattgtacgt	1860
gggtgggtattg aagctgttcc ttctgggtcaa atggaagcaa gtcgtagttt aggtatttct	1920
tacggcaaaa ctatgcaaaa ggttatcttg cctcaagcag tacgccttat gttaccaaac	1980
tttatcaacc aatttgtcat ctcatataag gatacaacaa ttgtatcagc aatcgggactt	2040
gtggaactct tccaaactgg taaaatcata attgcacgta actatcaatc attccgatatg	2100
tatgctatcc ttgcaattat gtatcttgta atcattaccc ttctcaccgc tctagcaaaa	2160
cgtttagaaa agaggcttaa ataa	2184

<210> 112

<211> 159

<212> DNA

<213> Streptococcus agalactiae

<400> 112	
atgggagata aaccgatatc atttcgtgat aaagatggga attttgtttc agcggccgat	60
gtctggaatg ctgaaaaatt agaagaactc ttttaacacat taaatcctaa tcgtaaaactt	120
cgtttagaac gcgaaaaatt agcaaaagaa aaaggatag	159

<210> 113

<211> 843

<212> DNA

<213> Streptococcus agalactiae

<400> 113	
atggaaacat atactctatc gaatactctt aacattccta aaattgggtt tgggacatgg	60
caactaactg aagggtgaaga agcttataag gcagtgactc atgctttaaa agttgggttat	120
actcatattg atactgctca gatttatggc aacgaacaca gtgttgacg tgctataaga	180
gacagtgggt tggcgcgaga aagtatcttt ttgacaacta agatttgga tgacaaacat	240
gactatcatt tagccaaagc ttctattgat gaatctctgc agaaattagg tgttgattat	300
attgatcttc ttttgattca ttggccaaat ccaaaagctc ttcgtgaaaa tgatgcgtgg	360
aaagctggga atgcaggcac ttggaaagcg atggaagaag cttataaaga aggaaaggta	420

GBS patentin.ST25

aattgccaaa tactctatga tcctgaaaat caattacaat cactcaaaga gagattcgaa	420
gtttcttatac ccagtcagtt acaaaaacaa attatcattc aaaatcgtaa cttattaact	480
ggcaagcttc cctcttacga taaacaaatt ataaaagccc ttaaagcca agactttgtt	540
agtactcacc atagaactac tgctttctta gattcctact ttgatattat ttttgactt	600
aataagttga cacatcctgg cgaaaaaaga atgatttcct atgctaagaa gaatgctaca	660
ttgcttccta aacatttcga agaaaatata attaaactat gtcatacaca ctccaacgaa	720
cacactgtta aagaaacatt aaacgatata ataatgcata tcgacgtcat gcttaaagaa	780
aattttcaac actttatagg ttaa	804

<210> 116

<211> 804

<212> DNA

<213> Streptococcus agalactiae

<400> 116

atgaaaaaaa ttatttatct tggtttagcc tgtgtcagta tattaacttt aagtggttgc	60
gagtcaattg agcgttctct aaaaggagac cgttatgttg accaaaaact agctgaaaac	120
tcttcaaagg aagctactga acaactaaac aaaaaaacta agcaagcctt aaaagctgat	180
aaaaaagctt ttcctcaatt ggacaaggct gttgccaaaa acgaggcaca agtgcttata	240
aaaacctcta aaggtgatat aaatatcaag ttatttccaa aatatgctcc tttagctggt	300
gaaaattttc taacacatgc aaaagaagga tactataatg ggtaagttt ccacagagtt	360
atcaaagatt ttatgatata atctggtgac cctaattggag acgggaccgg tggaaaatct	420
atatggaata gcaaagataa aaagaaagat tctggaaatg gttttgttaa tgaaatatcc	480
ccttacctct acaatatcag gggaagttha gcaatggcaa atgctggagc tgatactaat	540
ggcagccaat tctttatcaa tcaaagccag caagatcatt ccaaacaact gtcagataaa	600
aaagttccta aggtgattat taaagcctat tcagaggag gaaatccaag tttagatggt	660
ggttataaccg tctttggaca agtaatctct ggcattggaaa ctgtggataa aattgcttcg	720
gtagaagtta caaatcaga tcaacaaaaa gaaaaaatta ctattacaag tatcaaagtt	780
attaaagact acaaatthaa ataa	804

<210> 117

<211> 690

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

agtgcaactt tgcaaggggtt gagagctaga cgagcaaaga atgggcatat tgaattagat 1620
 aatattgcag catttcaatt atcagaactg tttgcaaadc aagataatgt tagcttttca 1680
 caacatTTTT accaattgat tgaagatttg agacaccag aaaagtttaa aatacctggt 1740
 ctatctgttt cagcttcctt gcgcgattat cagcttacag gtgtccgttg gttaagtatg 1800
 ttagatcatt atggctttgc agggatttta gctgatgata tggggcttgg aaaaacactt 1860
 caaacgattt catttttaag taaaaacta actagagatt ctctgtgtgct tattttatca 1920
 ccatcaagtt taatttataa ttggcaagat gaattccaca aatttgcgcc agacgtagat 1980
 gtagcagttg cctatgggtc taagattcgt agagatgaaa ttattgctga acgtcatcaa 2040
 gtaatcatta caagttattc atcatttagg caggattttg agacttattc tgaaggaaat 2100
 tatgattatt taattttgga tgaagcacag gttatgaaaa atgctcaaac taaaatagcc 2160
 catagcttga gatcttttga ggtcaaaaac tgttttgcat tatcgggaac acctattgag 2220
 aataaactgt tagaaatttg gtccattttc cagatcattt tacctgggtt attacctggt 2280
 aagaaagagt ttttgaagtt gaaccctaaa caagttgctc gttatatcaa accatttgtg 2340
 atgagacgtc gaaaagaaga agttctccca gaattaccgg atttgattga aatgaactat 2400
 ccaaagaaa tgacagacag tcaaaaagtt atctatttgg cgcaattacg ccaaattcaa 2460
 gaaagtatcc aacattctag tgacgctgac ttaaatcgtc gtaaaattga aattttatct 2520
 ggcattcacac gattacgtca aatttgcgac actccacgtc tttttatgga ttatgatggt 2580
 gaaagcggta agttagaaag cctacatcaa cttttaacac aaattaagga aaatggacat 2640
 cgtgctctga ttttttctca gttcaggggt atgtagata tcgcagaacg tgagatggta 2700
 gctatggggc ttacaactta taaaattact ggttctacac cagcaaatga acgtcatgaa 2760
 atgaccagag catttaatgc aggatcaaaa gatgctttct tgatttcttt aaaagctggt 2820
 ggcgttggtc tcaaccttac aggagctgat accgttggtc tgattgactt gtggtggaat 2880
 ccagctgttg aaatgcaggc gattagtcgc gcacataggt tggggcaaaa agagaatgtc 2940
 gaggtttatc gcttgattac tagaggcaca atcgaagaaa aaattctaga aatgcaagaa 3000
 actaaaaaac atttggttac aacagttctg gatggaaatg aaacccatgc tagcatgagt 3060
 gtagatgata ttcgagagat acttgaggtt tctaaataa 3099

<210> 122

<211> 534

<212> DNA

<213> streptococcus agalactiae

<400> 122

gtgttactta cagaaatcaa aaaatcacca gaggggcttt attttgataa aaaaatagat 60
 atcaaagagt cgcttatgga gcgtcattca gagataatgg atatttctga tattcaagtt 120

GBS patentin.ST25

aaagctattg gtgtttcgaa tttcatgaaa catcacttag aggcctttatt tgaaactgcc	480
gaaataaaaac ctatgggttaa tcaaattatc ctagcaccag gttgtgctca agaggatttg	540
gttcgcttct gtaaaggaaa tgatatctta ttagaagctt acagtccatt tggaacaggt	600
gctatTTTTg aaaatgaatc tataaaagct attgctgaaa aatatggtaa atcagttgca	660
caagtagctc ttcgctgggc acttgataat ggctttttac cattaccta gtcagcgact	720
cccaaaaata ttgaagcaaa ccttgatatt ttgattttc aattaaacga agatgatatt	780
actaccttaa tacaactaga ttcagggtatt aaacccaaag atccagataa tgtctcattt	840
taa	843

<210> 114

<211> 468

<212> DNA

<213> Streptococcus agalactiae

<400> 114	
atgggttaaag gtcaaggaaa cgttgtagca caaaataaaa aagcgcatca cgactatact	60
atcggtgaaa caatagaagc aggaattggt ttgacaggaa cagaaatcaa aagtgtccgc	120
gcagcgcgta ttacattgaa agatggatat gcacaaataa aaaatgggtga agcgtgggtg	180
attaatgttc atattacacc atacgatcaa ggtaatatat ggaatcaaga tcctgatcgt	240
acacgaaagt tattactaaa aaaacgtgag attgaaaaaa tatcaaatga actgaaaggg	300
actggatatga ctctgggtacc tctaaaagtt tacttaaaag atgggttttgc taaagttcta	360
ttgggttttg caaaaggaaa acatgattat gataagcgag agtctatcaa acgtcgtgag	420
caaaaccgtg atattgcccg tcagttaaaa aactataatt cacgatga	468

<210> 115

<211> 804

<212> DNA

<213> Streptococcus agalactiae

<400> 115	
atggaccatt tcacaaaact ctggcaagat ttctctaaac ttccaaatgt tgttgctata	60
gcactcggag gctcacgctc tgggtgacagt tttagcaaat cttccgatta tgatttgtat	120
gtttattgtg cagcaactcc tgatatcact agtcgtaaac gtatccttaa caagcactgt	180
cattacattg aacttaacaa tcattactgg gagcttgaag ataatggtag tttaaacgac	240
ggaactgata ttgatattct ctatcgtaac atagataact ttttatcaga cttagaagat	300
gtcgttgaac accacaattc tcgaattgga tacactactt gtttttggca taacctcatc	360

GBS patentin.ST25

<400> 117
 atgaaaattg gaattattgc agccatggag gaagagttaa aactccttgt ggaaaatctt 60
 gaggataaat ctcaagagac agtattatca aatgtatatt acagtggacg ttatggtgaa 120
 catgagcttg ttttagtaca gtctggtgtt gggaaagtca tgtcagcgat gagtgttgct 180
 attttagtag aaagctttta agttgatgct attattaata caggatcagc tgggtgcagta 240
 gcaacaggat tgaatgtagg agacgtcgtt gtcgcagata cattagttta tcacgatgta 300
 gatttaaccg cctttgggta tgactatgga caaatgtcaa tgcagccact ttattttcat 360
 tcggataaga cttttgtttc cacttttgaa gcagttttat ctaaagaaga aatgactagt 420
 aaagttgggt taattgcaac tggggatagt tttattgctg gccaggaaaa gattgatggt 480
 attaaggggc attttccaca ggttttagct gtcgagatgg aagggtgcagc aattgccc aa 540
 gctgctcaag ctacaggaaa gccctttgtg gtggtacgtg ctatgagtga tactgcagct 600
 catgatgcca atatcacatt tgatgaatgt atcattgaag ctggtaaacg ctctgccc aa 660
 gtattaatgg catttttgaa agcattataa 690

<210> 118

<211> 1167

<212> DNA

<213> Streptococcus agalactiae

<400> 118
 atggaaaaga gacttagttt aggagctctt gtttagcta gtacagttct tttagcagca 60
 tgtggaaatg tcggaggagg agcatcttcg acaggaacaa aaatagggaa agatattaag 120
 gtagggata actgggaatt atcaggaaac gtttcttcgt atggaaattc aatgaagaat 180
 ggagctgact tagcagtaaa agaaattaat gctgctggag gggttggcgg caagaagtta 240
 aaagtcctat cacaggataa taaatcagaa aatgcagagg cagcaacggt tgccacaaac 300
 ttggttacca aaggagctaa tgtcattatc ggaccagcaa catcgggtgc agctgcatct 360
 tcaactccaa aagtaaatgc agcagcagtt ccaatgattg cacctgctgc gacacaagac 420
 aatttagtct atggttctga tggaaaaacc ttaaatacagt atttcttccg agctactttt 480
 gtcgataatt atcaaggaaa gctattgtct cagtatgcta cagacaacct taaagctaaa 540
 aaagttgttc tattttatga taattcatca gattactcaa agggggtagc aaaatcattt 600
 aaggaaagt atagtggaaa aattgttgat agcatgacat tctccgctgg tgatactgat 660
 ttccaagcgt cattgactaa gttgaaaggg aaagaatatg atgctattgt gatgccaggt 720
 tactataccg agacaggatt aatagttaag caagcgcgtg atttaggtat ctctaaaccg 780
 gttcttgggc ctgatggttt tgatagtccg aaatttgtgc aatcggaac acctgtggga 840
 gcttcaaacg tttattattt gacaggtttc actacacaag gatcaaccaa agctaaagct 900
 ttccatgatc attacgttaa ggcataatgg gaagaacat ccatgttctc ggctttatca 960

GBS patentin.ST25

tacgatgccg	tgtatatggc	agctaaatct	gctaaaggag	ctaaaacttc	aattgatctt	1020
aaaaaagctt	tagctaagct	gaaagatttt	aaagggtgtga	cagggaaaat	gtctattgat	1080
aaaaatcata	atgttggtta	atcagcttac	gttgtcaa	tagacgatgg	aaaaacaagt	1140
agcgttaaca	ttatttcagc	aaaataa				1167

<210> 119

<211> 1353

<212> DNA

<213> Streptococcus agalactiae

<400> 119

atggagaatc	ataattctat	taaacagacc	tatggattaa	tgactacaat	tgctatgatt	60
gtagggttag	tgattgggtc	aggcatttat	tttaaagttg	atgacatcct	taaatttact	120
gggtggagatg	tctttttagg	catggtaatt	ttagtactag	gttctttttc	gattgttttt	180
ggaagtttgt	caatttctga	gctagctatt	agaacgagtg	aaagtgggtg	tattttttct	240
tactacgaaa	aatatgttag	cccagcttta	gcagcaactt	taggcttggt	tgctgttttt	300
ttgtatcttc	caactttaac	agcaatcggt	tcatgggtag	ctgcatttta	tacttttaggt	360
gaatcatcaa	gtttggaatc	acagattatt	ttagctgctg	tttatatttt	agcacttagt	420
ctcatgaata	tctttgctaa	gcgtattgca	gggggattcc	aatctttaac	gacctttgta	480
aaaatgattc	cttttagtct	aattgcttta	attggtgctt	tttgggtctga	taaagctcca	540
caacttccac	aacatttaac	agctattcag	ccgtcaaagt	ttggatggag	ttgggtgtca	600
gggtctggtag	cattgtattt	tgcatatgat	ggttggacaa	tttttggttag	tattgcacca	660
gaagtcaaga	atcccaagaa	gaatttacca	cttgcctttg	tcattgggtcc	agcgcttatc	720
ttattatcat	atttggcatt	tttctatggg	ttgacacaaa	tttttaggtgc	tagctttatt	780
atgacaaccg	gtaatgatgc	tattaattat	gcagctaaca	ttattttcgg	tcctagtgtt	840
gggcgtttat	tatctttcat	tgttatttta	tctgtattag	gtgttgccaa	tggaacttta	900
cttgggacga	tgctgtctacc	tcaagctttt	gcggaacgcg	gatggatcaa	aagtgagagg	960
atggctaaca	taaatttgaa	gtatcaaagt	tcattgccag	ctagtttgac	ggtgacggct	1020
gtagctattt	tttggctttt	tgttcacttt	atggttacaa	aatttaattt	attgccgggt	1080
agtgatatta	gtgaaattgc	tgtgggtgtt	aataatacta	gtttaatcat	tctttatggt	1140
ttagtactca	gcctttatct	caaaaaagat	attaaaaata	aatttaccgg	cttagtttca	1200
ccgattctag	caatttttagg	cggtttgatc	ctctttatcg	ggagtttggt	aagtaatttc	1260
tttacggttt	taattttcca	atgtttttgc	ttattattct	gtttgatttg	tcattatatc	1320
tatcaaaaaa	ataaccctaa	aactcatgaa	tag			1353

GBS patentin.ST25

<210> 120

<211> 1803

<212> DNA

<213> streptococcus agalactiae

<400> 120
 ttgaccgaat ttaatgacga tcagcattct aaccatgatc agaaaagttt taaagaacaa 60
 attctggcag agttagaaga agctaaccgt ttgagaaagt tgcgtgaaga agaactctat 120
 caaaaagagc aagaagccaa agaagctgct cgcagaacag cacaattgat ggcagattat 180
 gaagcgcaac gtttgaaaga cgaacaagaa gctagagcaa aggcgctaga gactaagcaa 240
 cgcttagaag agcaagagaa ggctcggatt gaggcgaaac ttctggcaga agctgctcga 300
 gaagaagaaa gacgtcaggc ggaacaagca ttagcttccc aagaagaaca agttatcaat 360
 caagggatgg aaccttcaag agagcttgat agcggctcca aatctagtga atttaggaca 420
 actgaaaatg tacctgacat agatttataaa gcagataaga ctgatgttgc aactgctgtg 480
 cctaatacaag aaacggaaga aatcttttctt gtgagagcaa cagatattcc tacagaaggt 540
 gaaaatgtaa aacttggtga gacatcagag ttagagcccg tagcaaagga acctatccga 600
 gtagaggatt tgtcaaaaga agaagaggat atagctttgt cagccaagaa caaacataac 660
 aagcgtgaaa gacgtcagaa agcagataat gtggcaaaac gaattgcacg tattctgata 720
 tcaattatca tacttgtatt gctcttgaca gcattttagt gttatcgttt tgtagatagt 780
 gctattaaac ctgttgattc caattcaaat aaatttgtac aagttgaaat tccgatagga 840
 tctgggaata aattaattgg tcaaatTTTA gaaaagcag gagtcattaa gagcgccaca 900
 gtctttaatt actattccaa gttcaaaaac tatagtaatt ttcaaagtgg atactacaat 960
 cttaaaaaaa gtatgacttt agatcagatt gctgctgaat tggaaaaagg cggaactgca 1020
 gaaccgacaa aaccagcttt aggtgaagata ttaattaccg agggttacac tattaacag 1080
 attgctaaag ctattgagtc taataaaatt gatacaaaga ctacaagtac acctataaa 1140
 gctgatgatt tcttgaaact tgttcaagat gaaacgttta ttaaaaaaat ggtagctaaa 1200
 tatccaaatt tactaggaag tctacctgat aaatcaaaag ctatttatca attggaagga 1260
 tatttattcc cagctactta caactattat aaagatacaa ccttagaagg acttggtgaa 1320
 gatatgattt caacaatgaa tactaagatg gcaccttact ataacactat taaagcgaag 1380
 aatatgtctg taaatgatgt tttagacatta tcatctcttg ttgaaaaaga gggatcaaca 1440
 gacgaagatc gccgtaaaat agcaagtgtc ttttataacc gattatcagc cggatcaagct 1500
 cttcaaagta acattgcaat ttgtgatgct atggggaaat taggtgataa aacaagttta 1560
 gctgaagatg ctcaaattaa tacttcaatt aaatcaccat acaacatcta tactaatact 1620
 ggtttgatgc ctggaccagt tgatagtcca agtatctcag caattgaagc gactataaaa 1680
 cctgcttcaa cagattatct ttattttgtc gctgatgtga agaccgaaa tgtatactac 1740

GBS patentin.ST25

gctaaagact ttgaaacaca caaggctaac gttgaaaaat atatcaatag tcaaattaac 1800
taa 1803

<210> 121

<211> 3099

<212> DNA

<213> Streptococcus agalactiae

<400> 121

atgagtagaa tgattccagg acgtattcga aatcaaggta tagaactcta cgaacaagggt 60
ttgggtgtcct tgatttctca agaaggtaat ctattaaaag ctaaagttgg ggattgtcag 120
attgaatatt cattagtaac agaagaaaca aaatgttctt gtgatttttt tgcaagaaaa 180
ggctattgtc aacatttagc tgctctggag catttcttga aaaacgaccc agagggtaaa 240
gcaatcttat ctaaagttca agttcaacaa gaaagtcaac aagaaactaa gaagaaaacc 300
tcttttggtg gtgttttttt agatagtcta attattaatg aagatgatac tataaaatat 360
caactatcgg ctcaaggaga acaaaatcct tatgctaattg atatctggtg gactttaaaa 420
attagacgac tgcctgatga tagaagttat gttattcgtg acatcaaagc ttttttaaat 480
actgttcgaa aagaagctta ttatcagatt ggaaaacaat actttgaaac tttgtctttg 540
atacagtttg atgagaccag tcaagaattg atagaatttt tatggaggct cattccaagt 600
cattcaagca aaattgatct agagtttatt ttaccaaadc aaggctcgta ccttagtctc 660
actcgtggtt tttttgaaga gggcggttact ttgatgaatg ctttagaaaa tttttcattt 720
gaaagtgatt ttcatcaatt taatcacctc tactttaagg aattagaagg tgaggatcat 780
ctttatcaat ttaaggttat tgtccatagg caatcaattg aattagaaat caaagagaaa 840
gacttaaac cactattttgc gaatttctat ttgttttatc gcgatacttt ctaccatctt 900
aatttgaagc aagaaaagat ggtaacggct attcgtagtc ttcccattga gggagattta 960
gcaaaacata tccatttttg tttagatgat caagataagt tagcagctca tttactggat 1020
tttaaggaga ttggactagt agatgctcca cggagcttct ctattcatga ttttaaggta 1080
aattttgagt tcgatattaa tagtcaaaat gaaattttat tgcaaattgg atttgattat 1140
ggtaattgatt taactgttca taatcgtcaa gaactagaac agttaacatt tgctagtcac 1200
ttcaaactg aagaaaaaat atttaaactc ttagaaagat atggcttttg accccacttt 1260
tcaaccagcc atccagcata cagtgcacaa gaattatacg atttttatac ctatatgctt 1320
ccacaattta aaaaaatggg aacagtgagc ttatccgcaa aattggaaag ttatcgtctc 1380
atagaacgac cgcaaattga tattgaagct aagggaagcc tgctagatat ttcttttgat 1440
ttctctgatt tactggaaaa cgatgttgat caagctctgg tagctttggt tgacaataat 1500
ccttattttg tgaataaatc agggcaatta gttatttttg atgaagagac taagaaagta 1560

GBS patentin.ST25

tcaggtcatg tgggtgatga agatgggtctc tatctacttg actataatat ggcttacgat	180
attacattac cgtctagtcg ttctatgaaa ccagttgttt tatctgaaaa gcaaactatt	240
aatgaagttt ttattgaagc tgaaaatggt agcactaaaa aagagctcgt tgatcaggat	300
ttgggtcttaa tattagagga agatgatatt aatttagaag aaagcgttat cgataatatc	360
ttgttaaata tacctcttcg tgttctggca gctgatgagg ttggggtaga agcggattta	420
tcaggtaaaa attggtcggt aatgactgaa aagcagtatg aagaaaaaca agctaaagaa	480
aaagaaaaat ctaatccttt cgcagcctta gaaggatatgt ttgatagtga ttag	534

<210> 123

<211> 579

<212> DNA

<213> Streptococcus agalactiae

<400> 123	
atggaagtaa aaactgcaat agaatggatg cacactttta accaaaaaat tcaatccaac	60
aaggactatt tatccgaact agatactcca ataggtgatg gcgaccatgg tggcaatatg	120
gcgcgtggta tgactgctgt tattgaaaac cttgataaca atgaatttag tagtgctgcc	180
gatgttttca aaaccgtatc catgcaactt ttaagcaaag taggcggagc atctggacca	240
ctctatgggt ctgcatttat gggaattaca aaagctgaac agagtgaag taccatttca	300
gaggcacttg gcgcaggact tgaaatgatt caaaaacgtg gtaaagctga acttaatgaa	360
aaaacaatgg ttgatgtttg gcacgggtgt attgaagcga ttgaaaaaaa tgaattgact	420
gaagaccgta ttgattcctt agtagatgct acaaaagga tgaaagcaac aaaaggacgc	480
gcttcttatg ttggagaacg ctcattagga cacattgatc cagggtcatt ttcttcagga	540
ttattattta aagcattact agaagttgga ggtgtctaa	579

<210> 124

<211> 2829

<212> DNA

<213> Streptococcus agalactiae

<400> 124	
atgcaagata aattaatgat aagaggagca agagctcaca atttaaaaaa tataagtgtc	60
gacatccac gagacaagtt agttgtcgtt acgggactat caggatcagg taagtctagt	120
ttggcctttg acactatcta tgcagaagga caacgtcgtt acgttgaaag tctttctgct	180
tacgcgcgcc aatttttggg aaatatggaa aagcctgatg tagattctat tgatggcctt	240
agtccagcta tttctattga tcagaaaaca acaagtaaga atcctcgctc tactgttggg	300

GBS patentin.ST25

actgtaacag	aaattaacga	ttattttacgt	ttgcttttatg	ctcgtgttgg	aaccccatat	360
tgtatcaatg	gtcacggagc	catcacagca	tcttctgtag	agcaaattgt	ggataaggta	420
ctagcgcttc	cagagcgaac	aaagatgcaa	attttagccc	caattatacg	tcgaaaaaaa	480
ggacaacaca	aatcaacatt	tgagaaaata	caaaaagatg	gttacgttcg	tgttcgtatt	540
gatggtgata	ttcacgatgt	tactgaggtg	cctgaattat	caaaaagtaa	gatgcacaat	600
attgatattg	tagtagatcg	attaattaat	aaagagggca	ttcgttcccg	cttatttgat	660
tccgttgaag	cggctctacg	tttgtcggat	ggttatgtcg	ttattgatac	aatggatggc	720
aatgagttat	tgttttcaga	gcattattct	tgtcctgaat	gtggttttac	tgttcctgaa	780
ttagagccac	gccttttttc	ttttaatgct	ccctttgggt	cttgtagcac	ctgtgatggc	840
ttaggaatta	agttagaagt	ggatatagat	ttggttattc	cagataaaag	caagaccctt	900
agagaagggg	ccttagttcc	ttggaatcca	atttcatcaa	attattatcc	aacgatgcta	960
gagcaagcta	tgactcaatt	tgatgttgat	atggatacgc	catttgaaaa	attaagcaag	1020
gcgagcagg	acctagccct	atatggttca	ggcgaacgag	agttccattt	ccattatatt	1080
aacgattttg	gaggcgagag	aaatattgat	ttgccttttg	aaggggttgt	caataatatt	1140
aatcgtcgtt	accatgaaac	taatagcgat	tacacacgca	atgttatgcg	agaatatatg	1200
aacgagctaa	aatgtaacac	ttgtcatggc	tatcgtctca	atgatcaagc	actttgcgta	1260
agagttgggg	gagaagaagg	tcttaatatt	gggcaagtct	cagatttatc	gatagcagac	1320
catttagaac	ttttagaaac	gttgcgttta	tcttcaaatg	aacaattaat	tgctcgacca	1380
attatcaaag	aaattcatga	ccgcctaagt	ttcttaataa	atgttgggct	taattattta	1440
aatctgtcac	gttctgcagg	aacgctttcc	gggggcgaga	gtcaacgtat	tcgtttggct	1500
actcaaattg	ggctctaatt	atcaggtgtc	ctttatgtac	ttgatgaacc	gtccattgga	1560
cttcatcagc	gagacaatga	ccgtttgatt	gatagtctta	agaaaatgcg	tgatttggggt	1620
aatacgctta	ttgttggtga	acatgatgaa	gatacaatga	tggcagctga	ttgggttaatc	1680
gatgtgggac	ctggcgctgg	tgcgtttggg	ggtagagattg	tggcctctgg	cacaccgaag	1740
caagtagcta	aaaataactaa	atctattaca	ggacaatatt	tgtaggtaa	gaaagtgatt	1800
cctgtgccat	ctgaacgaag	agtaggcaat	ggtcgctttt	tagaaatcaa	aggtgcggca	1860
gaaaacaacc	tacaaaattt	agatgtcaag	ttccctctcg	gtaaatttat	tgccgtaact	1920
gggtgtctcag	gttctggaaa	atcaacctta	attaatagta	ttttgaaaaa	agctgttgcg	1980
cagaagctta	accgtaactc	agataaacca	ggtaaataatg	tttctttaga	aggcattgaa	2040
tatgttgatc	gattgattga	tattgaccaa	agtccaattg	gtcggacccc	acgttctaata	2100
cccgaacct	atacaggtgt	ttttgatgat	attcgtgatc	tttttgctca	aactaatgag	2160
gcaaaaattc	gagggtataa	aaaaggacgc	ttctcattta	acgtcaaagg	tggacgttgt	2220
gagtccttgt	ctggtgatgg	tatcatcaaa	attgagatgc	attttttacc	agatgtctac	2280
gttccttgtg	aagtatgcc	cggcacgcgc	tataatagtg	agactctgga	agtacattac	2340

GBS patentin.ST25

aaagaaaaaa atattgcaca aattcttgat atgacagtga atgatgcagt tacatttttt	2400
gcagctattc ctaaaattgc tcgtaagtta cagactatta aggatgttgg tttgggatat	2460
gtcacttttg ggcaaccagc tacaacctta tcaggaggag aagctcagcg aatgaagttg	2520
gcaagtgaat tacataagcg ttcgacaggt aagagtcttt acatattaga cgaaccaaca	2580
acggggcttc atgcagatga tattgctcgc ttacttaagg ttttggatcg ttttgtagat	2640
gatggtaata cagtgcctgt tattgagcat aaccttgatg ttattaaaac tgctgaccac	2700
attattgatc tcggccctga aggaggtatt ggtggcggac aaattgtagc tatcggaaca	2760
ccagaagaag ttgctgaaaa tcctaaatcc tatacaggat attatttaaa agagaagtta	2820
gcaagatag	2829

<210> 125

<211> 1125

<212> DNA

<213> Streptococcus agalactiae

<400> 125

atgtggcctg aagatagaat cgcttctttt cgtcgcacac ttttaggggtg gtatgaccaa	60
gaaaaacgtg atctcccttg gcgaagaact actaatccat actatatttg ggtttctgaa	120
atcatgttgc aacaaacaca agttaatata gtaatccctt attataaacg ttttctagag	180
tggtttcctc aaataaaaga tttggcagac gctcctgaag aacaattact aaaggcatgg	240
gagggactag gttattattc tcgggtgcgt aatatgcaaa aggctgcaca gcaagtgatg	300
gttgattttg gtggcatatt tcctcacact tatgatgata ttgcttcatt aaaagggatt	360
ggtccttata ctgcagggtgc tatcgccagc atctcattca acttaccaga gcctgccgtt	420
gatggcaatg tgatgcgtgt catggctcgt ttgtttgaag ttaattatga catcggtgac	480
cctaaaaatc gtaaaatttt tcaagctatt atggaaatac taattgaccc tgacagaccc	540
ggtgatttta accaagcact tatggatctg ggtacagaca tcgaatccgc taagacacct	600
agacctgatg aaagccctat tcgtttcttt aatgctgctt atttgaatgg tacttatagt	660
aaatatccca taaaaaatcc taagaaaaag cctaaaccaa tgcgaattca ggcttttgtc	720
attcgtaacc aaaatggcca atatctactg gagaaaaata cttaaaggag acttctaggg	780
ggtttttggc catttcctat tatcgaaacg tcacctcttt ctcaacaatt agatttattt	840
gatgacaatc aatccaaccc cataatctgg caaaccacaa atgaaacttt ccaaagagaa	900
tatcaattaa agccccaatg gactgataat cactttccca atattaagca cacttttagt	960
caccagaagt ggacaataga actcatagag ggggtggtca aagcaacaga tttacctaat	1020
gctcctcacc taaagtgggc agcaattgag gacttttctc tgtatccctt tgcaacgcca	1080
caaaagaaaa tgctggagac ctacttaaaa cagaaaaatg cttaa	1125

GBS patentin.ST25

<210> 126
 <211> 849
 <212> DNA
 <213> Streptococcus agalactiae

<400> 126
 ttgatcgaaa tcacttggac tgtgaagtat atcacagaat ttatcgcaac cgcttttctt 60
 atcatcttag gaaatggggc tgtagctaac gttgacttaa aaggcacaaa aggaaataat 120
 tcaggttggga ttattattgc aattgggttat ggtttagggtg ttatgatgcc agcgcttatg 180
 tttggtaatg tctctggaaa ccatattaac ccagctttca cacttggatt ggcattttca 240
 ggtcttttcc cttgggcaca cgttggacaa tacattcttg cacaattttt gggagcaatg 300
 tttggacagt tagttgtcgt tatgggttat caaccttact ttgttaagac agaaaatcca 360
 aatcatgttc ttggatcatt ttcaactatt tctgcattag atgatggaca gaaatcaagt 420
 cgtaaagcgg cttacattaa tgggtttctta aatgaattcg ttgggttcttt tgttcttttc 480
 tttggagctt tggctttaac gaagaactat ttcggtgtag aacttgttgg taaacttggt 540
 caagctgggt atgaccaaac gacagcagcg acaaggattt caccatacgt aactgggtca 600
 cttgctgtag ctcacttagg tattgggttc ttggtaatga ctctagttgc ttcttttaggt 660
 ggaccgactg gacctgcatt gaaccctgcg cgtgaccttg gtccacgtat tgttcaccgc 720
 ttattaccaa aacaaattct tggacaagct aaagaagatt caaaatgggtg gtatgcatgg 780
 gtgccagttt tagcaccaat cgtagcaagt atactcgctg tagccttggtt caaactatta 840
 tatctttaa 849

<210> 127
 <211> 981
 <212> DNA
 <213> Streptococcus agalactiae

<400> 127
 atgtcatctt attggaataa ctatcctgaa cttaaaaaaa atattgatga aaccaatcaa 60
 ctaattcaag aaagaatata ggtcagaaat aaagatattg aagcggcgct aagccaactc 120
 acagctgcgg gaggaaaaca gtcagacca gcattctttt accttttttc tcaacttggt 180
 aataaggaga atcaagatac tcagcaacta aagaaaatcg ctgcttcttt agaaatcctt 240
 cacgttgcta cattaatcca tgatgatgtc attgatgact caccactaag acgtggaaat 300
 atgaccattc aaagcaagtt tggcaaagac atcgcagttt atactgggga tttacttttc 360
 acagtctttt tcgatcttat tttagaatct atggctgata caccatttat gaggattaat 420

GBS patentin.ST25

gcaaaatcta tgcgtaaaat tctcatggga gaattggacc agatgcacct tcgttacaat	480
caacaacaag gtatccatca ctattttacgt gcgatttcag gtaagacagc cgaactcttt	540
aaattagcta gcaaagaagg agcttacttt ggtgggtgcag agaaggaggt tgttcgtcta	600
gcaggccata tcggcctttaa catttggtatg acattccaaa ttttgatga tatcctggat	660
tatactgcag ataaaaaac atttaataag cctgtcttag aggatttaac acaaggcgtt	720
tacagccttc ctctacttct tgccattgaa gaaaatcctg atattttcaa acctatttta	780
gataaaaaaa cagatatggc tactgaagac atggaaaaaa ttgcttatct cgtcgtttcc	840
catagaggtg ttgacaaagc tcgccatcta gctcgtaaat ttactgagaa agctattagt	900
gacataaata agctaccca gaactctgca aaaaaacagt tgctacaatt aactaattac	960
cttttaaaac gcaaaattta a	981

<210> 128

<211> 1749

<212> DNA

<213> Streptococcus agalactiae

<400> 128

atgtttaaaa tccctttggt taaagaatta aagacagatc aatgggtaaa accatttttc	60
aaacaatata aagtttcctt agtaattgct cttttccttg gttttatgac tttcttttct	120
gccagtgctc ttatgtttta ttcgggctat ctgattagta agtcagcttc actaccgagt	180
aatattcttc tagtatatgt tccaattgta ctaacacgtg cttttggtat tggacgtcct	240
gtttttcggt atatagaacg cctaacgagt cacaattggg tattacgaat gacttcacaa	300
ctgcgcttga agctttacca ttccttagaa agcaatgcta tctttatgaa gcgtgatttt	360
cgtttaggag atgttatggg gcttttagcg gaggatatta attatttgca aaatttgat	420
cttaggacaa tatttccaac gattatagcg tggttattat atagctttat tattattgca	480
acaggcttct tttctctatg gtttgcttta atgatgttgc tttatttagc tattatgatt	540
tttctttttc cactttggtc gattttagct aatggtgctc gtcagactcg tgaaaaagaa	600
ttaaaaaatc atctttatac tgatttgacg gataatgtct taggtatttc agactggatt	660
tttagtcaac gtggtaaga gtacgtcgcc ttgcatgaac gttcggaaag tgaactaatg	720
gctattcaga aaaaaattcg ttcctttaat aatcgtagag ctcttattgt ggaattagtt	780
tttggttttc tagctatttt ggttattatt tgggctagta atcagtttat tggtcacaga	840
ggtggcgaag ctaactggat tgcagcattt gttctaacag tatttccctt gtcagaggca	900
tttgctgggt tgtctgctgc tgctcaagaa acaataaat attctgattc aattcatcgt	960
cttaatgaat tatcagaaac gtattttgaa acaactcaaa atcaattgcc taataagcca	1020
tatgattttt ccgtcaagaa ttttaagttt cagtataagc cacaagagaa atggggtttg	1080

GBS patentin.ST25

catcatttag atttggatat taaagaagga gaaaaaattg ctattttagg gcggagtggg	1140
tctggcaaga gtaccttagc tagtctactt cgtggcgact tgaaagcaag tcaagggaag	1200
attaccctag gcggtgctga tgtttcaata gttggtgatt gcatttctaa ctatattgga	1260
gtgatacaac aagcgcccta cttttttaat acaaccctgc taaataacat tcgcattgga	1320
aaccaagatg ctagtgaaga agatgtatgg aaagtctctg aacgagttgg attgaaagag	1380
atggctactg atttatcaga tgggtctctat acaatgggtg atgaagctgg acttaggttt	1440
tcagggtggcg aaaggcatag aattgctttg gctagaatct tactaaaaga tgtcccaatt	1500
gttatcttag atgagccaac tgttggactt gatcctatta ctgaacaagc cttactaagg	1560
gtatttatga aagaattgga aggtaagacc ttagtttgga ttacacatca cttaaaaggt	1620
attgaacatg ctgatcgtat cttattttata gaaaatgggc aattagagtt ggaaggttct	1680
cctcaagaat tgtctcaaag tagtcaacgt taccgtcagc tgaaagccgc tgatgatggg	1740
gatctatga	1749

<210> 129

<211> 447

<212> DNA

<213> Streptococcus agalactiae

<400> 129

atgaaaaaac ttattacaga aaaaaaagtc aacaacgtct caactgttaa ctatttgaaa	60
ctcgggtcttg tctcagcaat gtttgctgga ggagcattcg tagctcttgg ttctacacaa	120
gggtgtttcag cttcaacttt cacagcaccg caagcaacac atccaaaagc agaacgtcag	180
ttaacagatt cagaaatcta tgaacgtgcc caaaaacaag tgttaccaa atatatccaa	240
ggttctctct caggtatcct taaccaacat tcaacacttt acaacaaca aaacgcagca	300
gtgacaccgc aagtatcaag ccccaaagca gaacgtcagt taacagattc agaaatctat	360
gaacgtgccc aaaaacaagt attgccaaaa tatattcaag gttctctctc aggtatcctt	420
aaccaacatt caactttgaa tgcttaa	447

<210> 130

<211> 510

<212> DNA

<213> Streptococcus agalactiae

<400> 130

atggaggaaa acatgaacat aaaacaatta aagtctaaaa caatgcttgg aacagtggct	60
ttggtgtccg ctttttcatt tgcttcaaca aatgcagatg cgaatacata taactatgca	120

GBS patentin.ST25

gtagatgtag actacctagc aagtgcggag gaaattgctc aagcacatcc agctagtaat	180
acgtttccac taggtcaatg cacatggggg gtaaaggaga tggcaacatg ggcaggtaac	240
tggtggggaa acggtggtga ttgggctgcg agcgccgcat cagctgggta tacagtagga	300
acacaacctc gcgtgggttc tatcgtatgt tggactgatg gtagttatgg acatgtggct	360
tatgttacag ctgtagatcc tgtcactaat aaaattcagg ttttagaatc taattatgca	420
ggtcatcaat ggattgataa ttatcgtggt tggtttgatc cacaaaatac agcgacacca	480
ggggtagtta gctacattta tccgaattaa	510

<210> 131

<211> 942

<212> DNA

<213> Streptococcus agalactiae

<400> 131	
atgaaaatta accaaatgaa aaaagacgag ctttttgagg ggttttacct tataaagaaa	60
gcagaagttc gtaaaacgcg tgcaggtaaa gactttattg cctttacctt tcgagatgat	120
actggcgaaa tttcaggaaa tatgtgggat gcacaaacct ataatgtaga agagtttgta	180
gccggtaaaa ttgttcatat gaaagggcgt cgtgaagttt ataatggaac tccccaagtc	240
aaccaaatta cattaagaaa catcaaagat ggtgaaccta atgatacctag agattttaaa	300
gaaaaacctc caatcaatgt tgacaacgtg agagagtaca tggaacaaat gctctttaaa	360
attgaaaatg caacctggca gcgtgtggta agagcacctt atcgtaaata caataaggaa	420
ttttttacct atccagccgc caaaacaaac caccacgcct ttgaatcagg attggcatat	480
cacacggcaa cgatggttcg tttggcagat agtattggag atatctatcc agaacttaat	540
aaaagtttga tgtttgctgg tattatgcta catgatitag ccaaggatcat tgagttatcg	600
ggtcctgata atacagaata tactattcga ggtaacctta tcggtcatat ttcacttatt	660
gatgaggaat taacaaaaat actagcagag cttaatatgt atgatacaaa agaagagggt	720
acagtgttac gccatgttat tctgagtcac catggacaat tagaatatgg aagcccgggt	780
cgtcctagaa tcatggaggc agaaattatc catatgatcg ataacattga tgcaaatatg	840
atgatgatga caacagcttt aaatcgtgtc aacgaagggtg aaatgacaaa tcgcattttt	900
gccatggata accgttcttt ttataaaccg aacattaaat aa	942

<210> 132

<211> 852

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 132
atgttggttg acaagaagtg gcgttttgaa gatagtgcaa gttatttcgc ttgtcctaaa 60
tgtcaaaatc ccttgataaa agaaagtaac agcctcaa at gctctgataa tcattgtttt 120
gatttatcca aatttgata tgtaaatctt cttggaggaa agaagataga tgaacattat 180
gataaaaaat catttgaaaa tcggcagctt gtcttagaaa acgggtatta taatcatatt 240
ttagaagcta tttcaaagg tttggaaaat aattctcagt ttcattcgg ttttagatatt 300
ggttgtggag agggctttta ttctcgtcaa ttagttaaca agtatgagaa gactttcttg 360
gcttttgata tttctaaaga ttcgattcaa ttagctgcta aaagtgatca atctaggctt 420
gtgaaatgg tttgttctga tttagctaac cttcctattc aagactcatc aattgatatc 480
attttagaca ttttttctcc tgcaaattat aaagaattta ggcggttact gagtgatgat 540
ggtatccttg taaaggttgt tcctgtagct gaacatgtcc aagaattgag agaaaaagct 600
agtcaatact tgaacagaa agattactct aatcaaaaaa ttctagatca ctttagagaa 660
aattttgaaa ttatttctga gcagaaagtt gttcaaagtt ataactgttc tcaacaagaa 720
cgtcaagctt ttattgatat gacaccgttg ttattcagcg tagataaaac gactattgat 780
tgggcgagta tatcagaaat tacagtaggt gccttaatag taattggaaa aaagcgcagt 840
gtatctaaat aa 852

<210> 133

<211> 450

<212> DNA

<213> Streptococcus agalactiae

<400> 133
atgtgtctta tttgtcaacg tattgaaatg attgaacgaa atgagaatcc ttattttgtg 60
aaagaatatg aaacgggtta tcttgttctg ggagaccatc aatattttca aggttattgc 120
ctttttctct ctaaaaaaca cgtaacagag ttacatgaat tgcctagaga ttggcgaaat 180
cagtatcttt ccgaaatggc agatgcttct gaaatagttg ctaaggcttt tagagcagat 240
aagatgaata ttgagagttt gggaaatgga gacgctcatc tacattttca tctttttcca 300
agaaaaacag gtgatttaag gaactatggg cataatggaa aagggtccagt ttggtggtat 360
ccttttgaga agatgtatgc agatagtgtc agagcaactg gtgcagaaat agaaaaatta 420
aaagagaaat tgtagatgt ctaggatag 450

<210> 134

<211> 1188

<212> DNA

<213> Streptococcus agalactiae

<400> 134

atgttttagtg atttacgcaa aaaatttgtc tttttgacca tgtcaatcct tattgtcgtt	60
gttctctttc tctttgcagt gagtaatcgc tacaatcaat attgggatga atatgatgca	120
tataggattg ttaaattagt tgccaaaaat gattatttag gaataccagg cgatgaaccg	180
attgctttgg tgactataga taaccaaaag atggttaaga ttcaaagcaa taatactgat	240
ttgacaaatg atgttatcga aaaatctagt ttgaagctcc ttgagcaagg aaagaagtca	300
cgaaaatgga agtcttttat atattccata aaagaatata aagataaaac ctacaccata	360
gctattatgg atttggctag ttatgaagtc ccttatgcaa ggcgttttct aattcttggt	420
tttactattt ttggattttg tttattagca gctgtaagtc tttatctttc tcgatttatc	480
gtagggcctg tagagacaga aatgactcgc gaaaaacagt tcgtttcaga tgcgagtcac	540
gagctgaaga cccctattgc agctatacga gccaacgttc aggttctgga acagcaaatt	600
ccaggaaatc gttatctgga tcatgttggt tcggagacta agcgaatgga gtttttaatt	660
gaagatttgc ttaatttgtc tagacttgat gaaaaacgct ccaaggtaaa tttcaaaaag	720
ttaaacttat ctgtcttatg tcaagaagta cttctgacat atgaaagttt ggcataatgaa	780
gaagaaaagt gtttaaataa tacgattgaa gatgatgtct ggattgttgg agaagagagt	840
cagattaagc aaattttaat aattcttttg gataatgcta ttaggcattc tttgtcaaaa	900
tcagaaatcc agtttagtct taaacaggct cgaagaaaag ctattctgac aatatcaaat	960
ccaagtgcta tctattccaa agaggttatg gataatctct ttgagcgttt ttatcaagct	1020
aaagatgatc atgcagattc tctcagtttt ggtctaggct tatctattgc taaggcaatc	1080
gtggaacgcc ataaggggag aattagagca tatcaagaaa aagaccaatt acgtcttgaa	1140
gtccagttac caattgatgg attttgacc aataccatga ttaattaa	1188

<210> 135

<211> 1680

<212> DNA

<213> Streptococcus agalactiae

<400> 135

ttgattattc tcgataaaaa aagttatgac ctctctttt acctattgaa attagaggaa	60
cctgaaacag ttatggcaat tgccaacgca cttaatcagt ctaggcgtaa agtgtattat	120
cacttagaga agataaacga tgactgcct agcgatgtgc ctgagattgt tagttatcca	180
cgtgtaggaa tcttgctaac cgaaaacaa aaagcagcct gtcgtctttt attagatgaa	240
gtaactgatt atagttacgt catgaaaagt agtgagaggt tgcagctgtc tttagtatct	300
atcgtggtag ctaaggaccg cataacgatt gataggttga tgcaactaaa cgatgtttct	360

GBS patentin.ST25

cgaaatacta tcttaaacga tttaaacgaa ttaagaagtg agttagcaga gaaagaatat	420
aatttacagt tacaatcaac aaaatgtcgc gggtattttt tagatgggtca cccattgtcc	480
attatccagt acttatataa gctcttagat gatattctacc ataattggaag tagtagtttt	540
atagaccttt ttaatcataa actgtctcaa gcttttggtg ccagcacata tttttctaaa	600
gaggttcttg attattttca ccattatctc ttcatttctc aacgaagtct aggtaagaaa	660
atcaacagtc aagatgggtca gtttatgatt cagattttgc cttttatact aatggcttat	720
cgtaagatgc gattaagtcc tgaagtacag acctctctta atagtgattt tagcttggtt	780
tggcaacgta aggaatatga gattgctaaa gagttggctg atgagctgga agaaaatttt	840
cagttatcac tggatgagat tgaagtggga ctagtggcca tgcttatgct tagtttccgc	900
aaggaccgtg acaatcattt agagagccag gattatgatg atatgcgagc tactctaacc	960
agttttttga aagaattgga agaacgatat caccttcact ttgttcataa aaaggactta	1020
ctaagacaac ttctaactca ctgcaaggca ctcttatatc gttaaactgta tgggtatttt	1080
tctgttaatc ctttaacaga gcatattaaa gacaaatatg aagaactttt tgccataacc	1140
tcgtcttctg taaagctttt agagaaagct tggcaaatca aattgaccga tgatgatgta	1200
gcatatctaa cgattcattt aggaggggaa cttcgtaata gtcaacaatc tcctaataaa	1260
cttaagttag ttattgtatc tgatgaagga atagcgattc agaaacttct tttaaagcaa	1320
tgtcaacgct acttaacaaa cagtgatata gaagctgttt ttacaaccga acagtaccaa	1380
agtgtgagtg atcttatgca tgtagatatg gttgtctcta ctagtgacgc tttagaatct	1440
cgttttccga tgttagtagt tcacctgtt ttgacagatg atgatattat tcgcttgatt	1500
cgcttttcaa aaaaaggtaa ctgtgcaa atagtaaatcaat ttaccaatga acttgaaaaa	1560
acgattgctc aatatgtcaa ggaagatagt gaacgctacg tgctgaaatc taagattgag	1620
aaacttattc atcaagaatt gctccaagac gtccttcccc ttcaaagtac agtttgtaa	1680

<210> 136

<211> 648

<212> DNA

<213> Streptococcus agalactiae

<400> 136

atgaaatact ttttagatac tgccgatgtt tctgaaattc gtcgtcttaa tcgtttagga	60
atcgttgatg gtgttactac caatccgact attatttcac gtgaggggag tgactttaaa	120
gaagttatta acgaaatttg ccaaatcggt gatggcccag ttagtgcaga agtgacaggt	180
ttaacttggt atgaaatggt taccgaagct agagaaatcg ctaagtgggt accaaatgtt	240
gttggttaaa ttccaatgac tgaagaagggt ttagcagcag tttcacaatt atcaaaagaa	300
ggtataaaga caaatgtgac attaatattt actgtggctc aagggtctttc ggcaatgaaa	360

GBS patentin.ST25

gctggtgcaa catttattag tccttttgtg ggtcgtcttg aagatattgg aacagatgct	420
tatgctttga ttcgtgacct tcgtcacatt attgattttt atggtttcca atctgagatt	480
attgctgcta gcattcgtgg attggcgcat gtggagggcg tcgctaaatg cggtgcgcac	540
attgccacta ttccagataa aacatttgca tcactattta ctcacccgct tactgataaa	600
gggattgaaa ctttcttaaa agattgggat agtttcaaga agaagtag	648

<210> 137

<211> 2448

<212> DNA

<213> Streptococcus agalactiae

<400> 137	
atgagtcatt attccataaa attacaagaa gtattcagat tggcgcaatt tcaagcagca	60
cgctatgaaa gtcactattht agaaagctgg catcttcttt tagcaatggg tttagttcat	120
gattcagtag ctggtttgac atttgctgaa tatgagtctg aagttgcaat tgaagagtac	180
gaagcagcaa caatttttagc ttttaggtaga gcaccgaaag aagagattac caattatcaa	240
tttttagagc aatcaccagc tttgaaaaag atcttaaagt tagcagaaaa tattagtatc	300
gtagtaggag ctgaagatgt gggtagtgaa catgtcttgc ttgctatggt ggttaataaa	360
gatttattag ccacacgtat cttagagtta gttggcttta gaggtcaaga cgatggtgaa	420
tcagttcgta tggttgattt acgtaaggct ctagaacgtc atgccggttt tacaaaagat	480
gatatcaaaag caatttatga attacgtaat cctaaaaaag caaagtcggg tgcttctttt	540
tctgatatga tgaaaccacc gagtactgct ggtgatttag ctgatttcac acgtgattta	600
tcacagatgg cggttgatgg ggaaattgaa cctgttattg ggcgtgataa agaaatttca	660
cgtatgggcc aagtcttaag tcgtaaaaca aagaataatc ctgtcttagt tggagatgag	720
gggtgctgga aaacagcttt ggcgtacggg ctagcacaac gtattgctaa tggaaatatt	780
ccttatgagc ttagagatat gcgtgttcta gagttagata tgatgagcgt tgttgctgga	840
actcgttttc gtgggtgattt tgaggaacgt atgaatcaaa tcattgcaga tattgaagaa	900
gacggtcata ttattctttt cattgatgaa ctgcatacta ttatgggttc tggctctggt	960
attgatagca cacttgatgc tgctaataatt ttaaaaccag ctttggcccg aggcacttta	1020
cgcactgttg gagcaacaac tcaagaggaa tatcaaaagc atattgaaaa agatgctgct	1080
ttatctcgtc gctttgcaaa agtttttagta gaagaaccaa atcttgaaga cgcatatgaa	1140
attctacttg gattgaagcc agcgtatgaa gcctttcata atgttactat ttcagatgaa	1200
gcagttatga ctgctgtaaa agtggtcat cgttatttga caagtaagaa tttaccagac	1260
tcagctatag acttacttga tgaagcttct gccactgtgc aaatgatgat taagaaaat	1320
gctccttcgc ttttaacaga agttgaccaa gctatttttag atgatgatat gaaatctgct	1380

GBS patentin.ST25

tctaaagctc taaaagcaag ttataagggg aaaaagcgta agcctattgc cgtaacagaa	1440
gatcatatta tggcaactct cagtcgtcta tctgggtattc ctgttgaaaa attgacacaa	1500
gctgatagta aaaaatacct caatttagaa aaagaattgc ataaacgtgt tatcgggtcaa	1560
gatgatgcag ttactgccat tagtcgtgct atccgctcgca atcaatctgg cattcgtact	1620
ggtaagcgtc ctattgggtc ctttatgttc ttgggaccaa ctgggtgttg taagacagag	1680
ttagcaaaag ccttggcaga agtggtgttt gatgatgaat cagccctaatt tcgttttgat	1740
atgtcggaa atattggaaaa attcgcagct tctcacctga atggggcacc tccaggttat	1800
gttgggttatg atgaaggagg agagttgact gaaaaagtac gcaataaacc atattcagtt	1860
ttactttttg atgaagttga aaaagctcat ccagatattt ttaatgtatt attacaagtg	1920
cttgatgatg gcgttttaac agatagtcga ggacgaaaag ttgatttttc aaatactata	1980
atcattatga ctcttaattt aggagcaact gcattacgtg acgataaaac agttgggttt	2040
ggagctaagg atatcagcca tgattatact gctatgcaaa aacgtattat ggaggagctt	2100
aaaaaagctt atcgaccaga gtttatcaat cgtattgatg agaaagttgt attccatagt	2160
ctcagtcaag ataatatgcg tgaagttgtg aaaattatgg ttaaaccctt aattttagcg	2220
cttaaagata aaggtatgga tctgaaattc cagccttcag ccttgaaaca cttggcagag	2280
gatggctatg atatagaaat ggggtgctcg cactgcgta gaactattca aacgcaagta	2340
gaggatcatt tatcagaact actattggca aatcaagtga aagaggggca agtaattaag	2400
attggcgtat ccaaaggcaa attgaaattt gatattgcaa aatcataa	2448

<210> 138

<211> 1533

<212> DNA

<213> Streptococcus agalactiae

<400> 138

atgggtcttag ataaagaaat caaggctcaa ttagcgcaat atttagattt gctagaatct	60
gatattgtat tacaagctga tttaggagat aacgataatt ctcaaaaagt aaaggatttt	120
ctagatgaaa ttgtcgctat gtctgatcgc atcagccttg aatcaacaca tttaaacgt	180
caacctagtt ttggaattgc aaaaaagggt catgaaagtc gcgttatttt ttcaggcttg	240
ccaatggggc atgaattcac atctttcatt ttagctttgt tgcaagtctc tggtcgcgca	300
ccaaaagttg atgaagatat tatcaaacga attaagggga ttgagaaaac tatcaatcta	360
gaaacttatg tttcattaac ttgccataat tgtccagatg tcgttcaagc ctttaataa	420
atggctgttt tgaatccgaa tatcactcat actatgattg aaggaggcat gtatcaagac	480
gaagtcaaat caaaaggtat catgtctgtt cctactgttt ataaggacca agaagaattt	540
acttctggcc gtgctacaat tgaacagctt ttagaacaac tagatggacc tcttgatgct	600

GBS patentin.ST25

gaagcatttg ctgacaaagg tgtctatgat gttctagtta ttggtggtgg tcctgcaggt	660
aacagtgcctg caatttatgc cccccgtaaa gggttaaaaa caggtatttt agcagaaact	720
tttgggtggac aagttatcga aacagttggt attgagaaca tgattggtac actgtacaca	780
gaaggcccta aattaatggc tcaaattgaa gagcatacca aatcttacga tattgatatt	840
atcaagagtc aattagcaac tggcattgag aaaaaagaat tagttgaggt aacactggct	900
aacggagcta ttttacaagc taaaactgct atcctagctc tgggtgctaa gtggcgaaat	960
atcaacgttc ctggcgagga agaattccgc aataaagggtg ttacttactg tccacattgt	1020
gatggccctc ttttcgaagg aaaagatggt gctgttatag gtggtggtaa ttcaggtatg	1080
gaagctgctt tagatctagc cgggtgtcact aaacatgtta cagtcctaga attcttacct	1140
gagctcaaag cagaccaagt actgcaagaa cgagcagcta aaactgacaa ttttaactatt	1200
cttaagaatg ttgctactaa agatatcggt ggtgaagatc atgtcactgg tttaaactat	1260
accgatcgtg atacaaacga agaaaaacac attgatttag aagggtgtttt tgtacaaatt	1320
ggtcttgtag caagtacatc ttggctcaag gatagcggca ttgaactcaa tgaacgtcaa	1380
gaaattgtcg ttgataaatt tggctcaaca aatatccctg gtatttttgc tgcaggtgac	1440
tgtacagatg ctgcctacaa gcaaatcatt atttccatgg ggtctggtgc cacagctgcc	1500
attggcgcat ttgattattt aatcagacaa taa	1533

<210> 139

<211> 1896

<212> DNA

<213> Streptococcus agalactiae

<400> 139	
atgataaaat atcaagatga tttttaccaa gcggttaatg gggagtgggc taagacagct	60
gttatttctg atgacaaacc aaggacaggt ggtttttctg atcttgctga tgacattgaa	120
gcattaatgc tgtcaacgac agataagtgg ctggctgatg aaaataaacc aagtgatacg	180
attttaaatc attttattgc ttttcataaa atgacagctg attatcaaaa acgtgaagag	240
gtaggagtat caccagtatt accattaatt gaagaatata aaggcctaca atctttctct	300
gagtttgcac caaaagttgc agaatatgaa ctagagggtg aaccaaataa atttccattt	360
ggtgtggctc ctgactttat gaatgctcaa ttgaatgtac tttgggctga agcgcctggg	420
attattttac cagatacaac ttattatagt gaagataatg aaaaaggaaa ggaactcctt	480
gctttttggc gtaaaagtca agaagaccta ctgcctttgt ttggcctttc agaacaggaa	540
attaaagata tcttggataa ggttttagca ttggatgcaa aattggcaca atatgtctta	600
tctcgcgaag agagttcgga atatgttaaa ctttaccatc cttataactg ggaagatttc	660
acaaaattag cacctgaact tccattagat gctattttcc aaaagatatt aggacaaaaa	720

GBS patentin.ST25

ccagataaag	ttattgttcc	tgaagaacgt	ttctggacag	aatttgcac	tgactattac	780
tcagaatcta	attgggaatt	attaaaggca	gatcttattt	tatcagctgc	gaatgcctat	840
aatgcttact	taactgatga	tattcgtatc	aaatcgggag	tttacagtcg	agctttatca	900
ggcacaccac	aagcaatgga	taagaaaaaa	gcagcttact	accttgcttc	aggaccttac	960
aatcaagctc	taggtttgtg	gtatgcagga	gaaaaattct	ctccagaagc	taaagctgat	1020
gttgagcata	agattgcaac	gatgattgat	gtctataagt	cacgcttaga	aaaggcggat	1080
tggcttgac	agtcaacgcg	agaaaaagct	attatgaaac	ttaatgttat	cacaccacat	1140
attggatacc	ctgagaaact	accagagact	tatactaaaa	aaatcattga	tcctaaacta	1200
tcgcttgctg	aaaatgctac	taatttagac	aaaatttcaa	tagcctatgg	ttggagtaaa	1260
tggaataaac	cagttgatag	aagtgaatgg	catatgcctg	cccacatggg	caatgcgtat	1320
tatgatccac	aacaaaacca	aattgtcttc	ccagcagcca	ttttacaaga	accattttat	1380
gctttagagc	aaagttcatc	agcaaattat	gggggaattg	gtgcagtgat	tgacatgaa	1440
atatcacacg	cttttgacac	taatggagct	tcatttgatg	aacatggaag	tttgaataat	1500
tgggtggactg	atgaagattt	tgaagctttc	aaaaaactta	cagataaagt	agttgagcag	1560
tttgatggac	tggaatctta	tggcgcaaaa	gtcaatggta	aactaacagt	atcagaaaat	1620
gttgacagatt	taggtggagt	tgcttgctgct	ttagaagctg	cgcagcgtga	gtcagatttt	1680
tcagcgaggg	atttctttat	taactttgcg	acaatttggc	gtatgaaggc	acgtgatgag	1740
tatatgcaaa	tgtagctag	tgtagatggt	cacgcccag	cacaatggcg	aactaatatt	1800
acagtaacga	attttgaaga	attccataaa	gagtttgatg	ttaaagatgg	tgataacatg	1860
tggcgtccag	ttgaaaaacg	tgttattatt	tggtaa			1896

<210> 140

<211> 1008

<212> DNA

<213> Streptococcus agalactiae

<400> 140

atgtctaaga	ttcttttttt	cggtgaacct	ctcattcgca	tcactccaaa	agaaaatgac	60
tattttgcag	atagtatctc	aactaaacta	ttctatggtg	gctctgaagt	taataaccgca	120
agagctctac	aaggcttttg	gcaagatact	aaactcctct	cagccttacc	caataatccc	180
ataggtaata	gttttcttca	atttttaaaa	gcacagggta	ttgatactca	ttctattcag	240
tgggttgag	aacgtgttg	gttatatttt	ttagaagatt	cctttgcttg	cagaaaaggt	300
gaggtggtct	acgaccgcga	tcatagtagt	ttacatgact	ttaggataaa	tcaaattgat	360
ttcgatcaat	tatttgaagg	agtttctctc	tttcatttta	gtggtattac	actatcattg	420
gatgagtcta	tccaagagat	aacactgctt	cttttaaaag	aagctaaaaa	aagagagata	480

GBS patentin.ST25

acaatctcct tagatctcaa ttttcgcagt aaactaattt ctcctaaaaa tgccaaaatc	540
cttttttctc agttcgctac ctttgcggat atttgttttg gtattgaacc tcttatgggt	600
gactcacagg acactacctt cttcaatcgc gatgaagcta caatagagga cgtcaaagaa	660
cgaatgattt cgcttataaa tcactttgac tttcaagtca ttttccatac taaacgtcta	720
caggatgaat ggggacgaaa ccactacca gcttacatag caaatcgtaa acaagagttt	780
gtcacttcaa aagaaatcac cacagctgta aaccagagaa ttggaagcgg agatgctttt	840
gtggcgggag cgctatatca actacttcag cactcagaca gcaagacagt cattgatttc	900
gctgtcgccta gtgcatcttt aaaatgtgct ttggaagggg acaatatgtt tgagaccgtt	960
accgcagtta acaaagtact aaatcaatcg aaagacatta ttcgttag	1008

<210> 141

<211> 585

<212> DNA

<213> streptococcus agalactiae

<400> 141	
atgaaaagtc gaaaaaaaga taaattggta ttgaggttaa caacaacact attgggtttt	60
ggtttggttg gggtttggtt ttataattat aaaaatgata atgtcgaacc gacagtcact	120
agtgcacg atcaaacgac gacttttatt caaacgattt ctccaacagc tattgaaatt	180
tctaagacct atgatttgta tgcgtcagtc ttattagcac aagctatttt ggaatcatcc	240
agtggacaat cagatttgct taaggctcct aattataacc tctttggcat caaaggagaa	300
tataaaggta aatctgtcca aatgcctact ttagaagatg atgggaaagg caatatgact	360
caaatccaag ctctttttcg cgcctatcca aattattctg cttcactata tgattatgct	420
gagttagtag ctagtcaaaa gtatgcatct gtttggaat caaatcctc ttcttataag	480
gatgctactg cagctctaac aggtctttat gcgacagata ctgcttatgc tagtaaatta	540
aaccaaatta ttgaaaccta cagtctagat gcttatgata aatag	585

<210> 142

<211> 1338

<212> DNA

<213> Streptococcus agalactiae

<400> 142	
atggcagacg tgaaggtagt gaataatgag gattctagag gtcaaaagca agacttaaag	60
gctaaactat ttcatattaa gatagggtca gttcccctac cagtatatgt ttgttttagca	120
ttattgattc ttctagcagg ctttttataa aaattgccag tcaatatgct aggaggattt	180

GBS patentin.ST25

gcagttatct taacaatggg gtggttctta gggactatcg gagctagcat tcctggtttt	240
aaaaacttcg gtggcccagc tattttatct ttattagtag catctatttt ggtgtttttc	300
aacctcatta ataaaaatgt tttagaatca acaaatatgt tgatgaagca agctaacttt	360
ctttattttt atattgcttg tttagtgtcc ggtagtattt tagggatgaa tcggaaaatg	420
ttgattcagg gattgctaag aatgattttc cccatgttat taggaatggg ttgtgcatg	480
atggtaggga catttgctcg tgttatttta ggcttagagt ggcgacacac tttgttttat	540
atcgtaacac ccgttttagc tgggtggtatt ggtgaaggta tttaccatt atcgttaggc	600
tatagttcaa ttaccggtgt agctagttaa caactagttg ctcaactcat cccagccact	660
attattggta atttctttgc cattttatgt actgcactat tgaatcggtt gggagaaaag	720
aaaccacact tgtctggtca agggcaatta gtaagggtta ataaaggaga ggacatgtca	780
gatattattg ctgatcattc tggcccaatt gacgttaaga aaatgggtgg aggtgtttta	840
acagcatgta gtctctttat ttttggacat ttgttgcatg aattaactgg atttcctggt	900
cccgatttaa tgattgttgc agcagctatt ttgaaatata ttaatgttat tcctagagaa	960
acacaaaatg gagctaagca actttataaa tttatttctg gtaattttac atttcctcta	1020
atggcagggc taggattgct ttatatcccg ttaaaagatg ttgtggcaac gcttagcata	1080
caatatttca tagttgttat tagtgttgta tttacagtta tttctgttgg attctttgta	1140
tcgcgattcc ttaatatgaa tcctgttgaa gcagggtatta tttcagcttg tcaaagtggg	1200
atgggaggaa caggagatgt tgccatttta agtacagcag accgaatgaa cttgatgcca	1260
tttgctcaag ttgctacgcg tttaggagga gctattactg ttatcacaat gacagccatt	1320
ttacgcatgt tattctaa	1338

<210> 143

<211> 1239

<212> DNA

<213> Streptococcus agalactiae

<400> 143

agaggcaaaa aagctggtaa atacacaaca tctgatgggt acatttttga tgccaaagat	60
attaaaaaag atacaggtac aggttatgtc attccacata tgacacatga gcattgggta	120
ccaaagaaag atttatcaga gtcggaatta aaagcagctc aagaatttct ttcaggaaaa	180
tctgaagcaa atcaagacaa accaaaaaca ggtaaaacag ctcaagaaat ctatgaggca	240
attgaaccaa aagcaattgt taaacctgaa gatttattat ttggaattgc acaagcgaca	300
gactataaga atgggtacatt tgtaattcct cataaagatc attaccatta tgtggaatta	360
aaatggtttg atgaagaaaa agatctttta gctgattcag ataagacata ttcttttagaa	420
gactatttag ctacggctaa atattacatg atgcacccag aaaaacgtcc taaagttgaa	480

GBS patentin.ST25

ggatggggta aagatgctga aatttataag gaaaaggact ctaataaagc agataaacca	540
agtcctgcac caactgataa taaatcaaca tcaaattcta gtgacaaaaa cttaagtgtc	600
gcagaagtat tcaaacaagc aaaaccagaa aaaattgtac cgcttgataa aattgctgtc	660
cacatggcat atgcagttgg atttgaagat gatcaattga ttgttcctca tcatgatcat	720
tatcataatg ttcctatggc atggtttgac aagggttggtt tatggaaagc accagaaggc	780
tatacattac aacaactctt ctcaacaatt aaatactaca tggaacatcc taatgaatta	840
ccaaaagaaa aagggttgagg acacgacagt gatcataaca aaggctcaaa taaagacaat	900
aaagccaaaa attatgctcc agatgaagaa cctgaagatt cagggaaggt aactcacaac	960
tatggttttt atgatgttaa taaagggttca gacgaagaag aaccagaaaa acaagaagat	1020
gaatcagagc tagatgaata tgaactagga atggcacaaa atgctaagaa atatggtatg	1080
gatagacaat cttttgaaaa gcaactcatc caattatcaa ataaatatag tgtaagtttt	1140
gaaagcttta attatattaa tggtagtcaa gttcaagtta ctaaaaaaga tggctctaaa	1200
gtgcttggtg atattaaaac actaacagaa gtgaaataa	1239

<210> 144

<211> 1446

<212> DNA

<213> Streptococcus agalactiae

<400> 144

atgaatcgta aaaaaacagt tattattagt gctttatcag tagctctatt tgggtactggt	60
gtagggtgctt accaattagg tagctataat gcccaaaaat cagacaatag tgtttcttat	120
gtgaaaacag ataaatctga tagcaaagca caagcaacag ctgtaaataa aacgcccagc	180
caaatcagta aagaagaagg catatctgca gaacaaatcg ttgttaaaat tactgacgac	240
ggttatgtga cttctcatgg agaccattac cattattaca atgggaaagt gccatatgat	300
gccatcatta gtgaagaatt gattatgaaa gaccctagct atgtctttaa taaagctgat	360
gtcattaatg aagtcaaaga tggttatatt atcaaagtta acggtaagta ttacctctat	420
cttaaagaag gtagcaaacg aacaaatggt cgtacaaagg aacaaatcca aaagcaacgc	480
gaagaatggt ctaagggtgg ttctaaggga gaatcaggaa agcatagtag tgcaaaaact	540
caagctttat cagccagcgt acgtgaagcg aaagctagcg gtcgctatac tacagatgat	600
ggttatgttt ttagtccaac agatgtcatt gatgacatgg gagatgcctt tttagtacca	660
catggcgatc atttccatta tatcccgaag gctgatttat ctccatcaga gttatcagcc	720
gcacaggcat attggaaccg caagactggc cgatcaggta atagctcaaa accatcaaat	780
tcaagttcat acattcatgc aagtgcacca agcggtaatg tatcaacagg aagacatgct	840
aatgcccta tttctattcc aagagtcact cagcgaatc actggtcaaa accagctgggt	900

GBS patentin.ST25

aatcatgcta	cggcaccaaa	acaccatgca	cctacaacca	aaccaatcaa	caaagattct	960
gcttttagaca	aaatgttgaa	acgtttatat	gctcaaccgt	tatatgctcg	tcacgtagaa	1020
agtgatgggt	tggtttatga	cccagcacaa	gttaatgctt	tcacagcaat	cggtgtttct	1080
attccgcacg	gtaatcattt	ccactttatt	cactataagg	atatgtctcc	attagagtta	1140
gaagcaacaa	ggatggtggc	agagcataga	ggacatcata	ttgatgcatt	agggaaaaaa	1200
gattctacag	agaaaccaa	gcatattttct	catgaaccta	ataaggaacc	tcacacagag	1260
gaagaacacc	atgcagtaac	accgaaagac	caacgtaaag	gcaaaccaa	tagccagatt	1320
gtctacagt	ctcaagaaat	tgaagaggca	aaaaagctgg	taaatacaca	acatctgatg	1380
gttacatttt	tgatgccaaa	gatattaaaa	aagatacagg	tacaggttat	gtcattccac	1440
atatga						1446

<210> 145

<211> 471

<212> DNA

<213> Streptococcus agalactiae

<400> 145

atggcta	aat	ttggattttt	atcggtacta	gaagaagaat	tgataagca	tttacagtat	60
gactttgcca	tgattggga	taagaaaaat	catactgtag	aagtcacttt	tatattagaa		120
gcacaaaaca	gctctgctat	tgaaaccgtg	gacgaccagg	gggagacgag	tagcgaggac		180
atcgtttttg	aggactatgt	actcttttac	aaccctgtca	agtctcgctt	tgatgctgag		240
gactatctgg	tgactatccc	ctatgagcct	aagaagggct	tgctcgctga	gtttctggct		300
tattttg	cgg agactctcaa	cgaggttgcc	actgaaggg	gtgagcgacct	catggacttc		360
ctcaccgatg	acagtatcga	agagttcgg	ctttcttggg	atacggatgc	ttttgaaaat		420
ggcagagcag	aactgaaaga	gacagagttt	tacccttatc	cgagatatta	g		471

<210> 146

<211> 4713

<212> DNA

<213> Streptococcus agalactiae

<400> 146

atgaacacaa	aacagcgttt	ttcaatccgg	aatataagt	taggtgccgt	atctgtactt	60
ttgggaaccc	tatttttttt	aggtggtatc	acaaatgtag	ctgctgattc	tgtcataaat	120
aagccatctg	atattgcagt	tgaacagcaa	gtaaaagaca	gtccaacgag	catagcaa	180
gagacaccta	ctaacaacac	gtcatcagcc	cttgcgctga	cagctcaaga	caatcttggt	240

GBS patentin.ST25

acaaaggcta	ataatagtcc	aacagaaaca	caaccagtag	ctgagtctca	ctctcaagcc	300
accgagacat	tttcccagct	cgcaaatcaa	ccggttgaaa	gcactcaaga	agtttctaaa	360
actcctttta	ccaaacaaaa	tttagcagtc	aaatctacac	cagctatttc	taaagaaacc	420
cctcaaaaaca	ttgatagtaa	taaaattatc	actgtcccca	aagtatggaa	cacaggctac	480
aaaggagagg	gaactgttgt	agcaattatt	gactcaggac	tagatatcaa	tcacgatgct	540
ctccaattaa	atgattcgac	aaaagcaaaa	taccaaaccg	aacagcaaata	gaatgctgct	600
aaagcaaaag	ctggtataaa	ctatggaaaa	tggtataaca	acaaagtaat	ctttggtcac	660
aactatgttg	atgtcaatac	agagctaaaa	gaggtgaaaa	gcacttctca	tggtatgcac	720
gtaaccagta	tcgcaacagc	taatcctagc	aagaaagata	caaatgaatt	aatctatggt	780
gttgctcctg	aagcacaagt	aatgtttatg	agagtcttct	ctgatgaaaa	aagaggaact	840
ggaccagccc	tttatgttaa	agctattgaa	gatgccgtta	aactcgggtc	tgacagcatt	900
aatttaagtt	taggtggagc	taatgggtct	ttagttaatg	ccgatgaccg	acttataaaa	960
gcttttagaga	tggttagact	cgctggcggt	tctgttggtta	tagcagcagg	taacgacggt	1020
acatttggga	gtggagcatc	aaagccttct	gctctttatc	ctgattatgg	tttagttggt	1080
agtccatcaa	cagctcgtga	ggcattttct	gtagcatcat	ataataatac	aacactgggt	1140
aataaagtct	tcaacattat	cggattagaa	aacaacagaa	atctcaacaa	cggattagct	1200
gcttatgcag	atcctaaagt	tagtgataag	acctttgaag	tagggaaaca	atatgattat	1260
gttttcgtag	gaaaaggaaa	cgacaatgat	tataaggaca	aaactttaaa	tggtaaaatc	1320
gccttaattg	aacgtggaga	tattactttt	acaaaaaaag	tcgtcaatgc	tattaatcac	1380
ggtgctgtgg	gagctattat	ctttaataac	aaagctgggg	aagctaattct	aacaatgagt	1440
ttagatcctg	aagcaagtgc	tattcctgct	atttttacct	aaaaagagtt	tggagatggt	1500
ttagctaaaa	acaactataa	aattgtatgt	aacaatatca	aaaataaaca	agccaaccct	1560
aatgcagggtg	tcctatctga	cttttcaagc	tggggggttaa	cagcagacgg	acaattaaaa	1620
cctgacttat	ctgctcctgg	aggctctatt	tacgccgcta	tcaatgataa	tgaatatgat	1680
atgatgagtg	ggacaagtat	ggcttctccc	catgtcgctg	gtgctactgc	tctagttaaa	1740
caatacttat	tgaaagaaca	tccagaactt	aaaaaagggtg	acattgaaag	aactgtcaaa	1800
taccttctta	tgagtactgc	taaagcacac	ctaaacaaag	atacaggcgc	ttacacctca	1860
ccacgccaac	aaggagcagg	tattatcgat	gtcgcagcag	cagttcagac	aggattatac	1920
ctaactgggtg	gggaaaacaa	ctatggcagc	gttacattag	gaaatattaa	agataaaatt	1980
tcctttgatg	ttactgttca	taatatcaat	aaagttgcaa	aagattttaca	ctatacaacc	2040
tatttaaata	ctgatcaagt	taaagatggc	tttgtcacat	tggctcctca	acaacttggt	2100
acattttacag	ggaaaacgat	acggattgaa	ccagggcaaa	cccaaacgat	tacaattgat	2160
atagatgttt	cgaaatacca	tgacatgtta	aaaaaagtaa	tgccaaacgg	ctatttccta	2220
gaaggctacg	tacgttttac	agaccctgtt	gatgggtggg	aagttcttag	tattccttat	2280

GBS patentin.ST25

gttggattta agggagaatt ccaaaactta gaagtttttag aaaaatccat ttataagctt 2340
 gttgctaaca aagaaaaggg attttatttc caaccaaac aaacaaacga agttcctggt 2400
 tcagaagatt atactgcctt aatgactaca agttcagagc ctatctactc aacagacggt 2460
 actagtccta tccaattgaa agccttgga agctataagt ctatagatgg aaaatggatc 2520
 ttacaactag atcaaaaagg ccagcctcat ctagccattt cacctaata tgaccaaaat 2580
 caagatgccg ttgcagtga aggtgttttc ttacgtaatt tcaataattt aagagccaaa 2640
 gtctatcgtg cagatgatgt taatttaca aaaccactat gggtaagtgc tccccaagca 2700
 ggagataaaa attactacag cggaaatact gaaaatccaa aatctacatt tttatatgac 2760
 acagaatgga aaggaaccac tactgatggt attccttttag aagatggaaa atacaaatac 2820
 gttttaactt attactctga tgtccctggc tctaagccac aacaaatggt gtttgatattc 2880
 actttggata gacaagctcc tacactaaca acagcaactt atgacaaaga tagacgtatc 2940
 ttcaaagctc gtcctgcagt agaacacggg gaatctggta tcttttagaga acaagtttgt 3000
 tacttaaaaa aagataaaga tggtcattat aatagcgtct tacgtcaaca aggagaagac 3060
 ggtatccttg ttgaagataa caaagtattt atcaacaag aaaagaatgg tagctttatt 3120
 ctacctaaag aggttaacga tttctctcat gtctactata ctggtgaaga ttatgcaggc 3180
 aatctagtat cagcaaaact cgaagatttg atcaatattg gcaataaaaa tggtttagta 3240
 aacgtcaaag tgtttagccc tgagcttaac agtaatgtcg atattgattt ctcttactct 3300
 gtcaaagatg acaaaggtaa tatcatcaaa aagcaacatc acgggaaaga cctcaattta 3360
 ttgaaattgc cttttggtac ctatacgttt gatctattct tatacgatga ggaacgagca 3420
 aatctaata gtcctaaag tgctactgta actatttctg aaaaagatag ccttaaagac 3480
 gtcttattta aagttaactt actcaagaaa gcagccttac tcgttgaatt tgacaagctt 3540
 ttaccaaaag gagcaacagt ccagttggtt actaagacaa atactgttgt tgatctacca 3600
 aaagcaactt attctcttac tgactatggt aaaaacatac ctgtaggaga ctatcgttta 3660
 aacgtaacgc tgcctagtgg gtatagcact ttagagaact tagatgattt acttgatcc 3720
 gtaaaagaag atcaggtaaa cctaacaaaa ttgacgctga ttaataaagc tcctctgatt 3780
 aatgccctag cagaacaaac tgatattatt acccagcctg tgttttataa tgctggaact 3840
 cacttaaaaa ataattacct agctaactt gaaaaggcac aaactttaat taaaaataga 3900
 gtggaacaaa caagtattga taatgctatt gctgctttga gagaaagtcg ccaagctctt 3960
 aacggtaaaag aaacagatac ttctttactg gcaaaagcta ttttagctga aacagaaatc 4020
 aagggaaact atcaatttgt taatgctagt ccattaagcc aatcaactta tatcaatcaa 4080
 gtccaattgg cgaaaaacct tctacaaaaa cctaacgtca ctcaatcaga agtagacaaa 4140
 gccttagaaa atcttgatat tgctaaaaat caattaaatg gtcataaaac tgattactct 4200
 ggtttacacc atatgataat taaagcaaac gttctgaaac aaacatcatc taaatatcag 4260
 aacgccagtc aatttgctaa agaaaattat aataacctta tcaagaaagc agaattgctg 4320

GBS patentin.ST25

ctttccaata gacaagctac acaagctcaa gttgaagagt tattaaccca aataaaagca	4380
accgaacaag agcttgatgg ccgtgataga gtttcttccg cagagaatta tagtcaatca	4440
ctcaatgata atgactctct caataccaca cctatcaatc cgccaaatca gccccaggcg	4500
ttgatattca aaaaaggcat gactaaagaa agtgagggtg ctcagaagcg tgtcttaggg	4560
gtgactagcc aaaccgataa tcaaaaggta aagacaaaca agcttcctaa aacaggcgaa	4620
agcactccta aaataaccta tacaatattg ctatttagtc tctctatgct aggtctggca	4680
acaatcaaac taaagtctat caaaagagaa taa	4713

<210> 147

<211> 1932

<212> DNA

<213> Streptococcus agalactiae

<400> 147

atgaataata acgaaaaaaaa agtaaaatac tttttaagaa aaacagctta tggtttggcc	60
tcaatgtcag cagcgtttgc tgtatgtagt ggtattgtac acgcggatac tagttcagga	120
atatcggctt caattcctca taagaaacaa gttaatttag gggcggttac tctgaagaat	180
ttgatttcta aatatcgtgg taatgacaaa gctattgcta tacttttaag tagagtaa	240
gattttaata gagcatcaca ggatacactt ccacaattaa ttaatagtagt tgaagcagaa	300
attagaaata ttttatatca aggacaaatt ggtaagcaaa ataaaccaag tgtaactaca	360
catgctaaag ttagtgatca agaactaggt aagcagctca gacgttctca agatatcatt	420
aagtcattag gtttcctttc atcagaccaa aaagatattt tagttaaatc tattagctct	480
tcaaaagatt cgcaacttat tcttaaatTT gtaactcaag ccacgcaact gaataatgct	540
gaatcaacaa aagctaagca aatggctcaa aatgacgtgg ccttaataaa aaatataagc	600
cccgaagtct tagaagaata taaagaaaaa attcaagag ctagcactaa gagtcaagtt	660
gatgagtttg tagcagaagc taaaaaagtt gttaattcca ataaagaaac gttggtaa	720
caggccaatg gtaaaaagca agaaattgct aagttagaaa atttatctaa cgatgaaatg	780
ttgagatata atactgcaat tgataatgta gtgaaacagt ataataagagg taagctcaat	840
attactgctg caatgaatgc tttaaatagt attaagcaag cagcacagga agttgcccag	900
aaaaacttac aaaagcagta tgctaaaaaa attgaaagaa taagttcaaa aggattagcg	960
ttatctaaaa aggctaaaga aatttatgaa aagcataaaa gtattttgcc tacacctgga	1020
tattatgcag actctgtggg aacttatTTT aataggTTT gagataaaca aactttcgga	1080
aataggagtg tttggactgg tcaaagtTga cttgatgaag caaaaaaat gcttgatgaa	1140
gtcaaaaagc ttttaaaaga acttcaagac cttaccagag gtactaaaga agataaaaaa	1200
ccagacgtta agccagaagc caaaccagag gccaaaccaa atattcaagt acctaaacaa	1260

GBS patentin.ST25

gcacctacag aagctgcaaa accagctttg tcaccagaag ccttgacaag attgactaca	1320
tggtataatc aagctaaaga tctgcttaaa gatgatcaag taaaggacaa atacgtagat	1380
atacttgacag ttcaaaaagc tgttgaccaa gcttatgatc atgtggaaga gggaaaattt	1440
attaccactg atcaagcaaa tcaattagct aacaagctac gtgatgcttt acaaagtta	1500
gaattaaaag ataaaaaagt agccaaacca gaagccaaac cagaggccaa accagaagct	1560
aagccagaag ctaagccaga agctaagcca gaagctaagc cagaggccaa accagaagct	1620
aagccagacg ttaagccaga agctaaacca gacgttaaac cagaggctaa gccagaagct	1680
aaaccagagg ctaagtcaga agctaaacca gaggctaagc tagaagctaa accagaggcc	1740
aaaccagcaa ccaaaaaatc ggttaatact agcggaaact tggcggctaa aaaagctatt	1800
gaaaacaaaa agtatagtaa aaaattacca tcaacgggtg aagccgcaag tccactctta	1860
gcaattgtat cactaattgt tatgttaagt gcaggtctta ttacgatagt tttaaagcat	1920
aaaaaaaaatt aa	1932

<210> 148

<211> 1623

<212> DNA

<213> Streptococcus agalactiae

<400> 148

atggcaaaag atattaaatt ttcagcagat gcccgcctcag caatgggtgcg tggtgttgat	60
atcttagctg atacagtcaa agtaacatta ggtcctaaag gccgtaatgt tgttcttgaa	120
aaagcatttg gttctccttt aattacaaat gatgggtgtga caattgctaa agaaattgag	180
ctagaagatc actttgaaaa tatgggagct aaacttgtgt cagaagtggc ttcaaaaact	240
aatgatattg caggggatgg cactacaact gctactgttt tgaccaagc tattgtacgg	300
gaaggtctta aaaatgtaac tgcaggggca aatccgattg gcattcgtcg tggatttgaa	360
acagctgttt cagcagcagt tgaagagcta aaagagattg cacaaccagt ttcaggcaaa	420
gaagctattg ctcaagttgc ggctgtgtct tcacgttctg aaaaagttgg ggaatacatt	480
tctgaagcta tggggcgcgt gggtaatgat ggtgttatca ctattgaaga atcgcgaggt	540
atggaaacag agcttgaaat tgtggaagga atgcagtttg accgtgggta cttgtcacag	600
tatatggtaa ctgataacga gaaaatggc tctgaacttg agaatccgta tacccttatt	660
acagataaga aaatttcaaa tatccaagaa attttaccat tattagaaga ggttcttaaa	720
acaaatcgtc cgttgctaata catcgctgat gatgttgatg gagaagctct cccaacgctt	780
gttcttaaca aaattcgtgg aactttcaat gtcgtagctg ttaaagcgcc tggatttggt	840
gatcgtcgta aagccatgct ggaagatatt gctatcctaa caggaggaac tgctggtact	900
gaagaccttg gtttagactt aaaagatgct actatgcaag ttttaggaca gtctgctaaa	960

GBS patentin.ST25

gtaacagtag ataaagattc tactgttatt gtcgaagggtg ccggtgactc atcagcaatt	1020
gctaatacgcg tagctatcat taagtcacag atggaggcta caacttctga ttttgatcgt	1080
gaaaaattac aagaacgact tgctaagtta gccggtggtg tagcagtaat taaagttggt	1140
gcagcgactg aaacagaatt aaaagagatg aaacttcgca tcgaagatgc gttaaattgca	1200
acgcgtgctg cagttgaaga aggtattggt tcagggtggag gtacggctct tgtgaacggt	1260
attgaaaaag tagcggcact gaaacttaat ggtgatgagg agactggacg taatattggt	1320
cttcgtgctc tcgaagagcc tgttcgtcaa attgcttaca atgctggata tgaagggttca	1380
gttattattg aacgttttaa acagtctgaa attggtacag gatttaattgc ggccaatgga	1440
gaatgggtag atatggttac cacaggtatc attgaccctg tcaaagtaac acgttctgca	1500
cttcaaaatg cggcatctgt agcaagtctt atcttgacta cagaagcagt agtagcaaat	1560
aaacctgaac cagaagctcc tacagctcct gcaatggatc catctatgat ggggtggcttc	1620
taa	1623

<210> 149

<211> 1542

<212> DNA

<213> Streptococcus agalactiae

<400> 149	
gtggtagaaa acctagaaaa accaattgga gtgagctata aaaatagccc atcaatgagt	60
aaacgaacgg ctatcagaat gaagaaatct agtcgatttt caattttact atatagtgtt	120
ttgtcaactc tcttagcaat tgcaaactct ttattgactt attttgcaaa tggtttgcat	180
actcagaatc tctatacagg tttgatgatg accaaaggac agatccctta tagtgatgtt	240
tttgctacag gaggattttt atactatgta acgattgctc taagttacct tttagggctc	300
agtatctggt tactttattgt acagtttatt gcttactatg tatctggaat ttatttttat	360
aaattagttt attatgtggc acaaagtga atgtctcga taggcatgac gttgattttc	420
tatataatga atattgtctt aggattcggg ggtatgtacc caatacagtg ggcattacct	480
tttatgctca tttcgtatg gtttttaatt aaattttgtg tcgataatat cgttgatgaa	540
gcattttatat tttatggcat ttttagcagca ttctcactat ttatagatcc ccaaactg	600
attttttggc ttgtctctt tgttctctta acagcaacca atattaagca aaagcagtca	660
ctacgaggat tttatcagtt tttatgcgtt gtttttggtg tgattttaat tgcttatact	720
gttggttact ttatgtttta tctacagatt atctcttctt atattgacaa agctattttt	780
tacccttta cgtatttcgc taggacaaac cactcattcc ttcttagttt agcaattcaa	840
attgttgctc ttctaggggc aggttgctc tttggactat gggattttat tcaaaatcgt	900
aaaaaagcat cttatcaaat cggcttgaac tttattgcct gtatttttat tatttacgct	960

GBS patentin.ST25

ataatggcca	ttttttcaag	agatttttaac	ctttaccact	ttttacctgc	tttaccattt	1020
ggctcttttgc	taacgagtaa	taaaattact	attcttttacc	aaaaagtgat	tgacagacgt	1080
tcacatagac	gtcagtat	ctctggtaaa	tctcttatcg	tagacctttt	tgtaaagaaa	1140
acataattatt	tgccccctctt	actagtttcc	ttatcgatag	ggttactagt	ttataaatact	1200
tatcaaaatg	ttactcttag	taaagaaagg	cgtgacattt	cacattattt	gactacaaaa	1260
attgatagag	atggtaagat	ttatgtttgg	gacaaagttg	ctagcattta	tagccagact	1320
cggttaaaat	ctgcttctca	atgtgttttg	ccacatatta	atacagcgca	aaaaaataat	1380
gagaaaat	tgaaggacga	gctgcttcag	catggggcta	aatactttat	cttaaataaa	1440
aatgagaagt	taccaaata	actgaaatct	gatattaaga	agcactacca	agaagttcct	1500
ctatcaaata	tcactcattt	tgttctatat	cgtttcaa	at		1542

<210> 150

<211> 2577

<212> DNA

<213> Streptococcus agalactiae

<400> 150

atggccaagc	caacgatatc	accgggaatg	caacagtatc	tggatataaa	agagaattat	60
ccagatgctt	ttttgctttt	tagaatgggt	gatttttatg	aattatttta	tgatgatgcg	120
gtaaaagcag	cacaaatcct	ggaaattagc	ttgactagtc	gaaataagaa	cgcagaaaag	180
ccaatcccaa	tggcaggagt	tccctatcac	tcagctcaac	agtatattga	cgtttttagtt	240
gaattagggt	acaaagtagc	cattgctgag	cagatggaag	atcctaataa	agctgtggga	300
gtggtcaagc	gtgaggtagt	gcaagttggt	accccaggaa	cggttgtgga	gtcaacgaag	360
ccggatagtg	ctaataat	cttagtagcg	attgattcgc	aagatcaaca	aacatttggt	420
ctagcatata	tggatgtctc	aactggagag	tttcaggcaa	cccttttaac	agattttgag	480
tccgtccgta	gtgaaatact	aaatttaaaa	gctcgtgaga	ttgtagtagg	atatcaattg	540
acggacgaaa	aaaatcacct	actgacgaag	cagatgaact	tgcttttatc	atacgaagac	600
gaacgactta	atgatattca	tttgattgat	gagcagttaa	ctgatttgga	aatatctgct	660
gcggaaaaac	ttttacaata	tgtgcataga	acacaaaagc	gtgaacttag	tcatttacag	720
aaagtagttc	attatgaaat	aaaggactat	ttacaaatgt	catatgcaac	gaaaaatagt	780
ctagatttac	tggagaatgc	tagaacaagc	aagaagcatg	gaagtcttta	ctggttgtta	840
gatgagacta	aaacagcgat	gggaactcga	atgctgagaa	cttggattga	caggcctttg	900
gtaagtatga	atcgaatcaa	ggaacgtcaa	gatattattc	aagtgtttct	tgattatttt	960
tttgagagaa	acgatctcac	agaaagttta	aagggtgtat	atgatattga	acgcctagca	1020
agtcgagtat	ctttcggaaa	agccaaccct	aaagatctat	tgcaactcgg	acagacctta	1080

GBS patentin.ST25

tcacaaattc	ctcggattaa	aatgatttta	cagtccttca	atcaacctga	gcttgacatc	1140
attgtcaaca	aaattgacac	tatgcctgaa	ttagaaagtt	taattaatac	ggcgatagcc	1200
ccagaagcac	aggctactat	cactgaggga	aacattatca	agtctggatt	tgataagcaa	1260
ttggataatt	atcgaacagt	gatgcgtgaa	ggtacagggt	ggattgctga	tattgaagct	1320
aaggaaagag	cagcaagtgg	tatcgggtact	cttaaaattg	attataataa	aaaagacggt	1380
tattacttcc	atgttaccac	ttccaattta	tcactagtac	cggagcattt	tttccgtaaa	1440
gcgacattaa	aaaattctga	acgctatgga	acagcagaac	tagccaaaat	tgaagggtgaa	1500
atgctcgaag	ctcgcgagca	atcttcaaat	ttagaatatg	atatttttat	gcgtgttcgt	1560
gccaagtag	aatcttatat	taaacgtctt	caagagttag	caaagacgat	tgcaaccggt	1620
gatgttctac	agagtttggc	agtagttgca	gaaaattatc	actatgttcg	tcccaaattt	1680
aatgatcaac	atcagattaa	gattaagaat	gggcgtcatg	caactgttga	aaaagtgatg	1740
ggagtgcgaag	aatatattcc	caatagcatc	tattttgata	gtcagacaga	tatccagttg	1800
attacaggac	caaatatgag	tggttaagtcg	acctatatgc	gccagttagc	tttgacagtt	1860
attatggcac	aaatgggagg	ttttgtatcg	gcagacgaag	ttgatttgcc	tgtatttgat	1920
gcaatattta	ctaggattgg	tgctgctgac	gacttaattt	ctgggcaatc	aacctttatg	1980
gtagaaatga	tggaagcgaa	tcaagctgta	aaacgagcca	gtgataaatc	tttgattcct	2040
tttgatgaat	taggtcgagg	gacagccact	tatgatggta	tggcattagc	tcaatcgatt	2100
atagaatata	ttcatgaccg	tgttagggca	aaaacaatgt	ttgcgactca	ttaccatgag	2160
ttgacagatt	tatctgaaca	gttgacaagg	cttgtcaatg	tacacgtggc	tacttttagag	2220
agagatggag	aagttacctt	cttacataaa	attgaatctg	gacctgcgga	taagtcttat	2280
gggatacacg	tcgcaaaaat	agctgggtta	ccaattgact	tattggatag	ggcaactgat	2340
attttatcac	agttggaagc	tgatgcagta	cagttgatcg	tatcgccctc	ccaagaagct	2400
gttactgctg	acttaaatga	ggaactagat	tctgagaagc	aacaaggaca	attatcgctt	2460
tttgaagaac	cttcaaatgc	aggtaggggt	attgaggagt	tagaagcgat	agatataatg	2520
aatctaactc	caatgcaagc	tatgaatgct	atatttgact	taaagaaatt	attataa	2577

<210> 151

<211> 873

<212> DNA

<213> Streptococcus agalactiae

<400> 151

atgttgaaac	tggttttaaa	aacaaagata	aaagaagcta	ttttaattgc	ctttgggtgtg	60
gctctctata	ctttcggtt	tgtcaaat	aatatggcta	atcatttggc	tgaaggaggt	120
atttccggtg	tcactttgat	tatccatgca	cttttcggag	ttaatccagc	actttcatca	180

GBS patentin.ST25

cttctcctta atatcccgtt atttatatta ggggctagga ttttagggaa aaaatcctta	240
ttattaacta tatatggtac agtggtaatg tcttttttca tgtggttttg gcaacaaatc	300
cctgtaacag tccctttgaa aaacgatatg atgtaggtg cagtagctgc tggaaatttta	360
gcaggaactg gtagtggttt agtatattaga tatgggtgcaa ctacaggtgg tgcagatatt	420
attggctgta ttgtagagga aaaatctgga ataaaattag ggcaaaccctt attgtttatt	480
gatgctatag ttctaacgtc ttcacttggt tatattaatt tacaacagat gctatatacg	540
ttagtagcta gctttgtatt tagtcaagt ttaacaaatg ttgaaaatgg gggctacact	600
gttcgtggaa tgatcattat taccaaagaa tcagaatctg cagcagcaac cattttgcat	660
gaaattaata ggggtgtaac ttttttacgg ggccaaggtg cctactcagg tagagagcat	720
gatgtcttgt acgtagctct taaccaagt gaagtgcgtg atgtgaaaga aatcatggct	780
gatttagacc cagatgcttt tatttctggt ataaatgtag atgaagttat tagctcagat	840
tttaaaattc gacgaagaaa ttacgataaa taa	873

<210> 152

<211> 1752

<212> DNA

<213> Streptococcus agalactiae

<400> 152

atgaaacgta gtatgtatgc tgggcgtggt cgtagtgagc acataggaac atcgattact	60
ttaaaaggat gggttggtcg tcgtcgtgac cttggaggcc ttatttttat tgatcttcgc	120
gatcgcgagg gaatcatgca attagtattt aatcctgaag aagtagcagc ctcagttatg	180
gcaaccgcag aaagtctccg tagtgaattt gttatagagg ttagcgggtg agtgacagca	240
cgagaacaag ctaatgataa tttaaccaaca ggagaagttg aattaaaagt gcaagaatta	300
tcggttctta atacctcgaa aacaacacca tttgaaatta aagatggtat tgaggcaaat	360
gatgatacac gcatgcgtta ccgttacttg gatcttcgtc gtccggaaat gcttgaaaat	420
ttcaaattac gtgcgaaagt aacacactca atccgtaatt acctgacaa cttagagttt	480
attgatgtcg aaactccgat gctaacaaaa tcaactccag agggggcacg agactatttg	540
gttccatcac gtgtcaacca aggacatttt tatgcccttc cacaagccc tcaaattaca	600
aaacagctat tgatgaatgc aggatttgat cgttattatc aaattgtcaa atgttttcgt	660
gatgaggatt tacgtggaga tcgtcaacct gagtttacac aagttgactt agagacatca	720
ttccttagtg atcaagaaat tcaagacatt gttgagggtg tgattgctaa agtaatgaaa	780
gacactaaag gtttagaggt ttctttacca ttcccaagga tggcatatga tgatgcaatg	840
aataactacg ggtctgataa gcctgataca aggtttgata tgcttttaca agacttgaca	900
gaaattgtaa aagaagttga cttcaaggtg ttctcagaag cttcagtagt taaagcgatt	960

GBS patentin.ST25

gttgtcaaag acaaggcgga caagtactct cgaaaaaata ttgataaatt aacagaaatt	1020
gcaaaacaat acggtgccaa aggttttagca tggctaaaat atgtagataa tactatttca	1080
gggccggttg ctaagttctt gacagctatt gaaggtaggt tgacagaagc tttgcagcta	1140
gagaataatg acttaattct atttgtagca gatagtcttg aagtagctaa cgagacttta	1200
ggagcgcttc gtacacgcat tgcaaaagaa cttgaactca ttgattattc taaatttaat	1260
ttcctatggg ttgttgattg gccaatgttt gagtggtcag aagaagaggg acgatatatg	1320
tcggctcatc atccattcac cttgccaaca gcggagacag cgcattgagtt ggaaggggat	1380
ttggctaaag tacgtgcagt tgcctatgat attgttttga atggatatga gttaggcggg	1440
ggtagcctac gtattaacca aaaagataca caagagcgta tgttcaaggc tttaggattt	1500
agcgctgaat cagctcagga acagtttggt ttcttacttg aagctatgga ttacggcttc	1560
ccaccacatg gtggattggc aataggcctt gaccgctttg ttatgttggt agcaggcaag	1620
gacaatatc gagaaattat tgcattccct aaaaacaata aggctagtga tccaatgact	1680
caagctccta gtctcgtttc agaacaaca ttagaagaat taccacttac ttagaaggt	1740
tatgaaaact ag	1752

<210> 153

<211> 456

<212> DNA

<213> streptococcus agalactiae

<400> 153	
aaagaaaaag gaaaactaat aaagaaaaaa attctagaaa ataatactga tattattcca	60
aaaattatag aaaaaagtc tcaaaatctt attcttaca gtaattaca cagagttaat	120
attgataaaa taaaaaatat aaaaaatttt gataaaggat tcgaactagg ctttccactt	180
tttgaaaaag gagaaattct gagaaaagaa ggcgaaataa ctagtgcaat tgaattattt	240
gataaagcac gtgaactagg atatttttga cccgccttat acaattctta tgcatggct	300
tttaggaaaa taaagaatta tgatgatgaa attctaatac tacaagaagg aattgaaaga	360
ttcaaaaaaa gcaccctgtc atcaaatatt aacccaaaga caatcgatag atggagtact	420
cgtatttcta gagctaaaga tttaaaatgt aaataa	456

<210> 154

<211> 678

<212> DNA

<213> streptococcus agalactiae

GBS patentin.ST25

<400> 154

ttgaatgtaa	aaaaacatca	tttagcttat	ggagctatca	ctttagtagc	ccttttttca	60
tgtattttgg	ctgtaatggt	catcttttaa	agttcacaag	ttactactga	atctttgtca	120
aaagcagata	aagttcgcgt	agccaaaaaa	tcaaaaatga	ctaaggcgac	atctaaatca	180
aaagtagaag	atgtaaaaca	ggctccaaaa	ccttctcagg	catctaata	agccccaaaa	240
tcaagttctc	aatctacaga	agctaattct	cagcaacaag	ttactgagag	tgaagaggca	300
gctgtagaac	aagcagttgt	aacagaaaac	accctgcta	ccagtcaggc	acaacaagct	360
tatgctgtta	ctgagacaac	ttatagacct	gctcaacacc	agacgagtgg	ccaagtattg	420
agtaatggaa	atactgcagg	ggctattggc	tcagcagctg	cagcacaat	ggctgctgca	480
acaggagtcc	ctcagtctac	ttgggaacat	attattgccc	gtgaatcaaa	tggtaatcct	540
aatgttgcta	atgcctcagg	agcttcagga	cttttccaaa	cgatgccagg	ttggggttca	600
acagctacag	ttcaggatca	agttaattca	gctattaaag	cttatcgtgc	tcaagggtta	660
tcagcttggg	gttactag					678

<210> 155

<211> 1482

<212> DNA

<213> Streptococcus agalactiae

<400> 155

atgtcaaatt	gggatactaa	gtttttgaaa	aaagggttta	cttttgatga	tgttctgctt	60
attcctgctg	aaagccatgt	tttaccaaat	gaagttgata	tgaagacaaa	gttggctgat	120
aatttgacat	taaacattcc	aatcattaca	gctgcaatgg	atacagttac	agatagtaag	180
atggctattg	ctattgcacg	tgctgggtggg	cttggtatca	ttcataaaaa	tatgtcaata	240
gttgatcaag	cagaagaagt	tcgtaaagtt	aaacgctcag	aaaatgggtg	tattattgac	300
ccattcttct	tgacaccaga	taatactgtc	tctgaagctg	aggaattgat	gcaaaactat	360
cgcattagtg	gagttcctat	tgtagagaca	ctcgagaatc	gtaaattagt	tggaattatt	420
actaaccgtg	atatgcgttt	catttctgat	tataaacaac	taatctcaga	gcacatgaca	480
agtcaaaatc	ttgtaacagc	tcctattggg	acagatcttg	aaactgcaga	gcgtattctt	540
catgagcatc	gtattgaaaa	gctaccttta	gtagatgatg	agggacgtct	ttcaggactt	600
attactatta	aggatatcga	aaaagttatt	gaatttccta	aggcagcaaa	agatgaattt	660
ggacgtctct	tagttgcagg	tgtagtaggt	gtaacctctg	atacttttga	acgtgcagaa	720
gctttgtttg	aagcaggtgc	agatgctatt	gtcattgata	cagcacatgg	acattcagct	780
gggtgtgctcc	gtaaaattgc	tgaaattcgt	gctcacttcc	ctaactgcac	attgattgcg	840
ggaaatattg	ctacagcaga	aggagcgcgt	gcactttatg	atgcaggtgt	ggatgtcggt	900
aaagttggta	ttgggtccagg	ttcaatttgt	acgactcgtg	tcgttgctgg	ggtaggtggt	960

GBS patentin.ST25

cctcagatta	cagctattta	cgatgcagcg	gctgttgcgc	gtgagtacgg	taagactatc	1020
attgctgatg	gtggtattaa	atattcaggt	gatattgtaa	aagcacttgc	agcaggtgga	1080
aatgcagtta	tgctaggttc	aatgtttgca	ggaacagatg	aagcgccagg	agaaacagaa	1140
atcccccaag	ggcgtaagtt	caagacatac	cgtaggtatgg	gctcaattgc	agcaatgaaa	1200
aaaggttcaa	gcgatcgta	tttccaaggt	tctgtaaacg	aggctaacaa	attgggtcca	1260
gaagggtattg	aaggctcgtg	agcatacaaa	ggttcagtag	ccgatattgt	tttccaaatg	1320
cttggtggca	ttcgctctgg	tatgggatat	gtagggtcag	cgaacataaa	agaacttcat	1380
gataatgctc	aatttggtga	aatgtcagga	gctggcttga	aagaaagcca	tccccatgat	1440
gttcaaatta	caaatgaggc	accaaattat	tcagtacact	aa		1482

<210> 156

<211> 2580

<212> DNA

<213> Streptococcus agalactiae

<400> 156

atgacaatta	accactataa	gcttcgtata	ccttactata	caataagctt	tctacttccc	60
ttcataatca	tagtctgtat	cctctttact	aagaatattt	attggggaag	tccaacaacc	120
atattagcaa	gcgatggctt	tcatcaatat	gttatcttta	atcaagcatt	aagaaatatt	180
cttcatgggt	caaacagctt	attctatacc	tttacaagcg	gtttagggtt	aaatTTTTat	240
gctctgagta	gttactattt	gggaagtttt	ttatcccaa	tagttttattt	ctttaaccta	300
aaaaatatgc	ctgatgctat	ctacctttta	acaatatgta	aaatagggtt	gatagggttg	360
tcaatgtttg	tcactctttg	taaacgtcat	tgtaaagtta	atcgtgtctt	acttttagta	420
atttctactt	gctatagctt	aatgagtttc	tcaattagcc	aaattgaaat	taatagtgg	480
ctagatgtat	ttattcta	ttcccttggt	gttttaggag	ttgatcagct	actatgggaa	540
agaaaaccta	tactttattt	cctctctctg	acagccttat	tcattccaaa	ctattatttt	600
ggttttatga	ctgccatctt	tactagcctt	tacttcatcg	tacaaataac	ccgtaatact	660
gatagtaagg	ttgcatttaa	acaatttctt	cattttacct	ttttatctct	tttagctgg	720
atgactagta	gcattatgat	tttgccaact	tattttgatt	taactactca	tggtgaaaag	780
ttgacaaagg	tatcgaagat	gtttacagaa	aattcttggt	acatggattt	gtttgctaaa	840
aatatgattg	gagcctatga	tacaacaaaa	tttggctcta	ttcctatgat	ttatgtagg	900
ttacttcctt	tactcctttc	tttaactttac	tttacaataa	aggaagttcc	tcgaaggact	960
agattagcat	atggattttt	aataatattt	gttattgcta	gtttttatat	aacacctcta	1020
gatttatttt	ggcaagggat	gcattgctcca	aatatgtttc	tccatcgcta	ctcttgggta	1080
ctttcagtac	ttatctgtct	gctagctgct	gaatgccttg	agtatttaga	caacatttct	1140

GBS patentin.ST25

tggaaaaaga ttttaggggt caatttaatt ttagtaagtg gtttcataat cacgttttta	1200
tttaaaaagc attatcatta ccttaatcct gaattacttc ttttaacctt aactttcctc	1260
tcagcttata ttattctaac tattagtttt gtcagtaagc aaatccctaa attagttttt	1320
tatccctttc ttattgggtt tgttgtatta gagatgacat taaacacctt ttaccaacta	1380
aatagtctta acgatgaatg gatattttcca tctaggcaag gatatgctaa atataatcac	1440
agcattagca aacttgtcag aaagactgag agaaataact ctacattcct ccgtacagag	1500
cgctgggttag gacaaaccgg caacgactct atgaaatata attataatgg tatttcacaa	1560
ttttcatcta ttagaaatcg ttcttcaagt caagtgcctg atagacttgg ctttaaatca	1620
gatggtacaa atttaaatat acgttatcaa aataatactt tgatcgaga tagtctattt	1680
ggtgtgaagt ataaccttac agaatatcct ttgataaat ttggttttat caaaaaagct	1740
caagataaac aaaccattct ttacaaaaat cagtttgcca gtcaattagc tataactaacg	1800
aatcaagtat atcaagataa accatttact gtgaatactt tggataatca gacaactcct	1860
ttaaatcaat taagtgggtt gaaagagacg tattttgagc atcttattcc aaatagcggt	1920
tctgggcaaa ccactcttaa taaacaagta tttgttaaaa agaataaaca aggggaatact	1980
gaaattacct ataacataac tatccctaaa aacagtcagt tatatgttag tatgccgttt	2040
ataaatttta ataatgagga aaataaaatt gttcaaactc ccgttaataa tggaccattt	2100
gtaccttaata ctcttgataa tgcttattca ttttttaata ttggttcctt tgctgaaaac	2160
agtcgtatca aagtaaaatt tcaattttcca cacaatgac aagtttcttt cccaattcct	2220
cacttttatg ggctcaagtt agaagcttat caaaaagcta tgactgttat taataaacga	2280
aaagtaaaag taagaactga tcacaataaa gttattgcta attatacaag tcctaataka	2340
agttctcttt tcttcactat tccctatgat agggggttga aagcttatca aaataataaa	2400
gaaataaaaa ttttcaaagc tcagaaagggt tttatgaaaa taaatattcc taaaggaaaa	2460
ggcaaagtaa cattaatttt tatcccttac ggcttttaat ttggggtagg cctatctatt	2520
actggaatag tattattttac tgtctattat tttaaatttg gaaaaataa aataggatga	2580

<210> 157

<211> 45

<212> DNA

<213> Streptococcus agalactiae

<400> 157

tggtttatga agcactcggg tgggaagcgc cacaatttgg tcaca

45

<210> 158

<211> 90

GBS patentin.ST25

<212> DNA

<213> Streptococcus agalactiae

<400> 158

atgaaagatc acctaagggtg cttcctccat taccgatcca aaaacgttgg gaaaaatgga 60

acgagattga agggaggaaa gcctaattgac 90

<210> 159

<211> 99

<212> DNA

<213> Streptococcus agalactiae

<400> 159

gacaaacagc ttttccaatg cgtgcagggc ttccaaataa ggaacctcaa tggcaagaag 60

catgggatca agctgatatt tataaaaaac gtcaagcat 99

<210> 160

<211> 78

<212> DNA

<213> Streptococcus agalactiae

<400> 160

aacgaggaag ccatagatgg ggtgtccaag cttgggaaaa aaatcacat tctaggaaat 60

aattcatacc tttcttcc 78

<210> 161

<211> 93

<212> DNA

<213> Streptococcus agalactiae

<400> 161

atcaaacaat ggctattggt gatgaagaaa atgaccgtgc tatgcttgaa gttgttgga 60

atcctgttgt tatgcaaaac ggcaatcctg aac 93

<210> 162

<211> 57

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 162
aggcgcattt caaacaatct aggagtttta aaggaagcga ccggtataca cgccgta 57

<210> 163

<211> 108

<212> DNA

<213> Streptococcus agalactiae

<400> 163
gagctctgcc taaagctgag caacgtcaag ccaatctata tgccttggca cttcgagcaa 60
atcagtttga aaaaacaggt ttcaagggtt tatcacgctt tattcgaa 108

<210> 164

<211> 96

<212> DNA

<213> Streptococcus agalactiae

<400> 164
agaagctgct tcagtaggtg ctatccaaga tttaacagat tcagatatca ttttctcaaa 60
ccaccgtgga cacggacaaa ctattgcaaa aggtat 96

<210> 165

<211> 57

<212> DNA

<213> Streptococcus agalactiae

<400> 165
agatggtttg gttttagata tgacgatggc agaaaattta gctttacaaa cttatta 57

<210> 166

<211> 66

<212> DNA

<213> Streptococcus agalactiae

<400> 166
cccttaaaaa gtttgtcgat gacatcaaga atgaagctat tgaggttatc acaaagaaaa 60
gctatg 66

GBS patentin.ST25

<210> 167

<211> 90

<212> DNA

<213> Streptococcus agalactiae

<400> 167

aggcacttgc gaaagagaca aaagcaaaat catttaatga atttatgctt tctatgtgcc 60

gtgaaaaaat tgaaaaagga caatttaatt 90

<210> 168

<211> 90

<212> DNA

<213> Streptococcus agalactiae

<400> 168

aagttattta ttcagcctat tcaggaaaat atgaagcagc caatcgagat tatatcaa 60

tactatgcaa agcttgggtt aatgaaaatc 90

<210> 169

<211> 57

<212> DNA

<213> Streptococcus agalactiae

<400> 169

tatcaaactg attcgaaaaa ggcaagaaaa tttggttccg tttggcttaa acctaag 57

<210> 170

<211> 84

<212> DNA

<213> Streptococcus agalactiae

<400> 170

acgctgttat tccagatact tctcctgctt tctcatttga aaaagaacat ctttctggag 60

tggaatatgc acgctactta caat 84

<210> 171

<211> 210

<212> DNA

<213> Streptococcus agalactiae

<400> 171

```

aagaagtttt acgaaataat attagcaacc aagtaccaca catcagtgtt caaatggagt      60
ttaaaactca agaacaagtt gacgaatacc aaaaaaatct cggaagcatc atccgggaaa      120
ttggagatac acttggaaaca gcaactgaat tcaatgccaa aagtaacatt agcacttata      180
ctcttggtgg acaaatccaa cgcattattg      210

```

<210> 172

<211> 333

<212> DNA

<213> Streptococcus agalactiae

<400> 172

```

ttaaagcaaa tgttccgtcg cgtattgcat ttgctgtttc aagtgggtact gatagccgta      60
cgatccttga tgaaaatggg gctgaaaagc tcttgggacg gggtgacatg ctctttaagc      120
ctattgatga gaatcatcca gtacgactac aagggttcctt tatttcagat gatgatgttg      180
aaaggatcgt tggttttatc aaagaccaag ccgaggctga ctatgatgat gcctttgatc      240
ctggagaagt atctgaaaca gataacggct ctggtggtgg cggcggagta cctgaaagtg      300
atcctctttt tgaagaagcc aagggtactcg ttt      333

```

<210> 173

<211> 39

<212> DNA

<213> Streptococcus agalactiae

<400> 173

```

ggccggaaaa ttaatttttag tcgtccatca cgatttgag      39

```

<210> 174

<211> 81

<212> DNA

<213> Streptococcus agalactiae

<400> 174

```

agagttaagt ataaaaaatg ggaaccttta tcaatatccc gttcctgcta tgaaaaatct      60
tcgtcaacat caagcagaat t      81

```

GBS patentin.ST25

<210> 175

<211> 93

<212> DNA

<213> Streptococcus agalactiae

<400> 175

acttggtcaa gatgttgat tcccagggtg tactcgtggt gcaaaattag aagaagcaat 60
caatgctttg gaagatggac aagttctttt ggt 93

<210> 176

<211> 99

<212> DNA

<213> Streptococcus agalactiae

<400> 176

aaggagaatt tcgttcaaag gttgaggagt ctattgaaag caatcagcaa aaatataatc 60
atttatagtc tagtttctct accattagct agacacttg 99

<210> 177

<211> 177

<212> DNA

<213> Streptococcus agalactiae

<400> 177

agtataatca atattaaact agaaatatat gacatatgtc ctaaaactat ctcaaatagg 60
gagtcaatac atggatatag aaaactactg ccaagactac tgtttggaga ctatctttcc 120
aaaacattat ttcaaggatt tacaagtaat caccctaact gccggccaat ccgtctg 177

<210> 178

<211> 48

<212> DNA

<213> Streptococcus agalactiae

<400> 178

ctttctttca gaagaagtcg gcgaattggc tcaagccatt cgcaaata 48

<210> 179

<211> 42

GBS patentin.ST25

<212> DNA

<213> Streptococcus agalactiae

<400> 179

ttcattttca aggatagggtt taaaatgaga cacttcacgg ac

42

<210> 180

<211> 222

<212> DNA

<213> Streptococcus agalactiae

<400> 180

gggttgattt gtgcttgtaa agcctttatc tctgccatac tggctaactt attttgttcc

60

tctgttatcc ccattgccag ttgtcctgaa aatatttgcg ctaaaccaag gactaggttt

120

tcctccacct cagacattgt cttatctcct gcaaagtaca tttttaaggc acccacagtt

180

ttatcattta ttttagagg aactacaata gcagaattta ac

222

<210> 181

<211> 99

<212> DNA

<213> Streptococcus agalactiae

<400> 181

tcctcctctt tggacacca ttacaaacat agggagcttt tcttagtagc ggacagtcta

60

ggcagtcctt ggttgattct cttagttgct tatttcggt

99

<210> 182

<211> 75

<212> DNA

<213> Streptococcus agalactiae

<400> 182

cacctggtgc cactcaata tcataaacag aatctacctc ttgaatataa gaggctaaac

60

gctctagtc ccataaacag aatctacctc ttgaatataa gaggctaaac

75

<210> 183

<211> 72

<212> DNA

<213> Streptococcus agalactiae

<400> 183

gcacacctac acgaagggtg tcataagtat ccactaaaaa gacgcaatct ttatgagttt 60

ctgctgaagc tt 72

<210> 184

<211> 69

<212> DNA

<213> Streptococcus agalactiae

<400> 184

ccattgaaag agctccgcga acattatata attcctcgga aaattcgtct tcaaaacttt 60

ccccataga 69

<210> 185

<211> 63

<212> DNA

<213> Streptococcus agalactiae

<400> 185

aagtatacta ttgcaggctc tcgtgtcacc cagcgtcgac catcattttc tgttactaaa 60

gta 63

<210> 186

<211> 57

<212> DNA

<213> Streptococcus agalactiae

<400> 186

gcagcttttt catcaccagc agctaaaaac agagcattca ttacaacacg atcttca 57

<210> 187

<211> 141

<212> DNA

<213> Streptococcus agalactiae

<400> 187

tccatgggtta aacaaatata gttctctgac catttgatat cacgttttga aggcttatgc 60

GBS patentin.ST25

ttgaggcgat tttctgtgcg attccgtttg agacgctcac ttagctctgt ttctaattct 120
 acaaataata cctcttggtt g 141

<210> 188

<211> 129

<212> DNA

<213> Streptococcus agalactiae

<400> 188
 taccacgttc tttctcgata tcatttgaat ccattgcacg ttcttcaagc tctttacgct 60
 catcaagagt atgtgattgt tttaataatt catcaacgag agttgtttta ccgtgggtcaa 120
 cgtgggcaa 129

<210> 189

<211> 54

<212> DNA

<213> Streptococcus agalactiae

<400> 189
 gcacagcctt cttcaactag gatatcccct aaaattgatc gttttacacc taag 54

<210> 190

<211> 114

<212> DNA

<213> Streptococcus agalactiae

<400> 190
 tggaatagaa ctatcaatta ttttttgaat aacctgcaat tgggtgactaa tatcaagttg 60
 cccacgagaa aaattttcca gtcccaaaac aagtttctga gtttcatcaa aaac 114

<210> 191

<211> 36

<212> DNA

<213> Streptococcus agalactiae

<400> 191
 gtccaagaag gccataaaat tttccctctt caaaga 36

GBS patentin.ST25

<210> 192

<211> 87

<212> DNA

<213> Streptococcus agalactiae

<400> 192

caacaaagca ataacaccgc caattatagt cgcccctata aaccttggca taaaaagaaa 60

aatggattga gctgcagatg ctttagc 87

<210> 193

<211> 249

<212> DNA

<213> Streptococcus agalactiae

<400> 193

ttctttgatg ataccaaagt taacattcat tggttggaaa tgtttgctgt ctgtatgtgt 60

aatataatgt ggagtgac caatagcagt agtttggtgg aaaactactt cactctcccc 120

attaaagcga cgggcagcat tgattccgc tacaagacca cttgctgccg attctacata 180

accttcaaca ccggtcattt gtccagcaaa gaaaagattt gggttcttac gtgtagcaaa 240

ggtttggtc 249

<210> 194

<211> 243

<212> DNA

<213> Streptococcus agalactiae

<400> 194

gtgtattcgt tacgcatagc gacattggaa ctagaacgaa acttgataga caagcgacgt 60

gggaaaccaa ccgattctag gtcaatagag ttttagagg ttagtttagc aatattatct 120

tgcaagaata agttaatacc tgacatcatg ctagagaaga catttccctt agtttcttct 180

gaagcgaagt cagaagacct aaagtttaaa tcagccatat ctctaaattt ggaaaattgt 240

tct 243

<210> 195

<211> 168

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 195
ggccatagca atggcattaa agagggaaat ggaggtatct tcccagtatt ttgcattgcc 60
attaccgcta ccagggtttcg ttttacgata aatggcttct gcaaccgcat taacccttgt 120
ctgtgtcatt tcatagtaac ccttcttagc tgctgcaatc gcaagagc 168

<210> 196

<211> 489

<212> DNA

<213> Streptococcus agalactiae

<400> 196
agaatagaga aggctatcgt ccctaaaccg gccattagtg ttctgatgat aatctcaagg 60
atgggtattag gaacaccaga aaaagaacct gtcatttgtt ctgcaaaccg aataatttca 120
attgtaatag ccacacctgc tgatatagaa atacaaatga gtaaagcaga cataatcaaa 180
gctaaacctg ttgaaaaatt attctgtgaa aattctctca ccgaattaac aaaggcagcc 240
cctggcacca taaccattag tgcccctaata ataataatgc tacgatgctc acctaatacct 300
gaaaaatata ataaattagc acttaaagcc actacagaac tacctagaat ggtcaaaaga 360
aatcctgtat gtatacgact ttccatcaaa ttcagaaaat atcctaaaat taagcctgtt 420
acagcagcgg aaaatgaatc taataaggaa ctacctaagg ctaaagaaaa actaccgct 480
ccacaaaaa 489

<210> 197

<211> 267

<212> DNA

<213> Streptococcus agalactiae

<400> 197
ccatatttctg taacatatgc tgctccagta atttgtaatg gagcggattt agcacgacga 60
acagcatatg ctatgtcgtc atcagttaca aaaccttctg atgtagaaga attagttacc 120
ataggtgata gaacaaaacg attttctagg ctcaatccat tgggaagtat taatggacga 180
aataaattac cttggacatt attcatctct gctcaccgtc cccttattag ccatagactt 240
agcctgaaat ctatcaaact ctgcaac 267

<210> 198

<211> 54

<212> DNA

<213> Streptococcus agalactiae

<400> 198

gcccaaccata atgacaaaaa taatacgata agcgtaata aatttagtgc caaa

54

<210> 199

<211> 153

<212> DNA

<213> Streptococcus agalactiae

<400> 199

tcctttctgcg tattttgttg ccattccaaa aaaggcagct acccacatcc aaaacaaagc

60

tcctggtcct ccagatttaa tagccgtagc cacaccaacg atattacctg tccctaccgt

120

tgcagcaaga gcagttgcaa gggcagcata act

153

<210> 200

<211> 90

<212> DNA

<213> Streptococcus agalactiae

<400> 200

acattaggca tttcttttaa aataagaggg tgccatttct ccgcaaaacc ttttctaggg

60

ggtaaattctc ctgattttcc ttgacctggg

90

<210> 201

<211> 180

<212> DNA

<213> Streptococcus agalactiae

<400> 201

tttaatatatt ctaatagttc cttaggtttt ggtacttctg ctaaatacagc aagtacttcc

60

tcagctaatt cttccttaat aatttcttgt gataaggcca cacattcatt acaaatgaaa

120

acaccattac ctgcaataat tttttttact tcattcttggc ttttgccaca aaatgaacaa

180

<210> 202

<211> 105

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 202
 ggtgtttata aaaagcagag cctaagcctg attttccatc agattcacct gattgtttat 60
 cattttgatt ttttgcata taggtttgtg ccttattatc gagaa 105

<210> 203

<211> 261

<212> DNA

<213> Streptococcus agalactiae

<400> 203
 attttcttac gatcagtatg tggaaattca cgacaagctt taggtctgac atcgtatata 60
 ctacataagt tatcatcgcc taaaaacgga caaggcatcg ctttaaatac tttatctcca 120
 tcttcatcta cttctaaaaa taaatcttca aaagccgata acttcatccg gaaatgttta 180
 gaaatcctag aaatatcagc ttctgtaaat agaggacca aagttttaca acaattagca 240
 catgctgtac aatcaatttc t 261

<210> 204

<211> 390

<212> DNA

<213> Streptococcus agalactiae

<400> 204
 agtagaataa gtacaataac aataccaata aggataagcc caactttttt atatagagag 60
 gacttttctt caggacttaa aggatcggtt ggtctgagac tctcttcagt caaatatttt 120
 tttccatcta aggtatattg gaggagacca aagaacatac caatagcagc aagtgagaaa 180
 ccaagatgga aatttacttc ttgtccgagg taccacctta caatgggtga aataaaagca 240
 ccaagggtta taccaaaaac aaagatacta aaaccagcat cacgacgaga atcattttct 300
 ccatataaat taccaaccat ctctgataca ttgggtttta atagtccagt accaaggata 360
 attagagcaa tcgaaatgaa tagagctggt 390

<210> 205

<211> 78

<212> DNA

<213> Streptococcus agalactiae

<400> 205
 tcttttcttc gttcaaataa tttatgtgct tttaaagata agttcaaagtc tcgcacaagt 60

tctcgattag actgttta

78

<210> 206

<211> 123

<212> DNA

<213> Streptococcus agalactiae

<400> 206

atccattcat ttcatagaag gaaattaaat catcatggca agttaaactt ataccatctc 60

gttcttgaga aacaaccagg tctttcatcg ctgctaataa tgctgtacca atcccctgac 120

ctt 123

<210> 207

<211> 465

<212> DNA

<213> Streptococcus agalactiae

<400> 207

ctgtcttttt cgatagtatc ccatttatta actacaataa taataccttt accagcttca 60

tgtgcaaacc ctgcaatagc cttgtcatac tcacgaatac cttcctctgc attaatacacc 120

ataagaacaa catctgagcg gtcgatggcg cgcatagaac gcataacaga atattttctct 180

gtgttttcat ataccttacc agattttacgc ataccagcag tatcaatcat agtatactct 240

tgcccctggc tatcaacgaa attagtatca atagcatcgc gcgtagtacc agcaactggg 300

ctagcaataa cacggtcttc cccaaggatg gcattaatta aactagattt cccaacattt 360

ggacgtcaa tcaaactaaa acgaataata tctggatttt cattttcctc ttctaccgga 420

agattttcca caatagcatc caatatatca ccagtaccaa tacca 465

<210> 208

<211> 72

<212> DNA

<213> Streptococcus agalactiae

<400> 208

tgcccattcct cagatatagc tggaattaat ttaccacaaa atagcggaaa aatagataaa 60

caaaccgtta ca 72

<210> 209

GBS patentin.ST25

<211> 96

<212> DNA

<213> Streptococcus agalactiae

<400> 209

ccctttctca gaaatcattt ccataacaac gagaccagca ccaaattctt tagcgatagt 60

acgaaaagca gaattggtta tacctgccat cggtgc 96

<210> 210

<211> 150

<212> DNA

<213> Streptococcus agalactiae

<400> 210

gcgtcgacag gatcagcagc gaatccacag actacgccag gaaaactatt acaagcaagc 60

atcgctcaa ttcctgtccc acagcctgta ataacaaaat ctgcagcacc gctattaagt 120

aaaatagcag tcagtaaacc atttgtaca 150

<210> 211

<211> 141

<212> DNA

<213> Streptococcus agalactiae

<400> 211

gcaatgccta aacgttgctt cataccaccg gagtatgatg aaatcttctt ttacctaca 60

tcgcctaaac caacaagctc tagtaatcta ggaatttctt gtttagcttt cttttatca 120

acacctttta aggtagcgat a 141

<210> 212

<211> 147

<212> DNA

<213> Streptococcus agalactiae

<400> 212

cttttactga ttttaaaaaa tccagatact acacataaca ccaccataaa aagacaacct 60

aacaaacccc cttaaagtttt acgaaaaaga actgaaaaaa agagtattaa gcttatgaaa 120

agaataccga taaaccatgt tgcaccg 147

GBS patentin.ST25

<210> 213

<211> 132

<212> DNA

<213> streptococcus agalactiae

<400> 213

aaatttcaaag cacgaccacc aggtgttggt tcaggggttac caaacataac gcctactttt 60
tcccttaact ggttgataaa aattgcgatt gtctttgtct tgtaaatgga tgctgacaat 120
ttacgcattg ct 132

<210> 214

<211> 141

<212> DNA

<213> Streptococcus agalactiae

<400> 214

aaaagagtag ggatttgcca catatatcat gtatcccaat ccagctgttt ccacaacaat 60
aaatttagcc gttatttttac tcaattttcc tttaatataa tcgtacattc tattttccta 120
tctcaatatt tttcattttg g 141

<210> 215

<211> 237

<212> DNA

<213> streptococcus agalactiae

<400> 215

aattcaacga caagtgcctc attgatttct gggttaattt catcgcgttc tggaaggcga 60
gtcaatgaac cttcaagttt ttcagcatca aatgatacga aagctggacg tcctaaagta 120
gcttcaacag cttcaaggat tgcaggtact ttcattgatt tttcacgaac tgaaataact 180
tgtcctggag taacgcggta tgatgggata tcaacacgtt taccatcaac aaggata 237

<210> 216

<211> 111

<212> DNA

<213> Streptococcus agalactiae

<400> 216

acaagaccct tagtagaaat cttagttgat aaactagcgc catataagga agctaacttt 60

GBS patentin.ST25

tctcgaaatt cttgtacctt aggatactta gcatttgcag taactaacat t 111

<210> 217

<211> 861

<212> DNA

<213> Streptococcus agalactiae

<400> 217

agaactcgaa atgcaattag atatcctaaa gcaagcagcg gtgattatgg cacaaaaagg 60
 gaaataatca ctgctaataa ggataaatac agcatttcaa agatgtgtcg ctggctgaat 120
 atgccacgct caagttatta ctatcaagcc gtggagtcag tatctaaaac ggagtttgaa 180
 gaaactatta aaagaatttt tctcgatagc gagtctagat acggatccag aaaaatcaaa 240
 atatgcttga ataacgaagg tatcacactt tcacgtcgtc ggattcgacg cattatgaag 300
 cgactcaatt tggtttctgt ttatcagaaa gccaccttca aaccacattc tagaggcaag 360
 aatgaagccc ctattcccaa ccacttagac aggcaattta agcaagaaag accactacaa 420
 gccttagtca ctgacttaac ctatgttcgt gtaggcaatc gttgggctta tgtttgcctc 480
 atcattgacc tatacaaccg tgaaatcatc ggctgtctc ttggttgga caagaccgct 540
 gaactcgta agcaagccat acaaagcatc cttacgccc tgaccaaagt caagatgttc 600
 cattcagatc gtggcaaaga gtttgataat cagttaattg atgaaatatt ggaagccttt 660
 ggaatcacac gttcgcttag tcaggctggg tgtccttatg acaatgccgt agctgaaagt 720
 acgtatcgtg ctttcaaaaat tgaatttggt tatcaagaaa cttttcaatc gctggaagaa 780
 ctagctctta agactgaaaa ggcaacactt ttctgtacaa catttataaa gtgttgcctt 840
 ttcagggtttt taccaatgct a 861

<210> 218

<211> 428

<212> PRT

<213> Streptococcus agalactiae

<400> 218

Met Lys Lys Val Leu Thr Phe Leu Leu Cys Ser Leu Tyr Phe Val Ser
 1 5 10 15
 Ile Pro Ala Ile Ser Thr Glu Glu Pro Leu Thr Leu Ser Gln Asn Arg
 20 25 30
 Arg Tyr Ala Leu Thr Gln Thr Val Val Asp Lys Glu Met Tyr Phe Asp
 35 40 45

GBS patentin.ST25

Ala Ile Pro Glu Arg Pro Thr Thr Lys Ile Glu Ile Ser Ser Phe Gln
50 55 60

Asp Glu Ala Leu Thr Ile Thr Gly Glu Thr Leu Val Pro Asn Thr Leu
65 70 75 80

Leu Ser Ile Val Ser Leu Thr Ile Asn Ser Asn Gly Ile Pro Val Phe
85 90 95

Thr Leu Ser Asn Gly Gln Phe Ile Lys Ala Ser Arg Glu Ala Ile Phe
100 105 110

Asn Asp Leu Val Ser Lys Gln Gln Ser Val Ser Leu Asp Tyr Trp Leu
115 120 125

Lys Pro Ser Phe Val Thr Tyr Glu Ala Pro Tyr Thr Asn Gly Val Ser
130 135 140

Glu Val Lys Asn Asn Leu Lys Pro Tyr Ser Arg Val His Leu Val Glu
145 150 155 160

Gln Ala Glu Thr Glu His Gly Ile Tyr Tyr Lys Thr Asp Ser Gly Phe
165 170 175

Trp Ile Ser Val Glu Asp Leu Ser Val Ala Asp Asn Arg Met Ala Lys
180 185 190

Val Gln Glu Val Leu Leu Glu Lys Tyr Asn Lys Asp Lys Tyr Gly Ile
195 200 205

Tyr Ile Lys Gln Leu Asn Thr Gln Thr Val Ala Gly Ile Asn Ile Asp
210 215 220

Arg Ser Met Tyr Ser Ala Ser Ile Ala Lys Leu Ala Thr Leu Tyr Ala
225 230 235 240

Ser Gln Glu Gln Val Lys Leu Gly Lys Leu Ser Leu Asp Ser Lys Phe
245 250 255

Glu Tyr Lys Asp Asn Val Asn Gln Phe Pro Asn Ser Tyr Asp Pro Ser
260 265 270

Gly Ser Gly Lys Leu Glu Lys Lys Ala Asp His Lys Leu Tyr Thr Val
275 280 285

Lys Glu Leu Leu Glu Ala Thr Ala Lys Glu Ser Asp Asn Val Ala Thr
290 295 300

Asn Met Leu Gly Tyr Tyr Val Asn Asn Gln Tyr Asp Ser Met Phe Gln
305 310 315 320

GBS patentin.ST25

Thr Gln Val Asp Thr Ile Ser Gly Met His Trp Asp Met Lys Lys Arg
325 330 335

Gln Ile Ser Pro Gln Ala Ala Gly Lys Met Met Glu Ala Ile Tyr Tyr
340 345 350

Gln Asn Gly Asp Ile Val Asn Tyr Leu Ser Lys Thr Asp Phe Asp Asn
355 360 365

Thr Arg Ile Pro Lys Asn Ile Pro Val Lys Val Ala His Lys Ile Gly
370 375 380

Asp Ala Tyr Asp Tyr Lys His Asp Ala Ala Ile Val Tyr Ala Glu Gln
385 390 395 400

Pro Phe Ile Met Ile Ile Phe Thr Asp Lys Ser Ser Tyr Asp Asp Ile
405 410 415

Thr Lys Ile Ala Asp Asp Val Tyr Gln Val Leu Lys
420 425

<210> 219

<211> 447

<212> PRT

<213> streptococcus agalactiae

<400> 219

Met Lys Lys Arg Ile Leu Ser Ala Val Leu Val Ser Gly Val Thr Leu
1 5 10 15

Gly Thr Ala Ala Val Thr Val Asn Ala Asp Asp Phe Asp Ser Lys Ile
20 25 30

Ala Ala Thr Asp Ser Val Ile Asn Thr Leu Ser Gly Gln Gln Ala Ala
35 40 45

Ala Gln Asn Gln Val Thr Ala Ile Lys Gly Gln Val Gly Ala Leu Glu
50 55 60

Ser Gln Gln Ser Glu Leu Glu Ala Gln Asn Ala Gln Leu Glu Ala Val
65 70 75 80

Ser Gln Gln Leu Gly Gln Glu Ile Gln Thr Leu Ser Asn Lys Ile Val
85 90 95

Ala Arg Asn Glu Ser Leu Lys Lys Gln Val Arg Ser Ala Gln Lys Gly
100 105 110

GBS patentin.ST25

Asn Leu Thr Asn Tyr Ile Asn Thr Ile Leu Asn Ser Lys Ser Val Ser
115 120 125

Asp Ala Val Asn Arg Val Val Ala Ile Arg Glu Val Val Ser Ala Asn
130 135 140

Glu Lys Met Leu Ala Gln Gln Glu Ala Asp Lys Ala Ala Leu Glu Ala
145 150 155 160

Lys Gln Ile Glu Asn Gln Asn Ala Ile Asn Thr Val Ala Ala Asn Lys
165 170 175

Gln Ala Ile Glu Asn Asn Lys Ala Ala Leu Ala Thr Gln Arg Ala Gln
180 185 190

Leu Glu Ala Ala Gln Leu Glu Leu Ser Ala Gln Leu Thr Thr Val Gln
195 200 205

Asn Glu Lys Ala Ser Leu Ile Gln Ala Lys Ala Gln Ala Glu Glu Ala
210 215 220

Ala Arg Lys Ala Ala Glu Ala Gln Ala Ala Ala Glu Ala Lys Ala Gln
225 230 235 240

Ala Glu Ala Lys Ala Gln Ala Glu Ser Val Ala Lys Ala Gln Ala Ala
245 250 255

Ala Gln Val Glu Ser Ala Thr Ala Pro Thr Glu Thr Val Gln Thr Gln
260 265 270

Pro Arg Thr Glu Ile Lys Pro Ser Asn Leu Thr Ala Thr Ser Ser Ala
275 280 285

Thr Thr Val Ala Thr Thr Thr Ala Thr Ala Thr Asn Glu Pro Lys Val
290 295 300

Thr Gln Pro Ser Val Val Thr Lys Ala Val Glu Ala Pro Lys Ala Val
305 310 315 320

Val Ser Ser Thr Pro Arg Ala Val Ser Lys Pro Val Val Arg Ser Tyr
325 330 335

Asp Ser Ser Asn Thr Tyr Pro Met Gly Gln Cys Thr Trp Gly Ala Lys
340 345 350

Ser Met Ala Ser Trp Val Gly Asn Tyr Trp Gly Asn Ala Asn Gln Trp
355 360 365

Gly Ala Ser Ala Arg Ala Ala Gly Tyr Ser Val Gly Thr Thr Pro Arg
370 375 380

GBS patentin.ST25

Val Gly Ala Val Ala Val Trp Pro Tyr Asp Gly Gly Gly Tyr Gly His
385 390 395 400

Val Ala Val Val Thr Ser Val Ala Asn Asn Ser Ser Ile Gln Val Met
405 410 415

Glu Ser Asn Tyr Ala Gly Asn Met Ser Ile Gly Asn Tyr Arg Gly Ser
420 425 430

Phe Asn Pro Ser Ala Ser Gly Ser Val Tyr Tyr Ile Tyr Pro Asn
435 440 445

<210> 220

<211> 1241

<212> PRT

<213> streptococcus agalactiae

<400> 220

Met Asn Lys Arg Ile Phe Val Glu Lys Lys Ala Asp Phe Asp Ile Lys
1 5 10 15

Ser Ala Ser Leu Val Lys Glu Leu Thr His Asn Leu Gln Leu Thr Ser
20 25 30

Leu Lys Asp Leu Arg Ile Val Gln Val Tyr Asp Val Phe Asn Leu Ala
35 40 45

Glu Asp Leu Leu Ala Arg Ala Glu Lys His Ile Phe Ser Glu Gln Val
50 55 60

Thr Asp Cys Leu Leu Thr Glu Thr Glu Ile Thr Ala Glu Leu Asp Lys
65 70 75 80

Val Ala Phe Phe Ala Ile Glu Ala Leu Pro Gly Gln Phe Asp Gln Arg
85 90 95

Ala Ala Ser Ser Gln Glu Ser Leu Leu Leu Gly Ser Asp Ser Gln
100 105 110

Val Lys Val Asn Thr Ala Gln Leu Tyr Leu Val Asn Lys Asp Ile Ala
115 120 125

Glu Ala Glu Leu Glu Ala Val Lys Asn Tyr Leu Leu Asn Pro Val Asp
130 135 140

Ser Arg Phe Lys Asp Ile Thr Leu Pro Leu Glu Glu Gln Ala Phe Ser
145 150 155 160

GBS patentin.ST25

Val Ser Asp Lys Thr Ile Pro Ser Leu Asp Phe Phe Glu Thr Tyr Lys
165 170 175

Ala Asp Asp Phe Ala Ala Tyr Lys Ala Glu Gln Gly Leu Ala Met Glu
180 185 190

Val Asp Asp Leu Leu Phe Ile Gln Asp Tyr Phe Lys Ser Ile Gly Arg
195 200 205

Val Pro Thr Glu Thr Glu Leu Lys Val Leu Asp Thr Tyr Trp Ser Asp
210 215 220

His Cys Arg His Thr Thr Phe Glu Thr Glu Leu Lys Asn Ile Asp Phe
225 230 235 240

Ser Ala Ser Lys Phe Gln Lys Gln Leu Gln Ala Thr Tyr Asp Lys Tyr
245 250 255

Ile Ala Met Arg Asp Glu Leu Gly Arg Ser Glu Lys Pro Gln Thr Leu
260 265 270

Met Asp Met Ala Thr Ile Phe Gly Arg Tyr Glu Arg Ala Asn Gly Arg
275 280 285

Leu Asp Asp Met Glu Val Ser Asp Glu Ile Asn Ala Cys Ser Val Glu
290 295 300

Ile Glu Val Asp Val Asp Gly Val Lys Glu Pro Trp Leu Leu Met Phe
305 310 315 320

Lys Asn Glu Thr His Asn His Pro Thr Glu Ile Glu Pro Phe Gly Gly
325 330 335

Ala Ala Thr Cys Ile Gly Gly Ala Ile Arg Asp Pro Leu Ser Gly Arg
340 345 350

Ser Tyr Val Tyr Gln Ala Met Arg Ile Ser Gly Ala Gly Asp Ile Thr
355 360 365

Thr Pro Ile Ala Glu Thr Arg Ala Gly Lys Leu Pro Gln Gln Val Ile
370 375 380

Ser Lys Thr Ala Ala His Gly Tyr Ser Ser Tyr Gly Asn Gln Ile Gly
385 390 395 400

Leu Ala Thr Thr Tyr Val Arg Glu Tyr Phe His Pro Gly Phe Val Ala
405 410 415

Lys Arg Met Glu Leu Gly Ala Val Val Gly Ala Ala Pro Lys Glu Asn
420 425 430

GBS patentin.ST25

Val Val Arg Glu Lys Pro Glu Ala Gly Asp Val Val Ile Leu Leu Gly
 435 440 445
 Gly Lys Thr Gly Arg Asp Gly Val Gly Gly Ala Thr Gly Ser Ser Lys
 450 455 460
 Val Gln Thr Val Glu Ser Val Glu Thr Ala Gly Ala Glu Val Gln Lys
 465 470 475 480
 Gly Asn Ala Ile Glu Glu Arg Lys Ile Gln Arg Leu Phe Arg Asn Gly
 485 490 495
 Asn Val Thr Arg Leu Ile Lys Lys Ser Asn Asp Phe Gly Ala Gly Gly
 500 505 510
 Val Cys Val Ala Ile Gly Glu Leu Ala Asp Gly Leu Glu Ile Asp Leu
 515 520 525
 Asp Lys Val Pro Leu Lys Tyr Gln Gly Leu Asn Gly Thr Glu Ile Ala
 530 535 540
 Ile Ser Glu Ser Gln Glu Arg Met Ser Val Val Val Arg Pro Ser Asp
 545 550 555 560
 Val Asp Thr Phe Ile Ala Ala Cys Asn Lys Glu Asn Ile Asp Ala Val
 565 570 575
 Val Val Ala Thr Ile Thr Ala Lys Pro Asn Leu Val Met Thr Trp Asp
 580 585 590
 Gly Glu Thr Ile Val Asp Leu Glu Arg Arg Phe Leu Asp Thr Asn Gly
 595 600 605
 Val Arg Val Val Val Asp Ala Lys Val Val Asp Lys Asp Leu Thr Val
 610 615 620
 Pro Glu Val Arg Thr Thr Ser Ala Glu Thr Leu Glu Ala Asp Thr Leu
 625 630 635 640
 Lys Val Leu Ser Asp Leu Asn His Ala Ser Gln Lys Gly Leu Gln Thr
 645 650 655
 Ile Phe Asp Ser Ser Val Gly Arg Ser Thr Val Asn His Pro Ile Gly
 660 665 670
 Gly Arg Tyr Gln Ile Thr Pro Thr Glu Ser Ser Val Gln Lys Leu Pro
 675 680 685
 Val Gln His Gly Val Thr Thr Thr Ala Ser Val Met Ala Gln Gly Tyr
 690 695 700

GBS patentin.ST25

Asn Pro Tyr Ile Ala Glu Trp Ser Pro Tyr His Gly Ala Ala Tyr Ala
705 710 715 720

Val Ile Glu Ala Thr Ala Arg Leu Val Ala Thr Gly Ala Asp Trp Ser
725 730 735

Arg Ala Arg Phe Ser Tyr Gln Glu Tyr Phe Glu Arg Met Asp Lys Gln
740 745 750

Ala Glu Arg Phe Gly Gln Pro Val Ser Ala Leu Leu Gly Ser Ile Glu
755 760 765

Ala Gln Ile Gln Leu Gly Leu Pro Ser Ile Gly Gly Lys Asp Ser Met
770 775 780

Ser Gly Thr Phe Glu Glu Leu Thr Val Pro Pro Thr Leu Val Ala Phe
785 790 795 800

Gly Val Thr Thr Ala Asp Ser Arg Lys Val Leu Ser Pro Glu Phe Lys
805 810 815

Ala Ala Gly Glu Asn Ile Tyr Tyr Ile Pro Gly Gln Ala Ile Ser Glu
820 825 830

Asp Ile Asp Phe Asp Leu Ile Lys Ala Asn Phe Ser Gln Phe Glu Thr
835 840 845

Ile Gln Ala Gln His Lys Ile Thr Ala Ala Ser Ala Val Lys Tyr Gly
850 855 860

Gly Val Leu Glu Ser Leu Ala Leu Met Thr Phe Gly Asn Arg Ile Gly
865 870 875 880

Ala Ser Val Glu Ile Ala Glu Leu Asp Ser Ser Leu Thr Ala Gln Leu
885 890 895

Gly Gly Phe Val Phe Thr Ser Ala Glu Glu Ile Ala Asp Ser Val Lys
900 905 910

Ile Gly Gln Thr Gln Ala Ala Phe Thr Leu Thr Val Asn Gly Asn Asp
915 920 925

Leu Ala Gly Ala Ser Leu Leu Ser Val Phe Glu Gly Lys Leu Glu Glu
930 935 940

Val Tyr Pro Thr Glu Phe Glu Gln Ala Asp Ala Leu Glu Glu Val Pro
945 950 955 960

Ala Val Val Ser Asp Thr Val Ile Lys Ala Lys Glu Thr Ile Glu Lys
965 970 975

GBS patentin.ST25

Pro Val Val Tyr Ile Pro Val Phe Pro Gly Thr Asn Ser Glu Tyr Asp
980 985 990

Ser Ala Lys Ala Phe Glu Gln Val Gly Ala Ser Val Asn Leu Val Ala
995 1000 1005

Phe Val Thr Leu Asn Glu Ala Ala Ile Ala Asp Ser Val Asp Thr
1010 1015 1020

Met Val Ala Asn Ile Ala Lys Ala Asn Ile Ile Phe Phe Ala Gly
1025 1030 1035

Gly Phe Ser Ala Ala Asp Glu Pro Asp Gly Ser Ala Lys Phe Ile
1040 1045 1050

Val Asn Ile Leu Leu Asn Lys Lys Val Arg Ala Ala Ile Asp Ser
1055 1060 1065

Phe Ile Glu Lys Gly Gly Leu Ile Ile Gly Ile Cys Asn Gly Phe
1070 1075 1080

Gln Ala Leu Val Lys Ser Gly Leu Leu Pro Tyr Gly Asn Phe Glu
1085 1090 1095

Glu Ala Gly Glu Thr Ser Pro Thr Leu Phe Tyr Asn Asp Ala Asn
1100 1105 1110

Gln His Val Ala Lys Met Val Glu Thr Arg Ile Ala Asn Thr Asn
1115 1120 1125

Ser Pro Trp Leu Val Gly Val Glu Val Gly Asp Ile His Ala Ile
1130 1135 1140

Pro Val Ser His Gly Glu Gly Lys Phe Val Val Ser Ala Ser Glu
1145 1150 1155

Phe Ala Glu Leu Arg Asp Asn Gly Gln Ile Trp Ser Gln Tyr Val
1160 1165 1170

Asp Phe Asp Gly Gln Pro Ser Met Asp Ser Lys Tyr Asn Pro Asn
1175 1180 1185

Gly Ser Val Asn Ala Ile Glu Gly Ile Thr Ser Lys Asn Gly Gln
1190 1195 1200

Ile Ile Gly Lys Met Gly His Ser Glu Arg Trp Glu Asp Gly Leu
1205 1210 1215

Phe Gln Asn Ile Pro Gly Asn Lys Asp Gln Ala Leu Phe Ala Ser
1220 1225 1230

GBS patentin.ST25

Ala Val Lys Tyr Phe Thr Gly Lys
1235 1240

<210> 221

<211> 434

<212> PRT

<213> streptococcus agalactiae

<400> 221

Met Lys Met Asn Lys Lys Val Leu Leu Thr Ser Thr Met Ala Ala Ser
1 5 10 15

Leu Leu Ser Val Ala Ser Val Gln Ala Gln Glu Thr Asp Thr Thr Trp
20 25 30

Thr Ala Arg Thr Val Ser Glu Val Lys Ala Asp Leu Val Lys Gln Asp
35 40 45

Asn Lys Ser Ser Tyr Thr Val Lys Tyr Gly Asp Thr Leu Ser Val Ile
50 55 60

Ser Glu Ala Met Ser Ile Asp Met Asn Val Leu Ala Lys Ile Asn Asn
65 70 75 80

Ile Ala Asp Ile Asn Leu Ile Tyr Pro Glu Thr Thr Leu Thr Val Thr
85 90 95

Tyr Asp Gln Lys Ser His Thr Ala Thr Ser Met Lys Ile Glu Thr Pro
100 105 110

Ala Thr Asn Ala Ala Gly Gln Thr Thr Ala Thr Val Asp Leu Lys Thr
115 120 125

Asn Gln Val Ser Val Ala Asp Gln Lys Val Ser Leu Asn Thr Ile Ser
130 135 140

Glu Gly Met Thr Pro Glu Ala Ala Thr Thr Ile Val Ser Pro Met Lys
145 150 155 160

Thr Tyr Ser Ser Ala Pro Ala Leu Lys Ser Lys Glu Val Leu Ala Gln
165 170 175

Glu Gln Ala Val Ser Gln Ala Ala Ala Asn Glu Gln Val Ser Pro Ala
180 185 190

Pro Val Lys Ser Ile Thr Ser Glu Val Pro Ala Ala Lys Glu Glu Val
195 200 205

GBS patentin.ST25

Lys Pro Thr Gln Thr Ser Val Ser Gln Ser Thr Thr Val Ser Pro Ala
 210 215 220

Ser Val Ala Ala Glu Thr Pro Ala Pro Val Ala Lys Val Ala Pro Val
 225 230 235 240

Arg Thr Val Ala Ala Pro Arg Val Ala Ser Val Lys Val Val Thr Pro
 245 250 255

Lys Val Glu Thr Gly Ala Ser Pro Glu His Val Ser Ala Pro Ala Val
 260 265 270

Pro Val Thr Thr Thr Ser Pro Ala Thr Asp Ser Lys Leu Gln Ala Thr
 275 280 285

Glu Val Lys Ser Val Pro Val Ala Gln Lys Ala Pro Thr Ala Thr Pro
 290 295 300

Val Ala Gln Pro Ala Ser Thr Thr Asn Ala Val Ala Ala His Pro Glu
 305 310 315 320

Asn Ala Gly Leu Gln Pro His Val Ala Ala Tyr Lys Glu Lys Val Ala
 325 330 335

Ser Thr Tyr Gly Val Asn Glu Phe Ser Thr Tyr Arg Ala Gly Asp Pro
 340 345 350

Gly Asp His Gly Lys Gly Leu Ala Val Asp Phe Ile Val Gly Thr Asn
 355 360 365

Gln Ala Leu Gly Asn Lys Val Ala Gln Tyr Ser Thr Gln Asn Met Ala
 370 375 380

Ala Asn Asn Ile Ser Tyr Val Ile Trp Gln Gln Lys Phe Tyr Ser Asn
 385 390 395 400

Thr Asn Ser Ile Tyr Gly Pro Ala Asn Thr Trp Asn Ala Met Pro Asp
 405 410 415

Arg Gly Gly Val Thr Ala Asn His Tyr Asp His Val His Val Ser Phe
 420 425 430

Asn Lys

<210> 222

<211> 300

<212> PRT

<213> Streptococcus agalactiae

<400> 222

Met Leu Lys His Phe Gly Ser Lys Val Arg Asn Leu Arg Val Thr Arg
1 5 10 15

Asn Ile Thr Arg Glu Asp Phe Cys Gly Asp Glu Thr Glu Leu Ser Val
20 25 30

Arg Gln Leu Ala Arg Ile Glu Ser Gly Gln Ser Ile Pro Asn Leu Thr
35 40 45

Lys Ala His Tyr Ile Ala Lys Gln Leu Asn Val Lys Leu Asp Ile Leu
50 55 60

Thr Gly Gly Glu Ser Leu Glu Leu Pro Lys Arg Tyr Lys Glu Leu Lys
65 70 75 80

Tyr Lys Leu Leu Arg Thr Pro Thr Tyr Gly Asp Ala Asn Arg Leu Ala
85 90 95

Val Arg Glu Ala Tyr Phe Asp Glu Ile Tyr Glu Val Phe Tyr Glu Glu
100 105 110

Leu Pro Glu Asp Glu Arg Leu Ile Ile Asp Cys Met Gln Ser Lys Leu
115 120 125

Asp Val His Phe Ser Val Asn Asp Asn Phe Gly Ile Thr Ile Leu His
130 135 140

Asp Tyr Phe Asp Gln Ile Lys Lys Lys Lys Glu Tyr Thr Thr Asn Asp
145 150 155 160

Phe Val Met Ile Asp Leu Tyr Leu Leu Cys Phe Ser Ile Asn Tyr Gly
165 170 175

Met Lys Ser Leu Tyr Ser Leu Glu Asn Tyr His Phe Ile Met Ser Lys
180 185 190

Leu Leu Glu Gln Asp Asn Leu Leu Pro Glu Asp Asn Phe Gln Leu Asn
195 200 205

Asn Val Leu Leu Asn His Val Glu Leu Ala Phe Gln Phe Lys Gln Lys
210 215 220

Lys Tyr Val Gln Gln Ile Ile His Arg Ser Asn Ala Ile Met Thr Glu
225 230 235 240

Ile His Asp Phe Gln Lys Arg Pro Ile Leu Ser Leu Ile Glu Trp Lys
245 250 255

GBS patentin.ST25

Tyr Leu Leu Ile Ile Glu Lys Asp Arg Thr Lys Ala Glu Thr Cys Phe
260 265 270

Lys Gln Ser Ile Leu Phe Ala Glu Leu Ile Gly Asp Leu Tyr Leu Lys
275 280 285

Gly Lys Leu Ile Glu Glu Trp Asn Lys Asp Leu Thr
290 295 300

<210> 223

<211> 880

<212> PRT

<213> Streptococcus agalactiae

<400> 223

Met Thr Glu Lys Thr Lys Ala Val Glu Thr Thr Asp Val Ala Leu Ala
1 5 10 15

Ile Asp Thr Leu Val Gln Asn Gly Leu Lys Ala Leu Asp Glu Met Arg
20 25 30

Gln Leu Asn Gln Glu Gln Val Asp Tyr Ile Val Ala Lys Ala Ser Val
35 40 45

Ala Ala Leu Asp Ala His Gly Glu Leu Ala Leu His Ala Val Glu Glu
50 55 60

Thr Gly Arg Gly Val Phe Glu Asp Lys Ala Thr Lys Asn Leu Phe Ala
65 70 75 80

Cys Glu His Val Val Asn Asn Met Arg His Thr Lys Thr Val Gly Val
85 90 95

Ile Glu Glu Asp Asp Val Thr Gly Leu Thr Leu Ile Ala Glu Pro Val
100 105 110

Gly Val Val Cys Gly Ile Thr Pro Thr Thr Asn Pro Thr Ser Thr Ala
115 120 125

Ile Phe Lys Ser Leu Ile Ser Leu Lys Thr Arg Asn Pro Ile Ile Phe
130 135 140

Ala Phe His Pro Ser Ala Gln Glu Ser Ser Ala His Ala Ala Arg Ile
145 150 155 160

Val Arg Asp Ala Ala Ile Ala Ala Gly Ala Pro Glu Asn Cys Val Gln
165 170 175

GBS patentin.ST25

Trp Ile Glu Gln Pro Ser Ile Asp Ala Thr Asn Ala Leu Met Asn His
180 185 190

Asp Gly Ile Ala Thr Ile Leu Ala Thr Gly Gly Asn Ala Met Val Lys
195 200 205

Ala Ala Tyr Ser Cys Gly Lys Pro Ala Leu Gly Val Gly Ala Gly Asn
210 215 220

Val Pro Ala Tyr Val Glu Lys Ser Ala Asn Ile Arg Gln Ala Ala His
225 230 235 240

Asp Ile Val Met Ser Lys Ser Phe Asp Asn Gly Met Val Cys Ala Ser
245 250 255

Glu Gln Ala Val Ile Ile Asp Lys Glu Ile Tyr Lys Glu Phe Val Glu
260 265 270

Glu Phe Lys Ser Tyr His Thr Tyr Phe Val Asn Lys Lys Glu Lys Ala
275 280 285

Leu Leu Glu Glu Phe Cys Phe Gly Ala Lys Ala Asn Ser Lys Asn Cys
290 295 300

Ala Gly Ala Lys Leu Asn Pro Asn Ile Val Gly Lys Ser Ala Val Trp
305 310 315 320

Ile Ala Glu Gln Ala Gly Phe Thr Val Pro Glu Gly Thr Asn Ile Leu
325 330 335

Ala Ala Glu Cys Thr Glu Val Ser Glu Lys Glu Pro Leu Thr Arg Glu
340 345 350

Lys Leu Ser Pro Val Ile Ala Val Leu Lys Ala Glu Ser Thr Glu Asp
355 360 365

Gly Val Glu Lys Ala Arg Gln Met Val Glu Phe Asn Gly Leu Gly His
370 375 380

Ser Ala Ala Ile His Thr Lys Asp Ala Asp Leu Ala Arg Glu Phe Gly
385 390 395 400

Thr Arg Ile Arg Ala Ile Arg Val Ile Trp Asn Ser Pro Ser Thr Phe
405 410 415

Gly Gly Ile Gly Asp Val Tyr Asn Ala Phe Leu Pro Ser Leu Thr Leu
420 425 430

Gly Cys Gly Ser Tyr Gly Arg Asn Ser Val Gly Asp Asn Val Ser Ala
435 440 445

GBS patentin.ST25

Ile Asn Leu Leu Asn Ile Lys Lys Val Gly Arg Arg Arg Asn Asn Met
450 455 460

Gln Trp Phe Lys Val Pro Ser Lys Thr Tyr Phe Glu Arg Asp Ser Ile
465 470 475 480

Gln Tyr Leu Gln Lys Cys Arg Asp Val Glu Arg Val Met Ile Val Thr
485 490 495

Asp His Ala Met Val Glu Leu Gly Phe Leu Asp Arg Ile Ile Glu Gln
500 505 510

Leu Asp Leu Arg Arg Asn Lys Val Val Tyr Gln Ile Phe Ala Glu Val
515 520 525

Glu Pro Asp Pro Asp Ile Thr Thr Val Met Lys Gly Thr Asp Leu Met
530 535 540

Arg Thr Phe Lys Pro Asp Thr Ile Ile Ala Leu Gly Gly Gly Ser Pro
545 550 555

Met Asp Ala Ala Lys Val Met Trp Leu Phe Tyr Glu Gln Pro Glu Val
565 570 575

Asp Phe His Asp Leu Val Gln Lys Phe Met Asp Ile Arg Lys Arg Ala
580 585 590

Phe Lys Phe Pro Glu Leu Gly Lys Lys Thr Lys Phe Val Ala Ile Pro
595 600 605

Thr Thr Ser Gly Thr Gly Ser Glu Val Thr Pro Phe Ala Val Ile Ser
610 615 620

Asp Lys Ala Asn Asn Arg Lys Tyr Pro Ile Ala Asp Tyr Ser Leu Thr
625 630 635 640

Pro Thr Val Ala Ile Val Asp Pro Ala Leu Val Met Thr Val Pro Gly
645 650 655

Phe Ile Ala Ala Asp Thr Gly Met Asp Val Leu Thr His Ala Thr Glu
660 665 670

Ala Tyr Val Ser Gln Met Ala Asn Asp Tyr Thr Asp Gly Leu Ala Leu
675 680 685

Gln Ala Ile Lys Ile Val Phe Asp Tyr Leu Glu Arg Ser Val Lys Asp
690 695 700

Ala Asp Phe Glu Ala Arg Glu Lys Met His Asn Ala Ser Thr Met Ala
705 710 715 720

GBS patentin.ST25

Gly Met Ala Phe Ala Asn Ala Phe Leu Gly Ile Ser His Ser Met Ala
725 730 735

His Lys Ile Gly Ala Gln Phe His Thr Val His Gly Arg Thr Asn Ala
740 745 750

Ile Leu Leu Pro Tyr Val Ile Arg Tyr Asn Gly Thr Arg Pro Ala Lys
755 760 765

Thr Ala Thr Trp Pro Lys Tyr Asn Tyr Tyr Arg Ala Asp Glu Lys Tyr
770 775 780

Gln Asp Ile Ala Lys Leu Leu Gly Leu Pro Ala Ala Thr Pro Glu Glu
785 790 795 800

Ala Val Glu Ser Tyr Ala Lys Ala Val Tyr Asp Leu Gly Thr Arg Leu
805 810 815

Gly Ile Lys Met Asn Phe Arg Asp Gln Gly Ile Asp Glu Lys Glu Trp
820 825 830

Lys Glu Lys Ser Arg Glu Leu Ala Phe Leu Ala Tyr Glu Asp Gln Cys
835 840 845

Ser Pro Ala Asn Pro Arg Leu Pro Met Val Asp His Met Gln Glu Ile
850 855 860

Ile Glu Asp Ala Tyr Tyr Gly Tyr Glu Glu Arg Pro Gly Arg Arg Lys
865 870 875 880

<210> 224

<211> 277

<212> PRT

<213> Streptococcus agalactiae

<400> 224

Val Gly Ile Lys Val Tyr Lys Pro Thr Thr Asn Gly Arg Arg Asn Met
1 5 10 15

Thr Ser Leu Asp Phe Ala Glu Ile Thr Thr Asn Thr Pro Glu Lys Ser
20 25 30

Leu Leu Val Ser Leu Lys Asn Lys Ala Gly Arg Asn Asn Asn Gly Arg
35 40 45

Ile Thr Val Arg His Gln Gly Gly Gly His Lys Arg His Tyr Arg Leu
50 55 60

GBS patentin.ST25

Ile Asp Phe Lys Arg Asn Lys Asp Gly Val Glu Ala Val Val Lys Thr
65 70 75 80

Ile Glu Tyr Asp Pro Asn Arg Thr Ala Asn Ile Ala Leu Val His Tyr
85 90 95

Thr Asp Gly Val Lys Ala Tyr Ile Leu Ala Pro Lys Gly Leu Glu Val
100 105 110

Gly Gln Arg Ile Ile Ser Gly Pro Glu Ala Asp Ile Lys Val Gly Asn
115 120 125

Ala Leu Pro Leu Ala Asn Ile Pro Val Gly Thr Val Ile His Asn Ile
130 135 140

Glu Leu Gln Pro Gly Lys Gly Ala Glu Leu Ile Arg Ala Ala Gly Ala
145 150 155 160

Ser Ala Gln Val Leu Gly Gln Glu Gly Lys Tyr Val Leu Val Arg Leu
165 170 175

Gln Ser Gly Glu Val Arg Met Ile Leu Gly Thr Cys Arg Ala Thr Ile
180 185 190

Gly Thr Val Gly Asn Glu Gln Gln Ser Leu Val Asn Ile Gly Lys Ala
195 200 205

Gly Arg Asn Arg Trp Lys Gly Val Arg Pro Thr Val Arg Gly Ser Val
210 215 220

Met Asn Pro Asn Asp His Pro His Gly Gly Gly Glu Gly Lys Ala Pro
225 230 235 240

Val Gly Arg Lys Ala Pro Ser Thr Pro Trp Gly Lys Pro Ala Leu Gly
245 250 255

Leu Lys Thr Arg Asn Lys Lys Ala Lys Ser Asp Lys Leu Ile Val Arg
260 265 270

Arg Arg Asn Gln Lys
275

<210> 225

<211> 312

<212> PRT

<213> streptococcus agalactiae

GBS patentin.ST25

<400> 225

Met Ile Glu Phe Glu Lys Pro Ile Ile Thr Lys Ile Asp Glu Asn Lys
1 5 10 15

Asp Tyr Gly Arg Phe Val Ile Glu Pro Leu Glu Arg Gly Tyr Gly Thr
20 25 30

Thr Leu Gly Asn Ser Leu Arg Arg Val Leu Leu Ser Ser Leu Pro Gly
35 40 45

Ala Ala Val Thr Ser Ile Lys Ile Asp Gly Val Leu His Glu Phe Asp
50 55 60

Thr Ile Pro Gly Val Arg Glu Asp Val Met Gln Ile Ile Leu Asn Val
65 70 75 80

Lys Gly Leu Ala Val Lys Ser Tyr Val Glu Asp Glu Lys Ile Ile Glu
85 90 95

Leu Asp Val Glu Gly Pro Ala Glu Ile Thr Ala Gly Asp Ile Leu Thr
100 105 110

Asp Ser Asp Ile Glu Ile Val Asn Pro Asp His Tyr Leu Phe Thr Ile
115 120 125

Ala Glu Gly His Ser Leu Lys Ala Thr Met Thr Val Ala Lys Asn Arg
130 135 140

Gly Tyr Val Pro Ala Glu Gly Asn Lys Lys Asp Asp Ala Pro Val Gly
145 150 155 160

Thr Leu Ala Val Asp Ser Ile Tyr Thr Pro Val Lys Lys Val Asn Tyr
165 170 175

Gln Val Glu Pro Ala Arg Val Gly Ser Asn Asp Gly Phe Asp Lys Leu
180 185 190

Thr Ile Glu Ile Met Thr Asn Gly Thr Ile Ile Pro Glu Asp Ala Leu
195 200 205

Gly Leu Ser Ala Arg Val Leu Ile Glu His Leu Asn Leu Phe Thr Asp
210 215 220

Leu Thr Glu Val Ala Lys Ala Thr Glu Val Met Lys Glu Thr Glu Lys
225 230 235 240

Val Asn Asp Glu Lys Val Leu Asp Arg Thr Ile Glu Glu Leu Asp Leu
245 250 255

Ser Val Arg Ser Tyr Asn Cys Leu Lys Arg Ala Gly Ile Asn Thr Val
260 265 270

GBS patentin.ST25

Phe Asp Leu Thr Glu Lys Thr Glu Pro Glu Met Met Lys Val Arg Asn
275 280 285

Leu Gly Arg Lys Ser Leu Glu Glu Val Lys Ile Lys Leu Ala Asp Leu
290 295 300

Gly Leu Gly Leu Lys Asn Asp Lys
305 310

<210> 226

<211> 308

<212> PRT

<213> Streptococcus agalactiae

<400> 226

Met Lys Lys Ile Arg Leu Ser Lys Phe Ile Lys Met Ile Val Val Ile
1 5 10 15

Leu Phe Leu Ile Ser Val Ala Ala Ser Phe Tyr Phe Phe His Val Ala
20 25 30

Gln Val Arg Asp Asp Lys Ser Phe Ile Ser Asn Gly Gln Arg Lys Pro
35 40 45

Gly Asn Ser Leu Tyr Ala Tyr Asp Lys Ser Phe Asp Lys Leu Leu Lys
50 55 60

Gln Lys Ile Glu Met Thr Asn Gln Asn Ile Lys Gln Val Ala Trp Tyr
65 70 75 80

Val Pro Ala Ala Lys Lys Thr His Lys Thr Ala Val Val Val His Gly
85 90 95

Phe Ala Asn Ser Lys Glu Asn Met Lys Ala Tyr Gly Trp Leu Phe His
100 105 110

Lys Leu Gly Tyr Asn Val Leu Met Pro Asp Asn Ile Ala His Gly Glu
115 120 125

Ser His Gly Gln Leu Ile Gly Tyr Gly Trp Asn Asp Arg Glu Asn Ile
130 135 140

Ile Lys Trp Thr Glu Met Ile Val Asp Lys Asn Pro Ser Ser Gln Ile
145 150 155 160

Thr Leu Phe Gly Val Ser Met Gly Gly Ala Thr Val Met Met Ala Ser
165 170 175

GBS patentin.ST25

Gly Glu Lys Leu Pro Ser Gln Val Val Asn Ile Ile Glu Asp Cys Gly
180 185 190

Tyr Ser Ser Val Trp Asp Glu Leu Lys Phe Gln Ala Lys Glu Met Tyr
195 200 205

Gly Leu Pro Ala Phe Pro Leu Leu Tyr Glu Val Ser Thr Ile Ser Lys
210 215 220

Ile Arg Ala Gly Phe Ser Tyr Gly Gln Ala Ser Ser Val Glu Gln Leu
225 230 235 240

Lys Lys Asn Asn Leu Pro Ala Leu Phe Ile His Gly Asp Lys Asp Asn
245 250 255

Phe Val Pro Thr Ser Met Val Tyr Asp Asn Tyr Lys Ala Thr Ala Gly
260 265 270

Lys Lys Glu Leu Tyr Ile Val Lys Gly Ala Lys His Ala Lys Ser Phe
275 280 285

Glu Thr Glu Pro Glu Lys Tyr Glu Lys Arg Ile Ser Ser Phe Leu Lys
290 295 300

Lys Tyr Glu Lys
305

<210> 227

<211> 148

<212> PRT

<213> Streptococcus agalactiae

<400> 227

Met Ser Lys Val Arg Gly Phe Glu Leu Val Ser Gln Phe Ser Asn Lys
1 5 10 15

Glu Leu Leu Pro Lys Arg Glu Thr Ala His Ala Ala Gly Tyr Asp Leu
20 25 30

Lys Val Ala Lys Lys Thr Val Ile Glu Pro Gly Glu Ile Thr Leu Val
35 40 45

Pro Thr Gly Ile Lys Ala His Met Gln Pro Gly Glu Val Leu Tyr Leu
50 55 60

Tyr Asp Arg Ser Ser Asn Pro Arg Lys Lys Gly Ile Val Leu Ile Asn
65 70 75 80

GBS patentin.ST25

Ser Val Gly Val Ile Asp Gly Asp Tyr Tyr Asn Asn Gln Val Asn Glu
85 90 95

Gly His Ile Phe Ala Gln Met Gln Asn Ile Thr Asp Gln Ala Val Ile
100 105 110

Leu Glu Glu Gly Glu Arg Ile Val Gln Ala Val Phe Ala Pro Phe Leu
115 120 125

Leu Ala Asp Asp Asp Gln Ala Thr Gly Met Arg Thr Gly Gly Phe Gly
130 135 140

Ser Thr Gly Lys
145

<210> 228

<211> 322

<212> PRT

<213> Streptococcus agalactiae

<400> 228

Met Lys Phe Gly Lys Lys Leu Gly Phe Leu Ala Leu Leu Met Ser Ile
1 5 10 15

Val Leu Ile Leu Gly Ala Cys Gly Lys Thr Gly Leu Gly Asn Ser Thr
20 25 30

Gly Asn Ser Thr Lys Asn Val Thr Lys Lys Ser Ala Lys Asn Leu Lys
35 40 45

Leu Gly Val Ser Ile Ser Thr Thr Asn Asn Pro Tyr Phe Val Ala Met
50 55 60

Lys Asp Gly Ile Asp Lys Tyr Ala Ser Asn Lys Lys Ile Ser Ile Lys
65 70 75 80

Val Ala Asp Ala Gln Asp Asp Ala Ala Arg Gln Ala Asp Asp Val Gln
85 90 95

Asn Phe Ile Ser Gln Asn Val Asp Ala Ile Leu Ile Asn Pro Val Asp
100 105 110

Ser Lys Ala Ile Val Thr Ala Ile Lys Ser Ala Asn Asn Ala Asn Ile
115 120 125

Pro Val Ile Leu Met Asp Arg Gly Ser Glu Gly Gly Lys Val Leu Thr
130 135 140

GBS patentin.ST25

Thr Val Ala Ser Asp Asn Val Ala Ala Gly Lys Met Ala Ala Asp Tyr
145 150 155 160

Ala Val Lys Lys Leu Gly Lys Lys Ala Lys Ala Phe Glu Leu Ser Gly
165 170 175

Val Pro Gly Ala Ser Ala Thr Val Asp Arg Gly Lys Gly Phe His Ser
180 185 190

Val Ala Lys Ser Lys Leu Asp Ile Leu Ser Ser Gln Ser Ala Asn Phe
195 200 205

Asp Arg Ala Lys Ala Leu Asn Thr Thr Gln Asn Met Ile Gln Gly His
210 215 220

Lys Asp Val Gln Ile Ile Phe Ala Gln Asn Asp Glu Met Ala Leu Gly
225 230 235 240

Ala Ala Gln Ala Val Lys Ser Ala Gly Leu Gln Asn Val Leu Ile Val
245 250 255

Gly Ile Asp Gly Gln Pro Asp Ala His Asp Ala Ile Lys Lys Gly Asp
260 265 270

Ile Ser Ala Thr Ile Ala Gln Gln Pro Ala Lys Met Gly Glu Ile Ala
275 280 285

Ile Gln Ala Ala Ile Asp His Tyr Lys Gly Lys Lys Val Glu Lys Glu
290 295 300

Thr Ile Ser Pro Ile Tyr Leu Val Thr Lys Asp Asn Val Glu Lys Tyr
305 310 315 320

Asn. Trp

<210> 229

<211> 396

<212> PRT

<213> Streptococcus agalactiae

<400> 229

Met Gly Lys Glu Lys Leu Ile Leu Ala Tyr Ser Gly Gly Leu Asp Thr
1 5 10 15

Ser Val Ala Ile Ala Trp Leu Lys Lys Asp Tyr Asp Val Ile Ala Val
20 25 30

GBS patentin.ST25

Cys Met Asp Val Gly Glu Gly Lys Asp Leu Asp Phe Ile His Asp Lys
 35 40 45
 Ala Leu Thr Ile Gly Ala Ile Glu Ser Tyr Ile Leu Asp Val Lys Asp
 50 55 60
 Glu Phe Ala Glu His Phe Val Leu Pro Ala Leu Gln Ala His Ala Met
 65 70 75 80
 Tyr Glu Gln Lys Tyr Pro Leu Val Ser Ala Leu Ser Arg Pro Ile Ile
 85 90 95
 Ala Gln Lys Leu Val Glu Met Ala His Gln Thr Gly Ala Thr Thr Ile
 100 105 110
 Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val
 115 120 125
 Ala Ile Ala Ala Leu Asp Pro Glu Leu Lys Val Ile Ala Pro Val Arg
 130 135 140
 Glu Trp Lys Trp His Arg Glu Glu Glu Ile Thr Phe Ala Lys Ala Asn
 145 150 155 160
 Gly Val Pro Ile Pro Ala Asp Leu Asp Asn Pro Tyr Ser Ile Asp Gln
 165 170 175
 Asn Leu Trp Gly Arg Ala Asn Glu Cys Gly Val Leu Glu Asn Pro Trp
 180 185 190
 Asn Gln Ala Pro Glu Glu Ala Phe Gly Ile Thr Lys Ser Pro Glu Glu
 195 200 205
 Ala Pro Asp Cys Ala Glu Tyr Ile Asp Ile Thr Phe Gln Asn Gly Lys
 210 215 220
 Pro Ile Ala Ile Asn Asn Gln Glu Met Thr Leu Ala Asp Leu Ile Leu
 225 230 235 240
 Ser Leu Asn Glu Ile Ala Gly Lys His Gly Ile Gly Arg Ile Asp His
 245 250 255
 Val Glu Asn Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu Cys
 260 265 270
 Pro Ala Ala Met Val Leu Leu Ala Ala His Lys Glu Ile Glu Asp Leu
 275 280 285
 Thr Leu Val Arg Glu Val Ser His Phe Lys Pro Ile Leu Glu Asn Glu
 290 295 300

GBS patentin.ST25

Leu Ser Asn Leu Ile Tyr Asn Ala Leu Trp Phe Ser Pro Ala Thr Lys
305 310 315 320

Ala Ile Ile Ala Tyr Val Lys Glu Thr Gln Lys Val Val Asn Gly Thr
325 330 335

Thr Lys Val Lys Leu Tyr Lys Gly Ser Ala Lys Val Val Ala Arg His
340 345 350

Ser Ser Asn Ser Leu Tyr Asp Glu Asn Leu Ala Thr Tyr Thr Ala Ala
355 360 365

Asp Asn Phe Asp Gln Asp Ala Ala Val Gly Phe Ile Lys Leu Trp Gly
370 375 380

Leu Pro Thr Gln Val Asn Ala Gln Val Asn Lys Gly
385 390 395

<210> 230

<211> 62

<212> PRT

<213> Streptococcus agalactiae

<400> 230

Met Ala Lys Val Cys Tyr Phe Thr Gly Arg Lys Thr Val Ser Gly Asn
1 5 10 15

Asn Arg Ser His Ala Met Asn Gln Thr Lys Arg Thr Val Lys Pro Asn
20 25 30

Leu Gln Lys Val Thr Val Leu Ile Asp Gly Lys Pro Lys Lys Val Trp
35 40 45

Val Ser Ala Arg Ala Leu Lys Ser Gly Lys Val Glu Arg Val
50 55 60

<210> 231

<211> 551

<212> PRT

<213> Streptococcus agalactiae

<400> 231

Met Ala Lys Gln Lys Asn Asn Trp Arg Arg Val Gly Val Gly Val Leu
1 5 10 15

GBS patentin.ST25

Thr Leu Ala Ser Val Ala Thr Leu Ala Ala Cys Gly Ser Lys Ser Ala
20 25 30

Ser Gln Asp Ser Asn Gly Ala Ile Asn Trp Ala Ile Pro Thr Glu Ile
35 40 45

Asn Thr Leu Asp Leu Ser Lys Val Thr Asp Thr Tyr Ser Asn Leu Ala
50 55 60

Ile Gly Asn Ser Ser Ser Asn Phe Leu Arg Leu Asp Lys Asp Gly Lys
65 70 75 80

Thr Arg Pro Asp Leu Ala Thr Lys Val Asp Val Ser Lys Asp Gly Leu
85 90 95

Thr Tyr Thr Ala Thr Leu Arg Lys Gly Leu Lys Trp Ser Asp Gly Ser
100 105 110

Lys Leu Thr Ala Lys Asp Phe Val Tyr Ser Trp Gln Arg Leu Val Asp
115 120 125

Pro Lys Thr Ala Ser Gln Tyr Ala Tyr Leu Ala Val Glu Gly His Val
130 135 140

Leu Asn Ala Asp Lys Ile Asn Glu Gly Gln Glu Lys Asp Leu Asn Lys
145 150 155 160

Leu Gly Val Lys Ala Glu Gly Asp Asp Lys Val Val Ile Thr Leu Ser
165 170 175

Ser Pro Ser Pro Gln Phe Ile Tyr Tyr Leu Ala Phe Thr Asn Phe Met
180 185 190

Pro Gln Lys Gln Glu Val Val Glu Lys Tyr Gly Lys Asp Tyr Ala Thr
195 200 205

Thr Ser Lys Asn Thr Val Tyr Ser Gly Pro Tyr Thr Val Glu Gly Trp
210 215 220

Asn Gly Ser Asn Gly Thr Phe Thr Leu Lys Lys Asn Lys Asn Tyr Trp
225 230 235 240

Asp Ala Lys Asn Val Lys Thr Lys Glu Val Arg Ile Gln Thr Val Lys
245 250 255

Lys Pro Asp Thr Ala Val Gln Met Tyr Lys Arg Gly Glu Leu Asp Ala
260 265 270

Ala Asn Ile Ser Asn Thr Ser Ala Ile Tyr Gln Ala Asn Lys Asn Asn
275 280 285

GBS patentin.ST25

Lys Asp Val Thr Asp Val Leu Glu Ala Thr Thr Ala Tyr Met Gln Tyr
290 295 300

Asn Thr Thr Gly Ser Val Lys Gly Leu Asp Asn Val Lys Ile Arg Arg
305 310 315 320

Ala Leu Asn Leu Ala Thr Asn Arg Lys Gly Val Val Gln Ala Ala Val
325 330 335

Asp Thr Gly Ser Lys Pro Ala Ile Ala Phe Ala Pro Thr Gly Leu Ala
340 345 350

Lys Thr Pro Asp Gly Thr Asp Leu Ala Lys Tyr Val Ala Pro Gly Tyr
355 360 365

Glu Tyr Asn Lys Thr Glu Ala Ala Lys Leu Phe Lys Glu Gly Leu Ala
370 375 380

Glu Ser Gly Leu Thr Lys Leu Lys Leu Thr Ile Thr Ala Asp Ala Asp
385 390 395 400

Val Pro Ala Ala Lys Asn Ser Val Asp Tyr Ile Lys Ser Thr Trp Glu
405 410 415

Ala Ala Leu Pro Gly Leu Thr Val Glu Glu Lys Phe Val Thr Phe Lys
420 425 430

Gln Arg Leu Glu Asp Ser Arg Lys Gln Asn Phe Asp Ile Val Val Ser
435 440 445

Val Trp Gly Gly Asp Tyr Pro Glu Gly Ser Thr Phe Tyr Gly Leu Phe
450 455 460

Lys Ser Asp Ser Gln Asn Asn Asp Gly Lys Phe Ala Asn Lys Asp Tyr
465 470 475 480

Asp Ala Ala Tyr Asn Lys Ala Ile Ser Glu Asp Ala Leu Lys Pro Glu
485 490 495

Glu Ser Ala Lys Asp Tyr Lys Glu Ala Glu Lys Ile Leu Phe Glu Gln
500 505 510

Gly Ala Tyr Asn Pro Leu Tyr Phe Arg Ser Gly Lys Gly Leu Gln Asn
515 520 525

Pro Lys Leu Lys Gly Val Ile Arg Asn Thr Thr Gly Leu Ser Ile Asp
530 535 540

Phe Thr His Ala Tyr Lys Lys
545 550

GBS patentin.ST25

<210> 232

<211> 242

<212> PRT

<213> Streptococcus agalactiae

<400> 232

```

Met Glu Leu Leu Lys Thr Pro Ile Phe Gly Ile Cys Phe Ser Leu Ile
 1          5          10          15

Leu Tyr Thr Ile Gly Gln His Leu Phe Lys Lys Ser Lys Gly Phe Phe
          20          25          30

Leu Leu Gln Pro Leu Phe Phe Ala Met Val Ser Gly Ile Val Ile Leu
          35          40          45

Trp Leu Met Ser Lys Gly Leu Gly Thr Asp Val Lys Thr Phe Tyr Thr
 50          55          60

Gln Ala Tyr Lys Pro Gly Gly Asp Leu Ile Phe Trp Phe Leu Asn Pro
 65          70          75          80

Ala Thr Ile Ala Phe Ala Val Pro Leu Tyr Lys Lys Asn Asp Val Val
          85          90          95

Lys Lys Tyr Trp Val Glu Ile Leu Ser Ser Leu Val Ile Gly Met Ile
          100          105          110

Val Ser Leu Met Leu Ile Val Ala Ile Ser Lys Met Val Gly Leu Ser
          115          120          125

Gln Val Gly Ile Ala Ser Met Leu Pro Gln Ala Ala Thr Thr Ala Ile
          130          135          140

Ala Leu Pro Ile Thr Ala Ala Ile Gly Gly Asn Thr Ala Val Thr Ala
          145          150          155          160

Met Ala Cys Ile Leu Asn Ala Val Ile Ile Tyr Ala Leu Gly Lys Lys
          165          170          175

Leu Val Ser Phe Phe His Leu Asn Asp Ser Lys Ile Gly Ala Gly Leu
          180          185          190

Gly Leu Gly Thr Ser Gly His Thr Val Gly Ala Ala Phe Ala Leu Glu
          195          200          205

Leu Gly Glu Leu Gln Gly Ala Met Ala Ala Ile Ala Val Val Val Ile
          210          215          220

```

GBS patentin.ST25

Gly Leu Val Val Asp Leu Val Ile Pro Ile Phe Ser His Leu Ile Gly
225 230 235 240

Leu Leu

<210> 233

<211> 542

<212> PRT

<213> streptococcus agalactiae

<400> 233

Val Thr Lys Tyr Leu Lys Tyr Ile Ser Phe Val Ala Leu Phe Leu Ala
1 5 10 15

Ser Ile Phe Leu Val Ala Cys Gln Asn Gln Asn Ser Gln Thr Lys Glu
20 25 30

Arg Thr Arg Lys Gln Arg Pro Lys Asp Glu Leu Val Val Ser Met Gly
35 40 45

Ala Lys Leu Pro His Glu Phe Asp Pro Lys Asp Arg Tyr Gly Ile His
50 55 60

Asn Glu Gly Asn Ile Thr His Ser Thr Leu Leu Lys Arg Ser Pro Glu
65 70 75 80

Leu Asp Ile Lys Gly Glu Leu Ala Lys Lys Tyr Lys Ile Ser Lys Asp
85 90 95

Gly Leu Thr Trp Ser Phe Asp Leu Asn Asp Asp Phe Lys Phe Ser Asn
100 105 110

Gly Glu Pro Val Thr Ala Asp Asp Val Lys Phe Thr Tyr Asp Met Leu
115 120 125

Lys Ala Asp Gly Lys Ala Trp Asp Leu Thr Phe Ile Lys Asn Val Glu
130 135 140

Val Val Gly Lys Asn Gln Val Asn Ile His Leu Thr Glu Ala His Ser
145 150 155 160

Thr Phe Thr Ala Gln Leu Thr Glu Ile Pro Ile Val Pro Lys Lys His
165 170 175

Tyr Asn Asp Lys Tyr Lys Ser Asn Pro Ile Gly Ser Gly Pro Tyr Met
180 185 190

GBS patentin.ST25

Val Lys Glu Tyr Lys Ala Gly Glu Gln Ala Ile Phe Val Arg Asn Pro
195 200 205

Tyr Trp His Gly Lys Lys Pro Tyr Phe Lys Lys Trp Thr Trp Val Leu
210 215 220

Leu Asp Glu Asn Thr Ala Leu Ala Ala Leu Glu Ser Gly Asp Val Asp
225 230 235 240

Met Ile Tyr Ala Thr Pro Glu Leu Ala Ser Lys Lys Val Lys Gly Thr
245 250 255

Arg Leu Leu Asp Ile Ala Ser Asn Asp Val Arg Gly Leu Ser Leu Pro
260 265 270

Tyr Val Lys Lys Gly Val Val Lys Asn Ser Pro Asp Gly Tyr Pro Val
275 280 285

Gly Asn Asp Val Thr Ser Asp Pro Ala Ile Arg Lys Ala Leu Thr Ile
290 295 300

Gly Leu Asn Arg Gln Lys Val Leu Asp Thr Val Leu Asn Gly Tyr Gly
305 310 315 320

Lys Pro Ala Tyr Ser Ile Ile Asp Arg Thr Pro Phe Trp Asn Pro Lys
325 330 335

Thr Ala Ile Lys Asp Asn Lys Val Ala Lys Ala Lys Gln Leu Leu Thr
340 345 350

Lys Ala Gly Trp Lys Glu Gln Ala Asp Gly Ser Arg Lys Lys Gly Asn
355 360 365

Leu Lys Ala Glu Phe Asp Leu Tyr Tyr Pro Thr Asn Asp Gln Leu Arg
370 375 380

Ala Asn Leu Ala Val Glu Val Ala Glu Gln Ala Lys Ala Leu Gly Ile
385 390 395 400

Thr Ile Lys Leu Lys Ala Ser Asn Trp Asp Glu Met Ala Thr Lys Ser
405 410 415

His Asp Ser Ala Leu Leu Tyr Ala Gly Gly Arg His His Ala Gln Gln
420 425 430

Phe Tyr Glu Ser His Tyr Pro Ser Leu Ala Gly Lys Gly Trp Thr Asn
435 440 445

Ile Thr Phe Tyr Asn Asn Pro Thr Val Thr Lys Tyr Leu Asp Lys Ala
450 455 460

GBS patentin.ST25

Met Thr Ser Pro Asp Leu Asp Lys Ala Asn Lys Tyr Trp Lys Leu Ala
465 470 475 480

Gln Trp Asp Gly Lys Thr Gly Ala Ser Thr Leu Gly Asp Leu Pro Asn
485 490 495

Val Trp Leu Val Ser Leu Asn His Thr Tyr Ile Gly Asp Lys Arg Ile
500 505 510

Asn Val Gly Lys Gln Gly Val His Ser His Gly His Asp Trp Ser Leu
515 520 525

Leu Thr Asn Ile Ala Glu Trp Thr Trp Asp Glu Ser Ala Lys
530 535 540

<210> 234

<211> 381

<212> PRT

<213> Streptococcus agalactiae

<400> 234

Met Gly Gln Glu Pro Ile Ile Glu Tyr Gln Asn Ile Asn Lys Val Tyr
1 5 10 15

Gly Glu Asn Val Ala Val Glu Asp Ile Asn Leu Lys Ile Tyr Pro Gly
20 25 30

Asp Phe Val Cys Phe Ile Gly Thr Ser Gly Ser Gly Lys Thr Thr Leu
35 40 45

Met Arg Met Val Asn His Met Leu Lys Pro Thr Asn Gly Thr Leu Leu
50 55 60

Phe Lys Gly Lys Asp Ile Ser Thr Ile Asn Pro Ile Glu Leu Arg Arg
65 70 75 80

Arg Ile Gly Tyr Val Ile Gln Asn Ile Gly Leu Met Pro His Met Thr
85 90 95

Ile Tyr Glu Asn Ile Val Leu Val Pro Lys Leu Leu Lys Trp Ser Glu
100 105 110

Glu Ala Lys Arg Ala Lys Ala Arg Glu Leu Ile Lys Leu Val Glu Leu
115 120 125

Pro Glu Glu Tyr Leu Asp Arg Tyr Pro Ser Glu Leu Ser Gly Gly Gln
130 135 140

GBS patentin.ST25

Gln Gln Arg Ile Gly Val Ile Arg Ala Leu Ala Ala Asp Gln Asp Ile
145 150 155 160

Ile Leu Met Asp Glu Pro Phe Gly Ala Leu Asp Pro Ile Thr Arg Glu
165 170 175

Gly Ile Gln Asp Leu Val Lys Ser Leu Gln Glu Glu Met Gly Lys Thr
180 185 190

Ile Ile Leu Val Thr His Asp Met Asp Glu Ala Leu Lys Leu Ala Thr
195 200 205

Lys Ile Ile Val Met Asp Asn Gly Lys Met Val Gln Glu Gly Thr Pro
210 215 220

Asn Asp Leu Leu His His Pro Ala Thr Ser Phe Val Glu Gln Met Ile
225 230 235 240

Gly Glu Glu Arg Leu Leu His Ala Gln Ala Asp Ile Thr Pro Val Lys
245 250 255

Gln Ile Met Leu Asn Asn Pro Val Ser Ile Thr Ala Glu Lys Thr Leu
260 265 270

Thr Glu Ala Ile Thr Leu Met Arg Gln Lys Arg Val Asp Ser Leu Leu
275 280 285

Val Thr Asp Asn Gly Lys Leu Ile Gly Phe Ile Asp Leu Glu Ser Leu
290 295 300

Ser Ser Lys Tyr Lys Lys Asp Arg Leu Val Ser Asp Ile Leu Lys His
305 310 315 320

Thr Asp Phe Tyr Val Met Glu Asp Asp Leu Leu Arg Asn Thr Ala Glu
325 330 335

Arg Ile Leu Lys Arg Gly Leu Lys Tyr Ala Pro Val Val Asp His Glu
340 345 350

Asn Asn Leu Lys Gly Ile Val Thr Arg Ala Ser Leu Val Asp Met Leu
355 360 365

Tyr Asp Ile Ile Trp Gly Asp Thr Glu Thr Glu Asp Gln
370 375 380

<210> 235

<211> 235

<212> PRT

<213> Streptococcus agalactiae GBS patentin.ST25

<400> 235

Met Lys Ile Asp Lys Lys Glu Phe Leu Ala Leu Ile Ala Ser Ile Ile
1 5 10 15

Leu Leu Ile Phe Ala Ser Val Thr Phe Phe Leu Phe Lys Asp His Gly
20 25 30

Thr Thr Gln Met Asp Thr Val Glu Ser Ser Val Asn His Val Ser Asp
35 40 45

Ser Gln Leu Thr Glu Ala Gln Asp Met Leu Asp Lys Phe Glu Lys Lys
50 55 60

Pro Ser Glu Lys Leu Leu Lys Asp Val Glu Leu Ala Leu Asn Lys Leu
65 70 75 80

Ser Asn Ser Ser Lys Lys Glu Ala Leu Gln Lys Arg Phe Lys Lys Ala
85 90 95

Lys Asp Lys Tyr Leu Lys Asp Glu Ala Asp Lys Lys Ala Thr Lys Asp
100 105 110

Ala Thr Asp Leu Val Glu Ile Leu Glu Gln Ala Pro Ser Glu Glu Asn
115 120 125

Val Leu Lys Ala Glu Ala Ala Val Asn Lys Leu Thr Val Lys Glu Ser
130 135 140

Lys Glu Ala Leu Gln Lys Arg Ile Asp Thr Val Lys Thr Gln Tyr Gly
145 150 155 160

Leu Ile Gly Asn Gln Thr Pro Ser Ser Ser Val Ala Glu Thr Thr Glu
165 170 175

Gln Gly Thr Ala Asn Pro Ala Ser Gln Asp Thr Ser Ser Tyr Val Asn
180 185 190

Gln Asn Val Ala Pro Thr Tyr Glu Gln Pro Gln Thr Asn Asn Thr Pro
195 200 205

Val Thr Pro Gly Val Asn Asn Thr Val Pro Thr Pro Gly Thr Gly Thr
210 215 220

Ala Pro Ala Thr Asn Gly Thr Gly Val Ala Gln
225 230 235

<210> 236

GBS patentin.ST25

<211> 679

<212> PRT

<213> streptococcus agalactiae

<400> 236

Met Thr Lys Asp Leu Leu Leu Glu Leu Gly Leu Glu Glu Leu Pro Ala
1 5 10 15

Tyr Val Val Thr Pro Ser Glu Lys Gln Leu Gly Gln Lys Met Val Lys
20 25 30

Phe Leu Glu Asp His Arg Leu Ser Phe Glu Thr Val Gln Thr Phe Ser
35 40 45

Thr Pro Arg Arg Leu Ala Val Arg Val Lys Gly Leu Ala Asp Gln Gln
50 55 60

Thr Asp Leu Thr Glu Asp Phe Lys Gly Pro Ser Lys Lys Ile Ala Leu
65 70 75 80

Asp Ala Glu Gly Asn Phe Ser Lys Ala Ala Gln Gly Phe Val Arg Gly
85 90 95

Lys Gly Leu Ser Val Asp Asp Ile Glu Phe Arg Glu Val Lys Gly Glu
100 105 110

Glu Tyr Val Tyr Val Thr Lys His Glu Thr Gly Lys Ser Ala Ile Asp
115 120 125

Val Leu Ala Ser Val Thr Glu Val Leu Thr Glu Leu Thr Phe Pro Val
130 135 140

Asn Met His Trp Ala Asn Asn Ser Phe Glu Tyr Ile Arg Pro Val His
145 150 155 160

Thr Leu Val Val Leu Leu Asp Asp Gln Ala Leu Glu Leu Asp Phe Leu
165 170 175

Asp Ile His Ser Gly Arg Ile Ser Arg Gly His Arg Phe Leu Gly Ser
180 185 190

Asp Thr Glu Ile Leu Ser Ala Ser Ser Tyr Glu Asp Asp Leu Arg Gln
195 200 205

Gln Phe Val Ile Ala Asp Ala Lys Glu Arg Gln Gln Met Ile Val Asp
210 215 220

Gln Ile His Ala Ile Glu Glu Lys Glu Asn Ile Ser Val Glu Ile Asp
225 230 235 240

GBS patentin.ST25

Glu Asp Leu Leu Asn Glu Val Leu Asn Leu Val Glu Tyr Pro Thr Ala
245 250 255

Phe Leu Gly Ser Phe Asp Glu Lys Tyr Leu Asp Val Pro Glu Glu Val
260 265 270

Leu Val Thr Ser Met Lys Asn His Gln Arg Tyr Phe Val Val Arg Asp
275 280 285

Arg Asp Gly Lys Leu Leu Pro Asn Phe Ile Ser Val Arg Asn Gly Asn
290 295 300

Ala Glu His Ile Glu Asn Val Ile Lys Gly Asn Glu Lys Val Leu Val
305 310 315 320

Ala Arg Leu Glu Asp Gly Glu Phe Phe Trp Gln Glu Asp Gln Lys Leu
325 330 335

Asn Ile Ala Asp Leu Val Glu Lys Leu Lys Gln Val Thr Phe His Glu
340 345 350

Lys Ile Gly Ser Leu Tyr Glu His Met Asp Arg Val Lys Val Ile Ser
355 360 365

Gln Tyr Leu Ala Glu Lys Ala Asp Leu Ser Asp Glu Glu Lys Leu Ala
370 375 380

Val Leu Arg Ala Ala Ser Ile Tyr Lys Phe Asp Leu Leu Thr Gly Met
385 390 395 400

Val Asp Glu Phe Asp Glu Leu Gln Gly Ile Met Gly Glu Lys Tyr Ala
405 410 415

Leu Leu Ala Gly Glu Gln Pro Ala Val Ala Ala Ala Ile Arg Glu His
420 425 430

Tyr Met Pro Thr Ser Ala Asp Gly Glu Leu Pro Glu Thr Arg Val Gly
435 440 445

Ala Ile Leu Ala Leu Ala Asp Lys Phe Asp Thr Leu Leu Ser Phe Phe
450 455 460

Ser Val Gly Leu Ile Pro Ser Gly Ser Asn Asp Pro Tyr Ala Leu Arg
465 470 475 480

Arg Ala Thr Gln Gly Ile Val Arg Ile Leu Glu Ala Phe Gly Trp Asp
485 490 495

Ile Pro Leu Asp Glu Leu Val Thr Asn Leu Tyr Gly Leu Ser Phe Ala
500 505 510

GBS patentin.ST25

Ser Leu Asp Tyr Ala Asn Gln Lys Glu Val Met Ala Phe Ile Ser Ala
515 520 525

Arg Ile Glu Lys Met Ile Gly Ser Lys Val Pro Lys Asp Ile Arg Glu
530 535 540

Ala Val Leu Glu Ser Asp Thr Tyr Ile Val Ser Leu Ile Leu Glu Ala
545 550 555 560

Ser Gln Ala Leu Val Gln Lys Ser Lys Asp Ala Gln Tyr Lys Val Ser
565 570 575

Ile Glu Ser Leu Ser Arg Ala Phe Asn Leu Ala Glu Lys Val Thr His
580 585 590

Ser Val Ser Val Asp Tyr Ser Leu Phe Glu Asn Asn Gln Glu Lys Ala
595 600 605

Leu Tyr Gln Ala Ile Leu Ser Leu Glu Leu Thr Glu Asp Met His Asp
610 615 620

Asn Leu Asp Lys Leu Phe Ala Leu Ser Pro Ile Ile Asn Asp Phe Phe
625 630 635 640

Asp Asn Thr Met Val Met Thr Asp Asp Glu Lys Met Lys Gln Asn Arg
645 650 655

Leu Ala Leu Leu Asn Ser Leu Val Ala Lys Ala Arg Thr Val Ala Ala
660 665 670

Phe Asn Leu Leu Asn Thr Lys
675

<210> 237

<211> 661

<212> PRT

<213> Streptococcus agalactiae

<400> 237

Met Thr Phe Asp Thr Ile Asp Gln Leu Ala Val Asn Thr Val Arg Thr
1 5 10 15

Leu Ser Ile Asp Ala Ile Gln Ala Ala Asn Ser Gly His Pro Gly Leu
20 25 30

Pro Met Gly Ala Ala Pro Met Ala Tyr Val Leu Trp Asn Lys Phe Leu
35 40 45

GBS patentin.ST25

Asn Val Asn Pro Lys Thr Ser Arg Asn Trp Thr Asn Arg Asp Arg Phe
 50 55 60
 Val Leu Ser Ala Gly His Gly Ser Ala Leu Leu Tyr Ser Leu Leu His
 65 70 75 80
 Leu Ala Gly Tyr Asp Leu Ser Ile Asp Asp Leu Lys Gln Phe Arg Gln
 85 90 95
 Trp Gly Ser Lys Thr Pro Gly His Pro Glu Val Asn His Thr Asp Gly
 100 105 110
 Val Glu Ala Thr Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val
 115 120 125
 Gly Met Ala Met Ala Glu Ala His Leu Ala Ala Lys Phe Asn Lys Pro
 130 135 140
 Gly Phe Asp Leu Val Asp His Tyr Thr Tyr Thr Leu His Gly Asp Gly
 145 150 155 160
 Cys Leu Met Glu Gly Val Ser Gln Glu Ala Ala Ser Leu Ala Gly His
 165 170 175
 Leu Lys Leu Gly Lys Leu Val Leu Leu Tyr Asp Ser Asn Asp Ile Ser
 180 185 190
 Leu Asp Gly Pro Thr Ser Gln Ser Phe Thr Glu Asp Val Lys Gly Arg
 195 200 205
 Phe Glu Ser Tyr Gly Trp Gln His Ile Leu Val Lys Asp Gly Asn Asp
 210 215 220
 Leu Glu Ala Ile Ala Ala Ala Ile Glu Ala Ala Lys Ala Glu Thr Asp
 225 230 235 240
 Lys Pro Thr Ile Ile Glu Val Lys Thr Ile Ile Gly Phe Gly Ala Glu
 245 250 255
 Lys Gln Gly Thr Ser Ser Val His Gly Ala Pro Leu Gly Ala Glu Gly
 260 265 270
 Ile Thr Phe Ala Lys Lys Ala Tyr Gly Trp Glu Tyr Pro Asp Phe Thr
 275 280 285
 Val Pro Ala Glu Val Val Ala Arg Phe Ala Ser Asp Leu Gln Ala Arg
 290 295 300
 Gly Ala Lys Ala Glu Glu Ala Trp Asn Asp Leu Phe Ala Lys Tyr Glu
 305 310 315 320

GBS patentin.ST25

Val Glu Tyr Pro Glu₃₂₅ Leu Ala Ala Glu Tyr₃₃₀ Lys Glu Ala Phe Ala₃₃₅ Gly
 Gln Ala Glu Thr Val Glu Leu Lys Ala₃₄₅ His Asp Leu Gly Ser₃₅₀ Ser Val
 Ala Ser Arg₃₅₅ Val Ser Ser Gln Gln Ala Ile Gln Gln Leu₃₆₅ Ser Thr Gln
 Leu Pro Asn₃₇₀ Leu Trp Gly Gly₃₇₅ Ser Ala Asp Leu Ser₃₈₀ Ala Ser Asn Asn
 Thr Met Val Ala Ala Glu₃₉₀ Thr Asp Phe Gln Ala₃₉₅ Ser Asn Tyr Ala Gly₄₀₀
 Arg Asn Ile Trp Phe₄₀₅ Gly Val Arg Glu Phe₄₁₀ Ala Met Ala Ala Ala Met₄₁₅
 Asn Gly Ile Ala₄₂₀ Leu His Gly Gly Thr₄₂₅ Arg Val Tyr Gly Gly₄₃₀ Thr Phe
 Phe Val Phe₄₃₅ Ser Asn Tyr Leu Leu₄₄₀ Pro Ala Val Arg Met₄₄₅ Ala Ala Leu
 Gln Asn₄₅₀ Leu Pro Thr Val Tyr₄₅₅ Val Met Thr His Asp₄₆₀ Ser Ile Ala Val
 Gly Glu Asp Gly Pro Thr₄₇₀ His Glu Pro Ile Glu₄₇₅ Gln Leu Ala Ser Val₄₈₀
 Arg Ser Met Pro Asn₄₈₅ Leu Asn Val Ile Arg₄₉₀ Pro Ala Asp Gly Asn₄₉₅ Glu
 Thr Asn Ala Ala Trp Gln Arg Ala Val₅₀₅ Ser Glu Thr Asp Arg₅₁₀ Pro Thr
 Met Leu Val₅₁₅ Leu Thr Arg Gln Asn Leu Pro Val Leu Glu₅₂₅ Gly Thr Ser
 Glu Leu Ala Gln Glu Gly Val₅₃₅ Asn Lys Gly Ala Tyr₅₄₀ Ile Leu Ser Glu
 Ala Lys Gly Glu Leu Asp₅₅₀ Gly Ile Ile Ile Ala₅₅₅ Thr Gly Ser Glu Val₅₆₀
 Lys Leu Ala Leu Asp₅₆₅ Thr Gln Asp Lys Leu₅₇₀ Glu Ser Glu Gly Ile His₅₇₅
 Val Arg Val Val₅₈₀ Ser Met Pro Ala Gln₅₈₅ Asn Ile Phe Asp Glu Gln Glu₅₉₀

GBS patentin.ST25

Ala Ser Tyr Gln Glu Gln Val Leu Pro Ser Ala Val Thr Lys Arg Leu
595 600 605

Ala Ile Glu Ala Gly Ser Ser Phe Gly Trp Gly Lys Tyr Val Gly Leu
610 615 620

Asn Gly Leu Thr Leu Thr Ile Asp Thr Trp Gly Ala Ser Ala Pro Gly
625 630 635 640

Asn Arg Ile Phe Glu Glu Tyr Gly Phe Thr Val Glu Asn Ala Val Ser
645 650 655

Leu Tyr Lys Glu Leu
660

<210> 238

<211> 273

<212> PRT

<213> Streptococcus agalactiae

<400> 238

Met Thr Leu Gln Asp Gln Ile Ile Lys Glu Leu Gly Val Lys Pro Val
1 5 10 15

Ile Asn Pro Ser Gln Glu Ile Arg Arg Ser Val Glu Phe Leu Lys Asp
20 25 30

Tyr Leu Leu Lys His Ser Phe Leu Lys Thr Tyr Val Leu Gly Ile Ser
35 40 45

Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Ala Gln Leu Ala Val
50 55 60

Glu Glu Leu Arg Ala Asp Thr Gly Glu Asn Tyr Gln Phe Ile Ala Ile
65 70 75 80

Arg Leu Pro Tyr Gly Ile Gln Ala Asp Glu Glu Asp Ala Gln Lys Ala
85 90 95

Leu Asp Phe Ile Lys Pro Asp Ile Ala Leu Thr Ile Asn Ile Lys Glu
100 105 110

Ala Val Asp Gly Gln Val Arg Ala Leu Asn Ala Ala Gly Val Glu Ile
115 120 125

Thr Asp Phe Asn Lys Gly Asn Ile Lys Ala Arg Gln Arg Met Ile Ser
130 135 140

GBS patentin.ST25

Gln Tyr Ala Val Ala Gly Gln Tyr Ala Gly Ala Val Ile Gly Thr Asp
145 150 155 160

His Ala Ala Glu Asn Ile Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly
165 170 175

Gly Ala Asp Leu Leu Pro Leu Phe Arg Leu Asn Lys Ser Gln Gly Lys
180 185 190

Gln Leu Leu Ala Glu Leu Gly Ala Asp Lys Ala Leu Tyr Glu Lys Ile
195 200 205

Pro Thr Ala Asp Leu Glu Glu Asn Lys Pro Gly Ile Ala Asp Glu Ile
210 215 220

Ala Leu Gly Val Thr Tyr Gln Glu Ile Asp Ala Tyr Leu Glu Gly Lys
225 230 235 240

Val Val Ser Asp Lys Ser Arg Gly Ile Ile Glu Asn Trp Trp Tyr Lys
245 250 255

Gly Gln His Lys Arg His Leu Pro Ile Thr Ile Phe Asp Asp Phe Trp
260 265 270

Lys

<210> 239

<211> 745

<212> PRT

<213> Streptococcus agalactiae

<400> 239

Ile Lys Lys Glu Ser Val Ile Lys Leu Leu Lys Tyr Ala Phe Gly Ile
1 5 10 15

Ile Met Gly Phe Ile Ile Leu Ala Ile Val Ile Gly Gly Leu Leu Phe
20 25 30

Ala Tyr Tyr Val Ser Arg Ser Pro Lys Leu Thr Asp Gln Ala Leu Lys
35 40 45

Ser Val Asn Ser Ser Leu Val Tyr Asp Gly Asn Asn Lys Leu Ile Ala
50 55 60

Asp Leu Gly Ser Glu Lys Arg Glu Ser Val Ser Ala Asp Ser Ile Pro
65 70 75 80

GBS patentin.ST25

Leu Asn Leu Val Asn Ala Ile Thr Ser Ile Glu Asp Lys Arg Phe Phe
85 90 95

Lys His Arg Gly Val Asp Ile Tyr Arg Ile Leu Gly Ala Ala Trp His
100 105 110

Asn Leu Val Ser Ser Asn Thr Gln Gly Gly Ser Thr Leu Asp Gln Gln
115 120 125

Leu Ile Lys Leu Ala Tyr Phe Ser Thr Asn Lys Ser Asp Gln Thr Leu
130 135 140

Lys Arg Lys Ser Gln Glu Val Trp Leu Ala Leu Gln Met Glu Arg Lys
145 150 155 160

Tyr Thr Lys Glu Glu Ile Leu Thr Phe Tyr Ile Asn Lys Val Tyr Met
165 170 175

Gly Asn Gly Asn Tyr Gly Met Arg Thr Thr Ala Lys Ser Tyr Phe Gly
180 185 190

Lys Asp Leu Lys Glu Leu Ser Ile Ala Gln Leu Ala Leu Leu Ala Gly
195 200 205

Ile Pro Gln Ala Pro Thr Gln Tyr Asp Pro Tyr Lys Asn Pro Glu Ser
210 215 220

Ala Gln Thr Arg Arg Asn Thr Val Leu Gln Gln Met Tyr Gln Asp Lys
225 230 235 240

Asn Ile Ser Lys Lys Glu Tyr Asp Gln Ala Val Ala Thr Pro Val Thr
245 250 255

Asp Gly Leu Lys Glu Leu Lys Gln Lys Ser Thr Tyr Pro Lys Tyr Met
260 265 270

Asp Asn Tyr Leu Lys Gln Val Ile Ser Glu Val Lys Gln Lys Thr Gly
275 280 285

Lys Asp Ile Phe Thr Ala Gly Leu Lys Val Tyr Thr Asn Ile Asn Thr
290 295 300

Asp Ala Gln Lys Gln Leu Tyr Asp Ile Tyr Asn Ser Asp Thr Tyr Ile
305 310 315 320

Ala Tyr Pro Asn Asn Glu Leu Gln Ile Ala Ser Thr Ile Met Asp Ala
325 330 335

Thr Asn Gly Lys Val Ile Ala Gln Leu Gly Gly Arg His Gln Asn Glu
340 345 350

GBS patentin.ST25

Asn Ile Ser Phe Gly Thr Asn Gln Ser Val Leu Thr Asp Arg Asp Trp
355 360 365

Gly Ser Thr Met Lys Pro Ile Ser Ala Tyr Ala Pro Ala Ile Asp Ser
370 375 380

Gly Val Tyr Asn Ser Thr Gly Gln Ser Leu Asn Asp Ser Val Tyr Tyr
385 390 395 400

Trp Pro Gly Thr Ser Thr Gln Leu Tyr Asp Trp Asp Arg Gln Tyr Met
405 410 415

Gly Trp Met Ser Met Gln Thr Ala Ile Gln Gln Ser Arg Asn Val Pro
420 425 430

Ala Val Arg Ala Leu Glu Ala Ala Gly Leu Asp Glu Ala Lys Ser Phe
435 440 445

Leu Glu Lys Leu Gly Ile Tyr Tyr Pro Glu Met Asn Tyr Ser Asn Ala
450 455 460

Ile Ser Ser Asn Asn Ser Ser Ser Asp Ala Lys Tyr Gly Ala Ser Ser
465 470 475 480

Glu Lys Met Ala Ala Tyr Ser Ala Phe Ala Asn Gly Gly Thr Tyr
485 490 495

Tyr Lys Pro Gln Tyr Val Asn Lys Ile Glu Phe Ser Asp Gly Thr Asn
500 505 510

Asp Thr Tyr Ala Ala Ser Gly Ser Arg Ala Met Lys Glu Thr Thr Ala
515 520 525

Tyr Met Met Thr Asp Met Leu Lys Thr Val Leu Thr Phe Gly Thr Gly
530 535 540

Thr Lys Ala Ala Ile Pro Gly Val Ala Gln Ala Gly Lys Thr Gly Thr
545 550 555 560

Ser Asn Tyr Thr Glu Asp Glu Leu Ala Lys Ile Glu Ala Thr Thr Gly
565 570 575

Ile Tyr Asn Ser Ala Val Gly Thr Met Ala Pro Asp Glu Asn Phe Val
580 585 590

Gly Tyr Thr Ser Lys Tyr Thr Met Ala Ile Trp Thr Gly Tyr Lys Asn
595 600 605

Arg Leu Thr Pro Leu Tyr Gly Ser Gln Leu Asp Ile Ala Thr Glu Val
610 615 620

GBS patentin.ST25

Tyr Arg Ala Met Met Ser Tyr Leu Thr Gly Gly Tyr Ser Ala Asp Trp
625 630 635 640

Thr Met Pro Glu Gly Leu Tyr Arg Ser Gly Ser Tyr Leu Tyr Ile Asn
645 650 655

Gly Thr Thr Thr Thr Gly Thr Tyr Ser Ser Ser Val Tyr Lys Asn Ile
660 665 670

Tyr Gln Asn Ser Gly Gln Ser Ser Gln Ser Ser Ser Ser Thr Ser Ser
675 680 685

Glu Lys Gln Lys Glu Asp Lys Asn Thr Ala Asn Asp Ala Asn Ser Ser
690 695 700

Ser Pro Gln Val Glu Thr Pro Asn Asn Gly Asn Ala Thr Thr Pro Asn
705 710 715 720

Asn Ser Asn Gln Thr Val Pro Gly Thr Gly His Gly Asn Gly Asn Gly
725 730 735

Asn Asn Asn Thr Val Pro Asn Gly Asn
740 745

<210> 240

<211> 425

<212> PRT

<213> streptococcus agalactiae

<400> 240

Met Leu Asp Leu Lys Arg Ile Arg Thr Asp Phe Asp Val Val Ala Lys
1 5 10 15

Lys Leu Ala Thr Arg Gly Val Asp Gln Glu Thr Leu Thr Thr Leu Lys
20 25 30

Glu Leu Asp Ile Lys Arg Arg Glu Leu Leu Ile Lys Ala Glu Glu Ala
35 40 45

Lys Ala Gln Arg Asn Val Ala Ser Ala Ala Ile Ala Gln Ala Lys Arg
50 55 60

Asn Lys Glu Asn Ala Asp Glu Gln Ile Ala Ala Met Gln Thr Leu Ser
65 70 75 80

Ala Asp Ile Lys Ala Ile Asp Ala Glu Leu Ala Asp Val Asp Ala Asn
85 90 95

GBS patentin.ST25

Leu Gln Ser Met Val Thr Val Leu Pro Asn Thr Pro Ala Asp Asp Val
100 105 110

Pro Leu Gly Ala Asp Glu Asp Glu Asn Val Glu Val Arg Arg Trp Gly
115 120 125

Thr Pro Arg Glu Phe Asp Phe Glu Thr Lys Ala His Trp Asp Leu Gly
130 135 140

Glu Ser Leu Gly Ile Leu Asp Trp Glu Arg Gly Ala Lys Val Thr Gly
145 150 155 160

Ser Arg Phe Leu Phe Tyr Lys Gly Leu Gly Ala Arg Leu Glu Arg Ala
165 170 175

Ile Tyr Ser Phe Met Leu Asp Glu His Ala Lys Glu Gly Tyr Thr Glu
180 185 190

Val Ile Pro Pro Tyr Met Val Asn His Asp Ser Met Phe Gly Thr Gly
195 200 205

Gln Tyr Pro Lys Phe Lys Glu Asp Thr Phe Glu Leu Ala Asp Ser Pro
210 215 220

Phe Val Leu Ile Pro Thr Ala Glu Val Pro Leu Thr Asn Tyr Tyr Arg
225 230 235 240

Asp Glu Ile Ile Asp Gly Lys Glu Leu Pro Ile Tyr Phe Thr Ala Met
245 250 255

Ser Pro Ser Phe Arg Ser Glu Ala Gly Ser Ala Gly Arg Asp Thr Arg
260 265 270

Gly Leu Ile Arg Leu His Gln Phe His Lys Val Glu Met Val Lys Phe
275 280 285

Ala Lys Pro Glu Glu Ser Tyr Gln Glu Leu Glu Lys Met Thr Ala Asn
290 295 300

Ala Glu Asn Ile Leu Gln Lys Leu Asn Leu Pro Tyr Arg Val Ile Thr
305 310 315 320

Leu Cys Thr Gly Asp Met Gly Phe Ser Ala Ala Lys Thr Tyr Asp Leu
325 330 335

Glu Val Trp Ile Pro Ala Gln Asn Thr Tyr Arg Glu Ile Ser Ser Cys
340 345 350

Ser Asn Thr Glu Asp Phe Gln Ala Arg Arg Ala Gln Ile Arg Tyr Arg
355 360 365

GBS patentin.ST25

Asp Glu Val Asp Gly Lys Val Arg Leu Leu His Thr Leu Asn Gly Ser
370 375 380

Gly Leu Ala Val Gly Arg Thr Val Ala Ala Ile Leu Glu Asn Tyr Gln
385 390 395 400

Asn Glu Asp Gly Ser Val Thr Ile Pro Glu Val Leu Arg Pro Tyr Met
405 410 415

Gly Asn Ile Asp Ile Ile Lys Pro Asn
420 425

<210> 241

<211> 266

<212> PRT

<213> Streptococcus agalactiae

<400> 241

Val Thr Ile Ser Asn Gln Glu Leu Thr Leu Thr Pro Leu Arg Gly Lys
1 5 10 15

Ser Gly Lys Ala Tyr Ile Gly Thr Tyr Pro Asn Gly Glu Arg Val Phe
20 25 30

Val Lys Tyr Asn Thr Thr Pro Ile Leu Pro Ala Leu Ala Lys Glu Gln
35 40 45

Ile Ala Pro Gln Leu Leu Trp Ala Arg Arg Thr Ser Asn Gly Asp Met
50 55 60

Met Ser Ala Gln Glu Trp Leu Asp Gly Arg Thr Leu Thr Lys Glu Asp
65 70 75 80

Met Gly Ser Lys Gln Ile Ile His Ile Leu Leu Arg Leu His Lys Ser
85 90 95

Arg Pro Leu Val Asn Gln Leu Leu Gln Leu Gly Tyr Lys Ile Glu Asn
100 105 110

Pro Tyr Asp Leu Leu Met Asp Trp Glu Lys Gln Thr Pro Ile Gln Ile
115 120 125

Arg Glu Asn Thr Tyr Leu Gln Ser Ile Val Thr Glu Leu Lys Arg Ser
130 135 140

Leu Pro Glu Phe Arg Thr Glu Val Ala Thr Ile Val His Gly Asp Ile
145 150 155 160

GBS patentin.ST25

Lys His Ser Asn Trp Val Ile Thr Thr Ser Gly Leu Ile Tyr Leu Val
165 170 175

Asp Trp Asp Ser Val Arg Leu Thr Asp Arg Met Tyr Asp Val Ala Tyr
180 185 190

Ile Leu Ser His Tyr Ile Pro Gln Lys His Trp Lys Asp Trp Leu Ser
195 200 205

Tyr Tyr Gly Tyr Lys Asp Asn Glu Lys Val Trp Ser Lys Ile Ile Trp
210 215 220

Tyr Gly Gln Phe Ser Tyr Leu Ser Gln Ile Ile Lys Cys Phe Asp Lys
225 230 235 240

Arg Asp Met Glu His Val Asn Gln Glu Ile Tyr Glu Leu Arg Lys Phe
245 250 255

Arg Glu Leu Ile Lys Lys His Asn Ala Ser
260 265

<210> 242

<211> 521

<212> PRT

<213> streptococcus agalactiae

<400> 242

Met Lys Ile Ser Gln Tyr Asn Lys Trp Ser Ile Arg Arg Leu Lys Val
1 5 10 15

Gly Ala Ala Ser Val Met Ile Ala Ser Gly Ser Ile Val Ala Leu Gly
20 25 30

Gln Ser His Ile Val Ser Ala Asp Glu Met Ser Gln Pro Lys Thr Thr
35 40 45

Ile Thr Ala Pro Thr Ala Asn Thr Ser Thr Asn Val Glu Ser Ser Thr
50 55 60

Asp Lys Ala Leu Ser Lys Val Thr Thr Met Glu Thr Ser Ser Glu Met
65 70 75 80

Pro Lys Met Gln Asn Met Ala Lys Val Glu Lys Thr Ser Asp Lys Pro
85 90 95

Met Met Val Ala Thr Ser Val Arg Lys Met Met Ala Thr Pro Thr Pro
100 105 110

GBS patentin.ST25

Val Ala Met Thr Lys Thr Thr Ser Val Asp Glu Val Lys Lys Ser Thr
115 120 125

Asp Thr Ala Phe Lys Gln Thr Val Asp Val Pro Ala His Tyr Val Asn
130 135 140

Ala Ala Lys Gly Asn Gly Pro Phe Leu Ala Gly Val Asn Gln Thr Ile
145 150 155 160

Pro Tyr Glu Ala Phe Gly Gly Asp Gly Met Leu Thr Arg Leu Ile Leu
165 170 175

Lys Ser Ser Glu Gly Ala Lys Trp Ser Asp Asn Gly Val Asp Lys Asn
180 185 190

Ser Pro Leu Leu Pro Leu Lys Gly Leu Thr Lys Gly Lys Tyr Phe Tyr
195 200 205

Gln Val Ser Leu Asn Gly Asn Thr Thr Gly Lys Glu Gly Gln Ala Leu
210 215 220

Leu Asp Gln Ile Lys Ala Asn Asp Lys His Ser Tyr Gln Ala Thr Ile
225 230 235 240

Arg Val Tyr Gly Ala Lys Asp Gly Lys Val Asp Leu Lys Asn Met Ile
245 250 255

Ser Gln Lys Met Val Thr Ile Asn Ile Pro His Ile Thr Thr Asp Met
260 265 270

Glu Val Lys Asn Ser Leu Lys Met Ala Phe Lys Glu Lys Val Asp Val
275 280 285

Pro Ala Lys Tyr Val Ser Ala Ala Lys Ala Lys Gly Pro Phe Leu Ala
290 295 300

Gly Val Asn Glu Thr Ile Pro Tyr Glu Ala Phe Gly Gly Asp Gly Met
305 310 315 320

Leu Thr Arg Leu Ile Leu Lys Ala Ser Glu Gly Ala Lys Trp Ser Asp
325 330 335

Asn Gly Val Asp Lys Asn Ser Pro Leu Leu Pro Leu Lys Asp Leu Thr
340 345 350

Lys Gly Lys Tyr Phe Tyr Gln Val Ser Leu Asn Gly Asn Thr Ala Gly
355 360 365

Lys Lys Gly Gln Ala Leu Leu Asp Gln Ile Lys Ala Asn Gly Ser His
370 375 380

GBS patentin.ST25

Thr Tyr Gln Ala Thr Ile Thr Ile Tyr Gly Thr Lys Asp Gly Lys Val
385 390 395 400

Asp Met Asn Thr Ile Leu Gly Gln Lys Thr Val Met Ile His Ile Asn
405 410 415

Val Ala Lys Lys Asp Met Asn Ser Thr Ser Met Met Met Lys Lys Asp
420 425 430

Lys Met Thr Met Pro Met Lys Lys Glu Met Thr Ser Ser Lys Ile Asn
435 440 445

Thr Gly Met Met Met Ser Asn Asn Lys Met Ser Ala Asn Met Gln Met
450 455 460

Ser Ser Gln Ala Lys Ser Asn Asp Lys Ala Gly Lys Lys Met Ser Met
465 470 475 480

Met Ser Lys Asn Leu Pro Asn Thr Gly Glu Thr Lys Gln Gln Asn Val
485 490 495

Gly Val Leu Gly Met Leu Ser Leu Ala Phe Ala Thr Gly Leu Thr Ala
500 505 510

Leu Gly Leu Lys Lys Ser Lys Gln Arg
515 520

<210> 243

<211> 449

<212> PRT

<213> streptococcus agalactiae

<400> 243

Met Thr His Ile Thr Phe Asp Tyr Ser Lys Val Leu Gly Gln Phe Val
1 5 10 15

Gly Glu His Glu Leu Asp Tyr Leu Gln Pro Gln Val Ser Ala Ala Asp
20 25 30

Ala Phe Leu Arg Gln Gly Thr Gly Pro Gly Ser Asp Phe Leu Gly Trp
35 40 45

Met Asp Leu Pro Glu Asn Tyr Asp Lys Glu Glu Phe Ser Arg Ile Gln
50 55 60

Lys Ala Ala Glu Lys Ile Lys Ser Asp Ser Glu Val Leu Val Val Ile
65 70 75 80

GBS patentin.ST25

Gly Ile Gly Gly Ser Tyr Leu Gly Ala Lys Ala Ala Ile Asp Phe Leu
85 90 95

Asn Asn His Phe Ala Asn Leu Gln Thr Ala Glu Glu Arg Lys Ala Pro
100 105 110

Gln Ile Leu Tyr Ala Gly Asn Ser Ile Ser Ser Thr Tyr Leu Ala Asp
115 120 125

Leu Val Glu Tyr Val Gln Asp Lys Glu Phe Ser Val Asn Val Ile Ser
130 135 140

Lys Ser Gly Thr Thr Thr Glu Pro Ala Ile Ala Phe Arg Val Phe Lys
145 150 155 160

Glu Leu Leu Val Lys Lys Tyr Gly Gln Glu Glu Ala Asn Lys Arg Ile
165 170 175

Tyr Ala Thr Thr Asp Lys Val Lys Gly Ala Val Lys Val Glu Ala Asp
180 185 190

Ala Asn Asn Trp Glu Thr Phe Val Val Pro Asp Asn Val Gly Gly Arg
195 200 205

Phe Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Ala Ser Gly
210 215 220

Ala Asp Ile Thr Ala Leu Met Glu Gly Ala Asn Ala Ala Arg Lys Asp
225 230 235 240

Leu Ser Ser Asp Lys Ile Ser Glu Asn Ile Ala Tyr Gln Tyr Ala Ala
245 250 255

Val Arg Asn Val Leu Tyr Arg Lys Gly Tyr Ile Thr Glu Ile Leu Ala
260 265 270

Asn Tyr Glu Pro Ser Leu Gln Tyr Phe Gly Glu Trp Trp Lys Gln Leu
275 280 285

Ala Gly Glu Ser Glu Gly Lys Asp Gln Lys Gly Ile Tyr Pro Thr Ser
290 295 300

Ala Asn Phe Ser Thr Asp Leu His Ser Leu Gly Gln Phe Ile Gln Glu
305 310 315 320

Gly Tyr Arg Asn Leu Phe Glu Thr Val Val Arg Val Glu Lys Pro Arg
325 330 335

Lys Asn Val Thr Ile Pro Glu Leu Thr Glu Asp Leu Asp Gly Leu Gly
340 345 350

GBS patentin.ST25

Tyr Leu Gln Gly Lys Asp Val Asp Phe Val Asn Lys Lys Ala Thr Asp
355 360 365

Gly Val Leu Leu Ala His Thr Asp Gly Gly Val Pro Asn Met Phe Val
370 375 380

Thr Leu Pro Thr Gln Asp Ala Tyr Thr Leu Gly Tyr Thr Ile Tyr Phe
385 390 395 400

Phe Glu Leu Ala Ile Gly Leu Ser Gly Tyr Leu Asn Ser Val Asn Pro
405 410 415

Phe Asp Gln Pro Gly Val Glu Ala Tyr Lys Arg Asn Met Phe Ala Leu
420 425 430

Leu Gly Lys Pro Gly Phe Glu Glu Leu Ser Ala Glu Leu Asn Ala Arg
435 440 445

Leu

<210> 244

<211> 105

<212> PRT

<213> Streptococcus agalactiae

<400> 244

Met Lys Glu Lys Gln Thr Ala Gly Arg Arg Gln Leu Glu Glu Phe Ala
1 5 10 15

Pro Glu Phe Ala Arg Tyr Asn Asp Asp Ile Leu Phe Gly Glu Val Trp
20 25 30

Ala Lys Glu Asp His Leu Thr Asp Lys Thr Arg Ser Ile Ile Thr Ile
35 40 45

Ser Ala Leu Ile Ser Gly Gly Asn Leu Glu Gln Leu Glu His His Leu
50 55 60

Gln Phe Ala Lys Gln Asn Gly Val Thr Lys Glu Glu Ile Ala Asp Ile
65 70 75 80

Ile Thr His Leu Ala Phe Tyr Val Gly Trp Pro Lys Ala Trp Ser Ala
85 90 95

Phe Asn Lys Ala Lys Glu Ile Trp Ile
100 105

GBS patentin.ST25

<210> 245
 <211> 156
 <212> PRT
 <213> Streptococcus agalactiae

<400> 245

Ala Trp Arg Ala Leu Glu Asp Ala Gln Lys Ser Gly Lys Val Lys Ser
 1 5 10 15
 Ile Gly Val Ser Asn Phe Leu Glu Lys Asp Leu Glu Asn Ile Leu Lys
 20 25 30
 Asn Gly His Val Lys Pro Ala Val Asn Gln Ile Leu Ala His Ile Gly
 35 40 45
 Asn Thr Pro Phe Asp Leu Ile Asp Tyr Cys Gln Ser Lys Gly Ile Gln
 50 55 60
 Val Glu Ala Tyr Ser Pro Ile Ala His Gly Gln Ala Leu Lys Ser Asp
 65 70 75 80
 Gly Ile Gln Lys Met Ala Glu Lys Tyr Gly Val Ser Val Ala Gln Leu
 85 90 95
 Cys Ile Gln Tyr Leu Leu Gln Leu Asn Leu Ile Val Leu Pro Lys Ala
 100 105 110
 Ser Ser Lys Glu His Leu Gln Ser Asn Leu Asp Phe Asp Phe Val Ile
 115 120 125
 Ser Asp Glu Asp Met Ser Ile Leu Lys Ser Leu Met Phe Asp Asp Tyr
 130 135 140
 Gly Glu Phe Ser Asn Phe Pro Val Phe Ser Glu Lys
 145 150 155

<210> 246
 <211> 1126
 <212> PRT
 <213> Streptococcus agalactiae

<400> 246

Met Phe Arg Arg Ser Lys Asn Asn Ser Tyr Asp Thr Ser Gln Thr Lys
 1 5 10 15

GBS patentin.ST25

Gln Arg Phe Ser Ile Lys Lys Phe Lys Phe Gly Ala Ala Ser Val Leu
20 25 30

Ile Gly Leu Ser Phe Leu Gly Gly Val Thr Gln Gly Asn Leu Asn Ile
35 40 45

Phe Glu Glu Ser Ile Val Ala Ala Ser Thr Ile Pro Gly Ser Ala Ala
50 55 60

Thr Leu Asn Thr Ser Ile Thr Lys Asn Ile Gln Asn Gly Asn Ala Tyr
65 70 75 80

Ile Asp Leu Tyr Asp Val Lys Asn Gly Leu Ile Asp Pro Gln Asn Leu
85 90 95

Ile Val Leu Asn Pro Ser Ser Tyr Ser Ala Asn Tyr Tyr Ile Lys Gln
100 105 110

Gly Ala Lys Tyr Tyr Ser Asn Pro Ser Glu Ile Thr Thr Thr Gly Ser
115 120 125

Ala Thr Ile Thr Phe Asn Ile Leu Asp Glu Thr Gly Asn Pro His Lys
130 135 140

Lys Ala Asp Gly Gln Ile Asp Ile Val Ser Val Asn Leu Thr Ile Tyr
145 150 155 160

Asp Ser Thr Ala Leu Arg Asn Arg Ile Asp Glu Val Ile Asn Asn Ala
165 170 175

Asn Asp Pro Lys Trp Ser Asp Gly Ser Arg Asp Glu Val Leu Thr Gly
180 185 190

Leu Glu Lys Ile Lys Lys Asp Ile Asp Asn Asn Pro Lys Thr Gln Ile
195 200 205

Asp Ile Asp Asn Lys Ile Asn Glu Val Asn Glu Ile Glu Lys Leu Leu
210 215 220

Val Val Ser Leu Pro Asp Lys Ile Lys Tyr Ser Pro Glu Ala Lys His
225 230 235 240

Arg Thr Val Glu Gln His Ala Glu Leu Asp Ala Lys Asp Ser Ile Ala
245 250 255

Asn Thr Asp Glu Leu Pro Ser Asn Ser Thr Tyr Asn Trp Lys Asn Gly
260 265 270

His Lys Pro Asp Thr Ser Thr Ser Gly Glu Lys Asp Gly Ile Val Glu
275 280 285

GBS patentin.ST25

Val His Tyr Pro Asp Gly Thr Val Asp Asp Val Asn Val Lys Val Thr
290 295 300

Val Thr Ser Lys Lys Thr Asp Asn Thr Ala Pro Thr Leu Thr Val Thr
305 310 315 320

Pro Glu Gln Gln Thr Val Lys Val Asp Glu Asp Ile Thr Phe Thr Val
325 330 335

Thr Ala Glu Asp Glu Asn Glu Val Glu Leu Gly Leu Asp Asp Leu Lys
340 345 350

Ala Lys Tyr Glu Asn Asp Ile Ile Gly Ala Arg Val Lys Ile Lys Tyr
355 360 365

Leu Thr Lys Glu Pro Asn Lys Lys Val Met Glu Val Thr Ile Met Lys
370 375 380

Ala Thr Leu Ala Asp Lys Gly Ala Ile Thr Phe Thr Ala Lys Asp Lys
385 390 395 400

Ala Gly Asn Gln Ala Glu Pro Lys Thr Val Thr Ile Asn Val Leu Pro
405 410 415

Pro Asp Lys Ile Lys Tyr Ser Pro Glu Ala Lys His Arg Thr Val Glu
420 425 430

Gln His Ala Glu Leu Asp Ala Lys Asp Ser Ile Ala Asn Thr Asp Glu
435 440 445

Leu Pro Ser Asn Ser Thr Tyr Asn Trp Lys Asn Gly His Lys Pro Asp
450 455 460

Thr Ser Thr Ser Gly Glu Lys Asp Gly Ile Val Glu Val His Tyr Pro
465 470 475 480

Asp Gly Thr Val Asp Asp Val Asn Val Lys Val Thr Val Thr Ser Lys
485 490 495

Lys Thr Asp Asn Thr Ala Pro Thr Leu Thr Val Thr Pro Glu Gln Gln
500 505 510

Thr Val Lys Val Asp Glu Asp Ile Thr Phe Thr Val Thr Ala Glu Asp
515 520 525

Glu Asn Glu Val Glu Leu Gly Leu Asp Asp Leu Lys Ala Lys Tyr Glu
530 535 540

Asn Asp Ile Ile Gly Ala Arg Val Lys Ile Lys Tyr Leu Thr Lys Glu
545 550 555 560

GBS patentin.ST25

Pro Asn Lys Lys Val Met Glu Val Thr Ile Met Lys Ala Thr Leu Ala
565 570 575

Asp Lys Gly Ala Ile Thr Phe Thr Ala Lys Asp Lys Ala Gly Asn Gln
580 585 590

Ala Glu Pro Lys Thr Val Thr Ile Asn Val Leu Pro Pro Asp Lys Ile
595 600 605

Lys Tyr Ser Pro Glu Ala Lys His Arg Thr Val Glu Gln His Ala Glu
610 615 620

Leu Asp Ala Lys Asp Ser Ile Ala Asn Thr Asp Glu Leu Pro Ser Asn
625 630 635 640

Ser Thr Tyr Asn Trp Lys Asn Gly His Lys Pro Asp Thr Ser Thr Pro
645 650 655

Gly Glu Lys Asn Ala Val Val Val Val Thr Tyr Pro Asp Lys Ser Thr
660 665 670

Asp Glu Val Pro Val Lys Val Thr Val Val Asp Pro Arg Thr Asp Ala
675 680 685

Glu Lys Asn Asp Pro Ala Gly Lys Asp Gln Thr Val Lys Val Gly Glu
690 695 700

Gln Pro Asp Pro Thr Lys Ser Leu Glu Ala Val Pro Ala Gly Ser Thr
705 710 715 720

Val Ala Tyr Lys Glu Pro Val Asp Thr Lys Thr Pro Gly Glu Lys Asn
725 730 735

Ala Ile Val Val Val Thr Tyr Pro Asp Lys Ser Thr Asp Glu Val Pro
740 745 750

Val Lys Val Thr Val Val Asp Pro Arg Thr Asp Ala Glu Lys Asn Asp
755 760 765

Pro Ala Gly Lys Asp Gln Thr Val Lys Val Gly Glu Gln Pro Asp Pro
770 775 780

Thr Lys Ser Leu Glu Ala Val Pro Ala Gly Ser Thr Val Ala Tyr Lys
785 790 795 800

Glu Pro Val Asp Thr Lys Thr Pro Gly Glu Lys Asn Ala Ile Val Val
805 810 815

Val Thr Tyr Pro Asp Lys Ser Thr Asp Glu Val Pro Val Lys Val Thr
820 825 830

GBS patentin.ST25

Val Val Asp Pro Arg Thr Asp Ala Glu Lys Asn Asp Pro Ala Gly Lys
835 840 845

Asp Gln Thr Val Lys Val Gly Glu Gln Pro Asp Pro Thr Lys Ser Leu
850 855 860

Glu Ala Val Pro Ala Gly Ser Thr Val Ala Tyr Lys Glu Pro Val Asp
865 870 875 880

Thr Lys Thr Pro Gly Glu Lys Asn Ala Val Val Val Val Thr Tyr Pro
885 890 895

Asp Lys Ser Thr Asp Glu Val Pro Val Lys Val Thr Val Val Asp Pro
900 905 910

Arg Thr Asp Ala Glu Lys Asn Asp Pro Ala Gly Lys Asp Gln Thr Val
915 920 925

Lys Val Gly Glu Gln Pro Asp Pro Thr Lys Ser Leu Glu Ala Val Pro
930 935 940

Ala Gly Ser Thr Val Ala Tyr Lys Glu Pro Val Asp Thr Lys Thr Pro
945 950 955 960

Gly Glu Lys Asn Ala Val Val Val Val Thr Tyr Pro Asp Lys Ser Thr
965 970 975

Asp Glu Val Pro Val Lys Val Thr Val Val Asp Pro Arg Thr Asp Ala
980 985 990

Glu Lys Asn Asp Pro Ala Gly Gly Glu Thr Thr Val Pro Gln Gly Thr
995 1000 1005

Pro Ile Ser Asp Glu Glu Ile Thr Gly Leu Val Lys Ile Pro Glu
1010 1015 1020

Gly Ser Asn Gly Val Pro Lys Val Val Gly Asp Arg Pro Asn Thr
1025 1030 1035

Asp Val Pro Gly Asp Tyr Lys Val Thr Val Glu Val Thr Tyr Pro
1040 1045 1050

Asp Gly Thr Lys Asp Thr Val Ala Val Thr Val His Val Thr Pro
1055 1060 1065

Lys Pro Val Pro Asp Lys Asp Lys Tyr Asp Pro Thr Gly Lys Ser
1070 1075 1080

Gln Gln Val Asn Gly Lys Gly Asn Lys Leu Pro Ala Thr Gly Glu
1085 1090 1095

GBS patentin.ST25

Ser Ala Thr Pro Phe Phe Asn Val Ala Ala Leu Thr Ile Ile Ser
1100 1105 1110

Ser Val Gly Leu Leu Ser Val Ser Lys Lys Lys Glu Asp
1115 1120 1125

<210> 247

<211> 189

<212> PRT

<213> Streptococcus agalactiae

<400> 247

Met Gln Ile Leu Glu Asp Tyr Asp Gly Arg Ala Leu Pro Lys Leu Glu
1 5 10 15

Thr Asp Arg Leu Ile Leu Arg Gln Arg Thr Val Gly Asp Val Pro Ala
20 25 30

Met Phe Asp Tyr Val Cys Leu Glu Glu Val Ala Tyr Pro Ala Gly Leu
35 40 45

Ser Pro Ile Ala Ser Leu Glu Asp Glu Tyr Asp Tyr Phe Glu Asn Arg
50 55 60

Tyr Tyr Gln Asn Leu Glu Lys Ala Lys Leu Pro Ser Gly Tyr Gly Ile
65 70 75 80

Thr Val Lys Gly Ser Asp Arg Ile Ile Gly Ser Cys Ala Phe Asn His
85 90 95

Arg Arg Glu Asp Asp Val Phe Glu Ile Gly Tyr Leu Leu His Pro Asp
100 105 110

Tyr Trp Gly His Gly Tyr Met Thr Glu Ala Val Ala Ala Leu Ile Glu
115 120 125

Val Gly Phe Thr Leu Leu Asn Leu His Lys Ile Glu Ile Arg Cys Tyr
130 135 140

Asp Tyr Asn Lys Gln Ser Gln Arg Val Ala Glu Lys Leu Gly Phe Thr
145 150 155 160

Leu Glu Ala Thr Ile Arg Asp Arg Lys Asp Asn Gln Gly Asn Arg Cys
165 170 175

Val Asn Leu Ile Tyr Gly Leu Leu Arg Ser Glu Trp Glu
180 185

GBS patentin.ST25

<210> 248

<211> 884

<212> PRT

<213> Streptococcus agalactiae

<400> 248

Met Ser Lys Glu Leu Ser Pro Lys Tyr Asn Pro Ala Glu Val Glu Glu
1 5 10 15

Gly Arg Tyr Gln Thr Trp Leu Asp Gln Asp Val Phe Lys Pro Ser Gly
20 25 30

Asp Thr Glu Ala Lys Pro Tyr Ser Ile Val Ile Pro Pro Pro Asn Val
35 40 45

Thr Gly Lys Leu His Leu Gly His Ala Trp Asp Thr Thr Leu Gln Asp
50 55 60

Ile Ile Ile Arg Gln Lys Arg Met Gln Gly Phe Asp Thr Leu Trp Leu
65 70 75 80

Pro Gly Met Asp His Ala Gly Ile Ala Thr Gln Ala Lys Val Glu Glu
85 90 95

Arg Leu Arg Glu Gln Gly Ile Ser Arg Tyr Asp Leu Gly Arg Glu Lys
100 105 110

Phe Leu Asp Lys Val Trp Glu Trp Lys Asp Glu Tyr Ala Ala Thr Ile
115 120 125

Lys Ser Gln Trp Gly Lys Met Gly Leu Ser Val Asp Tyr Ser Arg Glu
130 135 140

Arg Phe Thr Leu Asp Glu Gly Leu Ser Lys Ala Val Arg Lys Val Phe
145 150 155 160

Val Asp Leu Tyr Asn Lys Gly Trp Ile Tyr Arg Gly Glu Phe Ile Ile
165 170 175

Asn Trp Asp Pro Ala Ala Arg Thr Ala Leu Ser Asp Ile Glu Val Ile
180 185 190

His Lys Asp Val Glu Gly Ala Phe Tyr His Met Asn Tyr Met Leu Glu
195 200 205

Asp Gly Ser Arg Ala Leu Glu Val Ala Thr Thr Arg Pro Glu Thr Met
210 215 220

GBS patentin.ST25

Phe Gly Asp Val Ala Val Ala Val Asn Pro Glu Asp Pro Arg Tyr Lys
225 230 235 240

Asp Leu Ile Gly Gln Asn Val Ile Leu Pro Ile Ile Asn Lys Pro Ile
245 250 255

Pro Ile Ile Ala Asp Glu His Ala Asp Pro Glu Phe Gly Thr Gly Val
260 265 270

Val Lys Ile Thr Pro Ala His Asp Pro Asn Asp Phe Ala Val Gly Gln
275 280 285

Arg His Asn Leu Pro Gln Val Asn Val Met Asn Asp Asp Gly Thr Met
290 295 300

Asn Glu Leu Ala Asp Glu Phe Asn Gly Met Asp Arg Phe Glu Ala Arg
305 310 315 320

Lys Ala Val Val Ala Lys Leu Glu Ser Leu Gly Asn Leu Val Lys Ile
325 330 335

Glu Lys Met Thr His Ser Val Gly His Ser Glu Arg Thr Gly Val Val
340 345 350

Val Glu Pro Arg Leu Ser Thr Gln Trp Phe Val Lys Met Asp Gln Leu
355 360 365

Ala Lys Asn Ala Ile Ala Asn Gln Asp Thr Glu Asp Lys Val Glu Phe
370 375 380

Tyr Pro Pro Arg Phe Asn Asp Thr Phe Met Ser Trp Met Glu Asn Val
385 390 395 400

His Asp Trp Val Ile Ser Arg Gln Leu Trp Trp Gly His Gln Ile Pro
405 410 415

Ala Trp Tyr Asn Val Asn Gly Glu Met Tyr Val Gly Glu Asp Ala Pro
420 425 430

Glu Gly Asp Gly Trp Thr Gln Asp Glu Asp Val Leu Asp Thr Trp Phe
435 440 445

Ser Ser Ala Leu Trp Pro Phe Ser Thr Met Gly Trp Pro Asp Thr Glu
450 455 460

Ala Ala Asp Phe Lys Arg Tyr Phe Pro Thr Ser Thr Leu Val Thr Gly
465 470 475 480

Tyr Asp Ile Ile Phe Phe Trp Val Ser Arg Met Ile Phe Gln Ser Leu
485 490 495

GBS patentin.ST25

Glu Phe Thr Gly Arg Gln Pro Phe Ser Asn Val Leu Ile His Gly Leu
500 505 510

Ile Arg Asp Glu Glu Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly
515 520 525

Ile Asp Pro Met Asp Val Ile Glu Lys Tyr Gly Ala Asp Ala Leu Arg
530 535 540

Trp Phe Leu Ser Asn Gly Ser Ala Pro Gly Gln Asp Val Arg Phe Ser
545 550 555 560

Tyr Glu Lys Met Asp Ala Ser Trp Asn Phe Ile Asn Lys Ile Trp Asn
565 570 575

Ile Ser Arg Tyr Ile Leu Met Asn Asn Glu Gly Leu Thr Leu Asp Gln
580 585 590

Ala Arg Glu Asn Val Glu Lys Val Val Asn Ser Gln Val Gly Asn Val
595 600 605

Thr Asp Arg Trp Ile Leu His Asn Leu Asn Glu Thr Val Gly Lys Val
610 615 620

Thr Glu Ser Phe Asp Lys Phe Glu Phe Gly Val Ala Gly His Ile Leu
625 630 635 640

Tyr Asn Phe Ile Trp Glu Glu Phe Ala Asn Trp Tyr Val Glu Leu Thr
645 650 655

Lys Glu Val Leu Tyr Ser Asp Asn Glu Asp Glu Lys Val Val Thr Arg
660 665 670

Ser Val Leu Leu Tyr Thr Leu Asp Gln Ile Leu Arg Leu Leu His Pro
675 680 685

Ile Met Pro Phe Val Thr Glu Glu Ile Phe Gly Gln Tyr Ala Glu Gly
690 695 700

Ser Ile Val Leu Ala Ser Tyr Pro Gln Val Asn Ala Thr Phe Glu Asn
705 710 715 720

Gln Thr Ala His Lys Gly Val Glu Ser Leu Lys Asp Leu Ile Arg Ser
725 730 735

Val Arg Asn Ser Arg Ala Glu Val Asn Val Ala Pro Ser Lys Pro Ile
740 745 750

Thr Ile Leu Val Lys Thr Ser Asp Ser Glu Leu Glu Ser Phe Phe Lys
755 760 765

GBS patentin.ST25

Asp Asn Ser Asn Tyr Ile Lys Arg Phe Thr Asn Pro Glu Thr Leu Glu
770 775 780

Ile Ser Ser Ala Ile Thr Ala Pro Glu Leu Ala Met Thr Ser Ile Ile
785 790 795 800

Thr Gly Ala Glu Ile Phe Leu Pro Leu Ala Asp Leu Leu Asn Val Glu
805 810 815

Glu Glu Leu Ala Arg Leu Glu Lys Glu Leu Ala Lys Trp Gln Lys Glu
820 825 830

Leu Asn Met Val Gly Lys Lys Leu Ser Asn Glu Arg Phe Val Ala Asn
835 840 845

Ala Lys Pro Glu Val Val Gln Lys Glu Lys Asp Lys Gln Thr Asp Tyr
850 855 860

Gln Thr Lys Tyr Asp Ala Thr Ile Ala Arg Ile Glu Glu Met Lys Lys
865 870 875 880

Leu Asn Asn Asp

<210> 249

<211> 244

<212> PRT

<213> streptococcus agalactiae

<400> 249

Met Val Glu Pro Ile Ile Ser Ile Gln Gly Leu His Lys Ser Phe Gly
1 5 10 15

Lys Asn Glu Val Leu Lys Gly Ile Asp Leu Asp Ile His Gln Gly Glu
20 25 30

Val Val Val Ile Ile Gly Pro Ser Gly Ser Gly Lys Ser Thr Phe Leu
35 40 45

Arg Thr Met Asn Leu Leu Glu Val Pro Thr Lys Gly Thr Val Thr Phe
50 55 60

Glu Gly Ile Asp Ile Thr Asp Lys Lys Asn Asp Ile Phe Lys Met Arg
65 70 75 80

Glu Lys Met Gly Met Val Phe Gln Gln Phe Asn Leu Phe Pro Asn Met
85 90 95

GBS patentin.ST25

Thr Val Leu Glu Asn Ile Thr Leu Ser Pro Ile Lys Thr Lys Gly Leu
100 105 110

Ser Lys Leu Asp Ala Gln Thr Lys Ala Tyr Glu Leu Leu Glu Lys Val
115 120 125

Gly Leu Lys Glu Lys Ala Asn Ala Tyr Pro Ala Ser Leu Ser Gly Gly
130 135 140

Gln Gln Gln Arg Ile Ala Ile Ala Arg Gly Leu Ala Met Asn Pro Asp
145 150 155 160

Val Leu Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val
165 170 175

Gly Glu Val Leu Thr Val Met Gln Asp Leu Ala Lys Ser Gly Met Thr
180 185 190

Met Val Ile Val Thr His Glu Met Gly Phe Ala Arg Glu Val Ala Asp
195 200 205

Arg Val Ile Phe Met Asp Ala Gly Ile Ile Val Glu Gln Gly Thr Pro
210 215 220

Lys Glu Val Phe Glu Gln Thr Lys Glu Ile Arg Thr Arg Asp Phe Leu
225 230 235 240

Ser Lys Val Leu

<210> 250

<211> 564

<212> PRT

<213> Streptococcus agalactiae

<400> 250

Met Asn Tyr Lys Glu Ile Tyr Gln Glu Trp Leu Glu Asn Asp Ser Leu
1 5 10 15

Gly Lys Asp Ile Lys Ser Asp Leu Glu Ala Ile Lys Gly Asp Glu Ser
20 25 30

Glu Ile Gln Asp Arg Phe Tyr Lys Thr Leu Glu Phe Gly Thr Ala Gly
35 40 45

Leu Arg Gly Lys Leu Gly Ala Gly Thr Asn Arg Met Asn Thr Tyr Met
50 55 60

GBS patentin.ST25

Val Gly Lys Ala Ala Gln Ala Leu Ala Asn Thr Ile Ile Asp His Gly
65 70 75 80

Pro Glu Ala Ile Ala Arg Gly Ile Ala Val Ser Tyr Asp Val Arg Tyr
85 90 95

Gln Ser Lys Glu Phe Ala Glu Leu Thr Cys Ser Ile Met Ala Ala Asn
100 105 110

Gly Ile Lys Ser Tyr Ile Tyr Lys Gly Ile Arg Pro Thr Pro Met Cys
115 120 125

Ser Tyr Ala Ile Arg Ala Leu Gly Cys Val Ser Gly Val Met Val Thr
130 135 140

Ala Ser His Asn Pro Gln Ala Tyr Asn Gly Tyr Lys Ala Tyr Trp Lys
145 150 155 160

Glu Gly Ser Gln Ile Leu Asp Asp Ile Ala Asp Gln Ile Ala Asn His
165 170 175

Met Asp Ala Ile Thr Asp Tyr Gln Gln Ile Arg Gln Ile Pro Phe Glu
180 185 190

Glu Ala Leu Ala Ser Gly Leu Ala Ser Tyr Ile Asp Glu Ser Ile Glu
195 200 205

Glu Ala Tyr Lys Lys Glu Val Leu Gly Leu Thr Ile Asn Asp Thr Asn
210 215 220

Ile Asp Lys Ser Val Arg Val Val Tyr Thr Pro Leu Asn Gly Val Gly
225 230 235 240

Asn Leu Pro Val Arg Glu Val Leu Arg Arg Arg Gly Phe Glu Asn Val
245 250 255

Tyr Val Val Pro Glu Gln Glu Met Pro Asp Pro Asp Phe Thr Thr Val
260 265 270

Gly Tyr Pro Asn Pro Glu Val Pro Lys Ala Phe Ala Tyr Ser Glu Ser
275 280 285

Leu Gly Lys Ser Val Asp Ala Asp Ile Leu Leu Ala Thr Asp Pro Asp
290 295 300

Cys Asp Arg Val Ala Leu Glu Val Lys Asp Ser Lys Gly Glu Tyr Ile
305 310 315 320

Phe Leu Asn Gly Asn Lys Ile Gly Ala Leu Leu Ser Tyr Tyr Ile Phe
325 330 335

GBS patentin.ST25

Ser Gln Arg Cys Ala Leu Gly Asn Leu Pro His His Pro Val Leu Val
340 345 350

Lys Ser Ile Val Thr Gly Asp Leu Ser Lys Val Ile Ala Asp Lys Tyr
355 360 365

Asn Ile Glu Thr Val Glu Thr Leu Thr Gly Phe Lys Asn Ile Cys Gly
370 375 380

Lys Ala Asn Glu Tyr Asp Ile Ser Lys Asp Lys Thr Tyr Leu Phe Gly
385 390 395 400

Tyr Glu Glu Ser Ile Gly Phe Cys Tyr Gly Thr Phe Val Arg Asp Lys
405 410 415

Asp Ala Val Ser Ala Ser Met Met Val Val Glu Met Thr Ala Tyr Tyr
420 425 430

Lys Glu Arg Gly Gln Thr Leu Leu Asp Val Leu Gln Thr Ile Tyr Asp
435 440 445

Glu Phe Gly Tyr Tyr Asn Glu Arg Gln Phe Ser Leu Glu Leu Glu Gly
450 455 460

Ala Glu Gly Gln Glu Arg Ile Ser Arg Ile Met Glu Asp Phe Arg Gln
465 470 475 480

Asp Pro Ile Leu Gln Val Gly Glu Met Arg Leu Glu Asn Ser Ile Asp
485 490 495

Phe Lys Asp Gly Tyr Lys Asp Phe Pro Lys Gln Asn Cys Leu Lys Tyr
500 505 510

Tyr Phe Asn Glu Gly Ser Trp Tyr Ala Leu Arg Pro Ser Gly Thr Glu
515 520 525

Pro Lys Ile Lys Cys Tyr Leu Tyr Thr Ile Gly Cys Thr Glu Ala Asp
530 535 540

Ser Leu Ser Lys Leu Asn Ala Ile Glu Ser Ala Cys Arg Ala Lys Met
545 550 555 560

Asn Ser Thr Lys

<210> 251

<211> 403

<212> PRT

<213> streptococcus agalactiae

<400> 251

Met Tyr Arg Glu Ile Thr Ala Val Glu His Asp Arg Phe Val Ser Glu
 1 5 10 15

Ser Asn Gln Thr Asn Leu Leu Gln Ser Ser Asn Trp Pro Lys Val Lys
 20 25 30

Asp Asn Trp Gly Ser Gln Leu Leu Gly Phe Phe Asp Gly Glu Thr Gln
 35 40 45

Ile Ala Ser Ala Ser Ile Leu Ile Lys Ser Leu Pro Leu Gly Phe Ser
 50 55 60

Met Leu Tyr Ile Pro Arg Gly Pro Ile Met Asp Tyr Ser Asn Leu Asp
 65 70 75 80

Ile Val Thr Lys Val Leu Lys Asp Leu Lys Ala Phe Gly Lys Lys Gln
 85 90 95

Arg Ala Leu Phe Ile Lys Cys Asp Pro Leu Ile Tyr Leu Lys Met Val
 100 105 110

Asn Ala Lys Asp Phe Glu Asn Ser Pro Asp Glu Lys Glu Gly Leu Ile
 115 120 125

Ala Ile Asp His Leu Gln Arg Ala Gly Ala Asp Trp Thr Gly Arg Thr
 130 135 140

Thr Asp Leu Ala His Thr Ile Gln Pro Arg Phe Gln Ala Asn Leu Tyr
 145 150 155 160

Ala Asn Gln Phe Gly Leu Asp Lys Met Ser Lys Lys Thr Arg Gln Ala
 165 170 175

Ile Arg Thr Ser Lys Asn Lys Gly Val Asp Ile Gln Phe Gly Ser His
 180 185 190

Glu Leu Leu Glu Asp Phe Ala Glu Leu Met Lys Lys Thr Glu Asp Arg
 195 200 205

Lys Gly Ile Asn Leu Arg Gly Ile Asp Tyr Tyr Gln Lys Leu Leu Asp
 210 215 220

Thr Tyr Pro Asn Asn Ser Tyr Ile Thr Met Ala Ser Leu Asp Val Ala
 225 230 235 240

Lys Arg Leu Glu Lys Ile Glu Lys Glu Cys Gln Ile Ala Gln Ser Glu
 245 250 255

GBS patentin.ST25

Arg Ile Lys Ser Leu Glu Leu Asn Arg Glu Lys Lys Val Lys Gln His
260 265 270

Gln Gly Thr Ile Asp Arg Leu Asn Lys Glu Ile Asp Phe Leu Lys Glu
275 280 285

Ala Gln Lys Ala Tyr Asp Arg Asp Ile Ile Pro Leu Ala Ala Thr Leu
290 295 300

Thr Leu Glu Phe Gly Asn Thr Ser Glu Asn Ile Tyr Ala Gly Met Asp
305 310 315 320

Asp Tyr Phe Lys Ser Tyr Ser Ala Pro Ile Tyr Thr Trp Phe Glu Thr
325 330 335

Ala Gln Arg Ala Phe Glu Arg Gly Asn Ile Trp Gln Asn Met Gly Gly
340 345 350

Ile Glu Asn Asp Leu Ser Gly Gly Leu Tyr His Phe Lys Ser Lys Phe
355 360 365

Glu Pro Ile Ile Glu Glu Phe Ile Gly Glu Phe Asn Ile Pro Val Asn
370 375 380

Arg Leu Leu Tyr Lys Ala Ser Asn Tyr Val Tyr Ala Leu Arg Lys Lys
385 390 395 400

Arg Asn Ser

<210> 252

<211> 465

<212> PRT

<213> Streptococcus agalactiae

<400> 252

Met Ala Cys Thr Thr Ile Leu Val Gly Lys Lys Ala Ser Tyr Asp Gly
1 5 10 15

Ser Thr Met Ile Ala Arg Thr Glu Asp Ser Val Asn Gly Asp Phe Thr
20 25 30

Pro Lys Lys Leu Lys Val Met Thr Ser Lys Asp Gln Pro Arg His Tyr
35 40 45

Lys Ser Val Leu Ser Asn Phe Glu Val Asp Leu Pro Asp Asn Pro Leu
50 55 60

GBS patentin.ST25

Pro Tyr Thr Ser Val Pro Asp Ala Leu Gly Lys Asp Gly Ile Trp Gly
65 70 75 80

Glu Ala Gly Ile Asn Ser Lys Asn Val Ala Met Ser Ala Thr Glu Thr
85 90 95

Ile Thr Thr Asn Ser Arg Val Leu Gly Ala Asp Pro Leu Val Ser Asp
100 105 110

Gly Ile Gly Glu Glu Asp Ile Leu Thr Leu Val Leu Pro Tyr Ile Gln
115 120 125

Ser Ala Arg Glu Gly Val Glu Arg Leu Gly Ala Ile Leu Glu Lys Tyr
130 135 140

Gly Thr Tyr Glu Ser Asn Gly Ile Ala Phe Ser Asp Thr Glu Glu Ile
145 150 155 160

Trp Trp Leu Glu Thr Ile Gly Gly His His Trp Ile Ala Arg Arg Val
165 170 175

Pro Asp Asp Val Tyr Val Thr Asn Pro Asn Gln Leu Gly Ile Asp His
180 185 190

Phe Glu Phe Asn Asn Cys Asp Asp Tyr Met Cys Ser Ser Asp Leu Lys
195 200 205

Glu Phe Ile Glu Gln Tyr His Leu Asp Leu Thr Tyr Ser Asn Glu His
210 215 220

Phe Asn Pro Arg Tyr Ala Phe Gly Ser Gln Arg Asp Lys Asp Arg His
225 230 235

Tyr Asn Thr Pro Arg Ser Trp Ala Met Gln Arg Phe Leu Asn Pro Glu
245 250 255

Ile Glu Gln Asp Pro Arg Ser Leu Phe Ile Pro Trp Cys Gln Lys Pro
260 265 270

Tyr Arg Lys Ile Thr Val Glu Asp Ile Lys Tyr Val Leu Ser Asp His
275 280 285

Tyr Gln Asp Ser Val Tyr Asp Pro Tyr Gly Pro Glu Gly Asp Ala Val
290 295 300

Ser Arg Arg Ala Phe Arg Ser Val Gly Ile Asn Arg Thr Ser Gln Thr
305 310 315 320

Ser Ile Leu Gln Leu Arg Pro Asn Lys Ser Leu Glu Thr Thr Gly Val
325 330 335

GBS patentin.ST25

Gln Trp Leu Ser Tyr Gly Ser Met Pro Phe Ala Thr Met Val Pro Leu
340 345 350

Phe Thr Gln Val Glu Thr Val Pro Asn Tyr Phe Ser Asn Thr Thr Lys
355 360 365

Asp Ala Ser Thr Asp Asn Phe Tyr Trp Thr Asn Arg Leu Ile Ala Ala
370 375 380

Leu Ala Asp Pro His Phe Tyr Gln His Glu Ala Asp Ile Glu Ser Tyr
385 390 395 400

Ile Glu Arg Thr Met Ala Gln Gly His Ala His Ile Asn Gly Val Asp
405 410 415

Arg Glu Val Ala Glu Asn Lys Glu Ile Asp Phe Gln Gln Lys Asn Gln
420 425 430

Glu Met Ser Asp Tyr Ile Gln Lys Glu Ser Gln Glu Leu Leu Asn Arg
435 440 445

Ile Leu Phe Asp Ala Ser Asn Leu Met Thr Asn Arg Phe Ser Met Gly
450 455 460

Asp
465

<210> 253

<211> 506

<212> PRT

<213> Streptococcus agalactiae

<400> 253

Met Arg Lys Lys Phe Leu Leu Leu Met Ser Phe Val Ala Met Phe Ala
1 5 10 15

Ala Trp Gln Leu Val Gln Val Lys Gln Val Trp Ala Asp Ser Lys Leu
20 25 30

Lys Val Val Thr Thr Phe Tyr Pro Val Tyr Glu Phe Thr Lys Asn Val
35 40 45

Val Gly Asp Lys Ala Asp Val Ser Met Leu Ile Lys Ala Gly Thr Glu
50 55 60

Pro His Asp Phe Glu Pro Ser Thr Lys Asn Ile Ala Ala Ile Gln Asp
65 70 75 80

GBS patentin.ST25

Ser Asn Ala Phe Val Tyr Met Asp Asp Asn Met Glu Thr Trp Ala Pro
85 90 95

Lys Val Ala Lys Ser Val Lys Ser Lys Lys Val Thr Thr Ile Lys Gly
100 105 110

Thr Gly Asp Met Leu Leu Thr Lys Gly Val Glu Glu Glu Gly Glu Glu
115 120 125

His Glu Gly His Gly His Glu Gly His His His Glu Leu Asp Pro His
130 135 140

Val Trp Leu Ser Pro Glu Arg Ala Ile Ser Val Val Glu Asn Ile Arg
145 150 155 160

Asn Lys Phe Val Lys Ala Tyr Pro Lys Asp Ala Ala Ser Phe Asn Lys
165 170 175

Asn Ala Asp Ala Tyr Ile Ala Lys Leu Lys Glu Leu Asp Lys Glu Tyr
180 185 190

Lys Asn Gly Leu Ser Asn Ala Lys Gln Lys Ser Phe Val Thr Gln His
195 200 205

Ala Ala Phe Gly Tyr Met Ala Leu Asp Tyr Gly Leu Asn Gln Val Pro
210 215 220

Ile Ala Gly Leu Thr Pro Asp Ala Glu Pro Ser Ser Lys Arg Leu Gly
225 230 235 240

Glu Leu Ala Lys Tyr Ile Lys Lys Tyr Asn Ile Asn Tyr Ile Tyr Phe
245 250 255

Glu Glu Asn Ala Ser Asn Lys Val Ala Lys Thr Leu Ala Asp Glu Val
260 265 270

Gly Val Lys Thr Ala Val Leu Ser Pro Leu Glu Gly Leu Ser Lys Lys
275 280 285

Glu Met Ala Ala Gly Glu Asp Tyr Phe Ser Val Met Arg Arg Asn Leu
290 295 300

Lys Val Leu Lys Lys Thr Thr Asp Val Ala Gly Lys Glu Val Ala Pro
305 310 315 320

Glu Glu Asp Lys Thr Lys Thr Val Glu Thr Gly Tyr Phe Lys Thr Lys
325 330 335

Asp Val Lys Asp Arg Lys Leu Thr Asp Tyr Ser Gly Asn Trp Gln Ser
340 345 350

GBS patentin.ST25

Val Tyr Pro₃₅₅ Leu Leu Gln Asp Gly₃₆₀ Thr Leu Asp Pro Val₃₆₅ Trp Asp Tyr
 Lys Ala₃₇₀ Lys Ser Lys Lys Asp₃₇₅ Met Thr Ala Ala Glu₃₈₀ Tyr Lys Lys Tyr
 Tyr Thr Ala Gly Tyr Lys₃₉₀ Thr Asp Val Glu Ser₃₉₅ Ile Lys Ile Asp Gly₄₀₀
 Lys Lys His Gln Met₄₀₅ Thr Phe Val Arg Asn₄₁₀ Gly Lys Ser Gln Thr₄₁₅ Phe
 Thr Tyr Lys Tyr₄₂₀ Ala Gly Tyr Lys Ile₄₂₅ Leu Thr Tyr Lys Lys₄₃₀ Gly Asn
 Arg Gly Val₄₃₅ Arg Tyr Leu Phe Glu₄₄₀ Ala Lys Glu Lys Asp₄₄₅ Ala Gly Gln
 Phe Lys₄₅₀ Tyr Ile Gln Phe Ser₄₅₅ Asp His Gly Ile Lys₄₆₀ Pro Asn Lys Ala
 Glu His Phe His Ile Phe₄₇₀ Trp Gly Ser Glu Ser₄₇₅ Gln Glu Lys Leu Phe₄₈₀
 Glu Glu Met Glu Asn₄₈₅ Trp Pro Thr Tyr Phe₄₉₀ Pro Ala Lys Met Ser₄₉₅ Gly
 Arg Glu Val Ala₅₀₀ Gln Asp Leu Met Ser₅₀₅ His

<210> 254

<211> 554

<212> PRT

<213> Streptococcus agalactiae

<400> 254

Met Lys Leu Ser₅ Lys Lys Leu Leu Phe Ser₁₀ Ala Ala Val Leu Thr Met₁₅
 Val Ala Gly Ser₂₀ Thr Val Glu Pro Val₂₅ Ala Gln Phe Ala Thr Gly Met₃₀
 Ser Ile Val₃₅ Arg Ala Ala Glu Val₄₀ Ser Gln Glu Arg Pro₄₅ Ala Lys Thr
 Thr Val Asn Ile Tyr Lys₅₅ Leu Gln Ala Asp Ser₆₀ Tyr Lys Ser Glu Ile

GBS patentin.ST25

Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
65 70 75 80

Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
85 90 95

Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
100 105 110

Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
115 120 125

Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
130 135 140

Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
145 150 155 160

Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
165 170 175

Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser
180 185 190

Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr
195 200 205

Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile
210 215 220

Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu
225 230 235 240

Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu
245 250 255

Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn
260 265 270

Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn
275 280 285

Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu
290 295 300

Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys
305 310 315 320

Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala
325 330 335

GBS patentin.ST25

Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr
340 345 350

Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys
355 360 365

Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg
370 375 380

Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu
385 390 395 400

Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala
405 410 415

Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val
420 425 430

Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu
435 440 445

Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala
450 455 460

Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile
465 470 475 480

Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr
485 490 495

Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr
500 505 510

Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly Gly Ile Gly
515 520 525

Thr Ala Ile Phe Val Ala Ile Gly Ala Ala Val Met Ala Phe Ala Val
530 535 540

Lys Gly Met Lys Arg Arg Thr Lys Asp Asn
545 550

<210> 255

<211> 890

<212> PRT

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 255

Met Lys Lys Arg Gln Lys Ile Trp Arg Gly Leu Ser Val Thr Leu Leu
 1 5 10 15

Ile Leu Ser Gln Ile Pro Phe Gly Ile Leu Val Gln Gly Glu Thr Gln
 20 25 30

Asp Thr Asn Gln Ala Leu Gly Lys Val Ile Val Lys Lys Thr Gly Asp
 35 40 45

Asn Ala Thr Pro Leu Gly Lys Ala Thr Phe Val Leu Lys Asn Asp Asn
 50 55 60

Asp Lys Ser Glu Thr Ser His Glu Thr Val Glu Gly Ser Gly Glu Ala
 65 70 75 80

Thr Phe Glu Asn Ile Lys Pro Gly Asp Tyr Thr Leu Arg Glu Glu Thr
 85 90 95

Ala Pro Ile Gly Tyr Lys Lys Thr Asp Lys Thr Trp Lys Val Lys Val
 100 105 110

Ala Asp Asn Gly Ala Thr Ile Ile Glu Gly Met Asp Ala Asp Lys Ala
 115 120 125

Glu Lys Arg Lys Glu Val Leu Asn Ala Gln Tyr Pro Lys Ser Ala Ile
 130 135 140

Tyr Glu Asp Thr Lys Glu Asn Tyr Pro Leu Val Asn Val Glu Gly Ser
 145 150 155 160

Lys Val Gly Glu Gln Tyr Lys Ala Leu Asn Pro Ile Asn Gly Lys Asp
 165 170 175

Gly Arg Arg Glu Ile Ala Glu Gly Trp Leu Ser Lys Lys Ile Thr Gly
 180 185 190

Val Asn Asp Leu Asp Lys Asn Lys Tyr Lys Ile Glu Leu Thr Val Glu
 195 200 205

Gly Lys Thr Thr Val Glu Thr Lys Glu Leu Asn Gln Pro Leu Asp Val
 210 215 220

Val Val Leu Leu Asp Asn Ser Asn Ser Met Asn Asn Glu Arg Ala Asn
 225 230 235 240

Asn Ser Gln Arg Ala Leu Lys Ala Gly Glu Ala Val Glu Lys Leu Ile
 245 250 255

Asp Lys Ile Thr Ser Asn Lys Asp Asn Arg Val Ala Leu Val Thr Tyr
 260 265 270

GBS patentin.ST25

Ala Ser Thr Ile Phe Asp Gly Thr Glu Ala Thr Val Ser Lys Gly Val
275 280 285

Ala Asp Gln Asn Gly Lys Ala Leu Asn Asp Ser Val Ser Trp Asp Tyr
290 295 300

His Lys Thr Thr Phe Thr Ala Thr Thr His Asn Tyr Ser Tyr Leu Asn
305 310 315 320

Leu Thr Asn Asp Ala Asn Glu Val Asn Ile Leu Lys Ser Arg Ile Pro
325 330 335

Lys Glu Ala Glu His Ile Asn Gly Asp Arg Thr Leu Tyr Gln Phe Gly
340 345 350

Ala Thr Phe Thr Gln Lys Ala Leu Met Lys Ala Asn Glu Ile Leu Glu
355 360 365

Thr Gln Ser Ser Asn Ala Arg Lys Lys Leu Ile Phe His Val Thr Asp
370 375 380

Gly Val Pro Thr Met Ser Tyr Ala Ile Asn Phe Asn Pro Tyr Ile Ser
385 390 395 400

Thr Ser Tyr Gln Asn Gln Phe Asn Ser Phe Leu Asn Lys Ile Pro Asp
405 410 415

Arg Ser Gly Ile Leu Gln Glu Asp Phe Ile Ile Asn Gly Asp Asp Tyr
420 425 430

Gln Ile Val Lys Gly Asp Gly Glu Ser Phe Lys Leu Phe Ser Asp Arg
435 440 445

Lys Val Pro Val Thr Gly Gly Thr Thr Gln Ala Ala Tyr Arg Val Pro
450 455 460

Gln Asn Gln Leu Ser Val Met Ser Asn Glu Gly Tyr Ala Ile Asn Ser
465 470 475 480

Gly Tyr Ile Tyr Leu Tyr Trp Arg Asp Tyr Asn Trp Val Tyr Pro Phe
485 490 495

Asp Pro Lys Thr Lys Lys Val Ser Ala Thr Lys Gln Ile Lys Thr His
500 505 510

Gly Glu Pro Thr Thr Leu Tyr Phe Asn Gly Asn Ile Arg Pro Lys Gly
515 520 525

Tyr Asp Ile Phe Thr Val Gly Ile Gly Val Asn Gly Asp Pro Gly Ala
530 535 540

GBS patentin.ST25

Thr Pro Leu Glu Ala Glu Lys Phe Met Gln Ser Ile Ser Ser Lys Thr
545 550 555 560

Glu Asn Tyr Thr Asn Val Asp Asp Thr Asn Lys Ile Tyr Asp Glu Leu
565 570 575

Asn Lys Tyr Phe Lys Thr Ile Val Glu Glu Lys His Ser Ile Val Asp
580 585 590

Gly Asn Val Thr Asp Pro Met Gly Glu Met Ile Glu Phe Gln Leu Lys
595 600 605

Asn Gly Gln Ser Phe Thr His Asp Asp Tyr Val Leu Val Gly Asn Asp
610 615 620

Gly Ser Gln Leu Lys Asn Gly Val Ala Leu Gly Gly Pro Asn Ser Asp
625 630 635 640

Gly Gly Ile Leu Lys Asp Val Thr Val Thr Tyr Asp Lys Thr Ser Gln
645 650 655

Thr Ile Lys Ile Asn His Leu Asn Leu Gly Ser Gly Gln Lys Val Val
660 665 670

Leu Thr Tyr Asp Val Arg Leu Lys Asp Asn Tyr Ile Ser Asn Lys Phe
675 680 685

Tyr Asn Thr Asn Asn Arg Thr Thr Leu Ser Pro Lys Ser Glu Lys Glu
690 695 700

Pro Asn Thr Ile Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg
705 710 715 720

Glu Phe Pro Val Leu Thr Ile Ser Asn Gln Lys Lys Met Gly Glu Val
725 730 735

Glu Phe Ile Lys Val Asn Lys Asp Lys His Ser Glu Ser Leu Leu Gly
740 745 750

Ala Lys Phe Gln Leu Gln Ile Glu Lys Asp Phe Ser Gly Tyr Lys Gln
755 760 765

Phe Val Pro Glu Gly Ser Asp Val Thr Thr Lys Asn Asp Gly Lys Ile
770 775 780

Tyr Phe Lys Ala Leu Gln Asp Gly Asn Tyr Lys Leu Tyr Glu Ile Ser
785 790 795 800

Ser Pro Asp Gly Tyr Ile Glu Val Lys Thr Lys Pro Val Val Thr Phe
805 810 815

GBS Patentin.ST25

Thr Ile Gln Asn Gly Glu Val Thr Asn Leu Lys Ala Asp Pro Asn Ala
820 825 830

Asn Lys Asn Gln Ile Gly Tyr Leu Glu Gly Asn Gly Lys His Leu Ile
835 840 845

Thr Asn Thr Pro Lys Arg Pro Pro Gly Val Phe Pro Lys Thr Gly Gly
850 855 860

Ile Gly Thr Ile Val Tyr Ile Leu Val Gly Ser Thr Phe Met Ile Leu
865 870 875 880

Thr Ile Cys Ser Phe Arg Arg Lys Gln Leu
885 890

<210> 256

<211> 201

<212> PRT

<213> Streptococcus agalactiae

<400> 256

Gly Ala Lys Lys Ala Gly Trp Thr Glu Tyr Ala Arg Met Leu Glu Val
1 5 10 15

Arg Glu Gln Val Asp His Val Met Ile Pro Lys Ile Asn Gln Asp Leu
20 25 30

Pro Ile Tyr Ala Gly Pro Glu Glu Asp Asn Leu Gln Arg Gly Val Gly
35 40 45

His Leu Glu Gly Ile Ser Leu Pro Ile Gly Gly Ala Ser Thr His Ala
50 55 60

Val Leu Ser Gly Gln Arg Gly Met Pro Ala Ala Arg Leu Phe Ala Asp
65 70 75 80

Leu Asp Lys Met Lys Lys Gly Asp Tyr Phe Tyr Val Thr Asn Leu Lys
85 90 95

Glu Thr Leu Ala Tyr Gln Val Asp Arg Ile Met Val Ile Glu Pro Ser
100 105 110

Gln Leu Asp Ala Val Ser Ile Glu Glu Asp Lys Asp Tyr Val Thr Leu
115 120 125

Leu Thr Cys Thr Pro Tyr Met Gly Ser Leu Ser Thr Val Met Gly Asp
130 135 140

GBS patentin.ST25

Leu Ser Leu Thr Thr Arg Glu Asn Gln Leu Gly Ser Leu Ser Phe Trp
145 150 155 160

Met Phe Lys Ala Met Arg Ile Leu Leu Leu Lys Phe Leu Lys Leu Arg
165 170 175

Lys Pro Lys Ala Cys Arg Leu Met Ser Leu Ile Ser Leu Leu Val Ala
180 185 190

Ser Asn Leu Ala Leu Glu Arg Asp Ser
195 200

<210> 257

<211> 352

<212> PRT

<213> streptococcus agalactiae

<400> 257

Met Ser Asp Val Val Glu Lys Gln Thr Ala Lys Ser Phe Ile Met Asn
1 5 10 15

Val Leu Asn Gly Leu Ala Leu Gly Thr Val Ile Val Leu Ile Pro Gly
20 25 30

Ala Ile Leu Gly Glu Leu Met Lys Ala Leu Leu Pro Met Trp Ser Gly
35 40 45

Phe Ala Thr Leu Ile Ala Ala Thr Ala Val Ala Thr Ser Met Met Gly
50 55 60

Leu Val Ile Gly Ile Met Val Gly Leu Asn Phe Lys Phe Asn Pro Ile
65 70 75 80

Gln Ser Ala Ser Leu Gly Leu Ala Val Met Phe Ala Gly Gly Ala Ala
85 90 95

Thr Phe Leu Lys Gly Ala Ile Met Leu Lys Gly Thr Gly Asp Ile Ile
100 105 110

Asn Met Gly Ile Thr Ala Ala Leu Gly Val Leu Leu Ile Gln Phe Leu
115 120 125

Ser Asp Lys Thr Lys Ser Phe Thr Leu Ile Val Ile Pro Thr Val Thr
130 135 140

Leu Leu Leu Val Gly Gly Val Gly His Val Leu Leu Pro Tyr Val Lys
145 150 155 160

GBS patentin.ST25

Met Ile Thr Thr Met Ile Gly Gln Gly Ile Ala Ser Leu Leu Gly Leu
165 170 175

Gln Pro Val Leu Met Ser Ile Leu Ile Ala Met Ile Phe Cys Phe Leu
180 185 190

Ile Val Ser Pro Ile Thr Thr Val Gly Ile Ala Leu Ala Ile Ser Leu
195 200 205

Ser Gly Ile Gly Ser Gly Ala Ala Asn Leu Gly Ile Cys Ala Ala Ser
210 215 220

Phe Gly Leu Cys Met Ala Gly Trp Ser Val Asn Ser Lys Gly Thr Ala
225 230 235 240

Leu Ala His Val Leu Gly Ser Pro Lys Ile Ser Met Ala Asn Val Leu
245 250 255

Ala Lys Pro Lys Ile Met Leu Pro Met Ile Ser Ser Ala Ala Ile Leu
260 265 270

Gly Ile Leu Gly Ala Leu Phe Asn Ile Gln Gly Thr Pro Ala Ser Ala
275 280 285

Gly Phe Gly Ile Ser Gly Leu Ile Gly Pro Ile Asn Ala Leu Asn Leu
290 295 300

Ala Lys Gly Gly Trp Ser Val Met Asn Met Leu Leu Ile Ile Ile Ile
305 310 315 320

Phe Val Ala Ala Pro Ile Ile Leu Asn Phe Ile Phe Asn Tyr Leu Phe
325 330 335

Ile Lys Val Leu Lys Ile Ile Asp Pro Met Asp Tyr Lys Leu Asp Ile
340 345 350

<210> 258

<211> 223

<212> PRT

<213> Streptococcus agalactiae

<400> 258

Met Ala Arg Pro Leu Val Glu Gln Thr Ala Asp Arg Leu Leu His Leu
1 5 10 15

Ile Leu Glu Arg Glu Tyr Pro Val Gly Ala Lys Leu Pro Asn Glu Tyr
20 25 30

GBS patentin.ST25

Glu Leu Ala Glu Asp Leu Asp Val Gly Arg Ser Thr Ile Arg Glu Ala
35 40 45

Val Arg Ser Leu Ala Thr Arg Asn Ile Leu Glu Val Arg Gln Gly Ser
50 55 60

Gly Thr Tyr Ile Ser Ser Lys Lys Gly Val Ser Glu Asp Pro Leu Gly
65 70 75 80

Phe Ser Leu Ile Lys Asp Thr Asp Arg Leu Thr Ser Asp Leu Phe Glu
85 90 95

Leu Arg Leu Leu Leu Glu Pro Arg Ile Ala Glu Leu Val Ala Tyr Arg
100 105 110

Ile Thr Asp Asp Gln Leu Gln Leu Leu Glu Lys Leu Val Gly Asp Ile
115 120 125

Glu Asp Ala Val His Ala Gly Asp Pro Lys His Leu Leu Leu Asp Val
130 135 140

Glu Phe His Ser Met Leu Ala Lys Tyr Ser Gly Asn Ile Ala Met Asp
145 150 155 160

Ser Leu Leu Pro Val Ile Asn Gln Ser Ile His Leu Ile Asn Ala Asn
165 170 175

Tyr Thr Asn Arg Gln Met Lys Ser Asp Ser Leu Glu Ala His Arg Glu
180 185 190

Ile Ile Lys Ala Ile Arg Glu Lys Asn Pro Val Ala Ala His Asp Ala
195 200 205

Met Leu Met His Ile Met Ser Val Arg Arg Ser Ala Leu Lys Ala
210 215 220

<210> 259

<211> 188

<212> PRT

<213> Streptococcus agalactiae

<400> 259

Met Ile Lys Lys Asn Lys Val Phe Leu Gly Val Leu Leu Val Leu Val
1 5 10 15

Val Ile Leu Gly Gly Gly Val Leu Phe Tyr Gln Ser Gln Phe Gln Lys
20 25 30

GBS patentin.ST25

Thr Thr Asn Gln Ala Leu Ala Ile Ala Tyr Lys Asp Ala Lys Val Ala
35 40 45

Lys Lys Asp Val Ile His Gln Lys Ile Asp Lys Glu Phe Glu Asn Phe
50 55 60

Arg Gly Ser Tyr Glu Ile Glu Phe Asn Thr Lys Ser Ala Glu Tyr Ser
65 70 75 80

Tyr His Val Asp Ala Lys Thr Gly Gln Ile Leu Glu Arg Asp Met Asp
85 90 95

Asn Asn Gly Phe Ser Lys Ser Thr Ser Gln Ser Ser Ser Ser Ser Ser
100 105 110

Gln Lys Ser His Lys Ile Ser Gln Glu Glu Ala Lys Lys Ile Ala Phe
115 120 125

Lys Asp Ala Asn Ile Glu Glu Ser Glu Val Ser Asn Leu Lys Ile Lys
130 135 140

Glu Glu Ile Glu Asn Gly Lys Ser Val Tyr Asp Ile Asp Phe Val Asp
145 150 155 160

Leu Lys Asn Lys Asn Glu Val Asp Tyr Gln Ile Asp Ala Glu Thr Gly
165 170 175

Lys Ile Ile Glu Arg Ser Arg Asp His Met Asn Asp
180 185

<210> 260

<211> 680

<212> PRT

<213> Streptococcus agalactiae

<400> 260

Leu Asn Arg Lys Lys Arg Tyr Arg Leu Thr Val Lys Lys Gln Asn Ala
1 5 10 15

Ser Ile Pro Arg Arg Leu Asn Leu Leu Phe Phe Ile Ile Val Leu Leu
20 25 30

Phe Thr Val Leu Ile Leu Arg Leu Glu Gln Met Gln Ile Gly Gln Gln
35 40 45

Ser Phe Tyr Met Lys Lys Leu Thr Ala Leu Thr Ser Tyr Thr Val Lys
50 55 60

GBS patentin.ST25

Glu Ser Lys Ala Arg Gly Gln Ile Phe Asp Ala Lys Gly Val Val Leu
 65 70 75 80
 Val Glu Asn Asp Glu Arg Pro Thr Val Ala Phe Ser Arg Gly Asn Asn
 85 90 95
 Ile Ser Ser Gln Ser Ile Lys Glu Leu Ala Asn Lys Leu Ser His Tyr
 100 105 110
 Ile Thr Leu Thr Glu Val Ala Ser Ser Asp Arg Ala Lys Arg Asp Tyr
 115 120 125
 Tyr Leu Ala Asp Lys Ala Asn Tyr Lys Lys Val Val Glu Ser Leu Pro
 130 135 140
 Asp Ser Lys Arg Tyr Asp Lys Phe Gly Asn His Leu Ala Glu Ser Thr
 145 150 155 160
 Val Tyr Ala Asn Ala Val Ala Ala Val Pro Val Ser Ala Ile Asn Tyr
 165 170 175
 Ser Glu Asp Glu Leu Lys Val Val Ala Leu Phe Asn Gln Met Asn Ala
 180 185 190
 Thr Pro Thr Phe Gly Ser Val Lys Leu Ser Thr Gly Glu Leu Ser Asp
 195 200 205
 Asp Gln Ile Lys Lys Leu Asp Ala Asp Lys Lys Glu Leu Leu Gly Ile
 210 215 220
 Ser Val Thr Ser Asn Trp His Arg Arg Lys Lys Gly Thr Ser Leu Ser
 225 230 235 240
 Asp Ile Leu Gly Thr Ile Ser Thr Glu Lys Ala Gly Leu Pro Arg Glu
 245 250 255
 Glu Val Lys Lys Tyr Leu Lys Lys Gly Tyr Ser Leu Asn Asp Arg Val
 260 265 270
 Gly Thr Ser Tyr Leu Glu Lys Gln Tyr Glu Asp Asp Leu Gln Gly Ile
 275 280 285
 Arg Gln Ile Arg Lys Val Val Val Asn Lys Lys Gly Lys Val Val Ser
 290 295 300
 Asp Asn Ile Thr Gln Glu Gly Lys Ser Gly Arg Asn Leu Lys Leu Thr
 305 310 315 320
 Ile Asp Leu Asn Tyr Gln Asn Lys Val Glu Ser Ile Leu Lys Gln Tyr
 325 330 335

GBS patentin.ST25

Tyr Gly Ser Glu₃₄₀ Leu Ser Ser Gly Arg₃₄₅ Ala Ser Phe Ser Glu₃₅₀ Gly Met

Tyr Ala Val₃₅₅ Ala Ile Glu Pro Ser₃₆₀ Thr Gly Lys Val Leu₃₆₅ Ala Met Ala

Gly Leu₃₇₀ Lys Asn Asp His Gly₃₇₅ Asn Leu Val Asp Asp₃₈₀ Ser Leu Gly Thr

Ile Ala Lys Asn Phe Thr₃₉₀ Pro Gly Ser Val Val₃₉₅ Lys Gly Ala Thr Leu₄₀₀

Ser Ser Gly Trp Glu₄₀₅ Asn Lys Val Leu Arg₄₁₀ Gly Asn Glu Val Leu₄₁₅ Tyr

Asp Gln Glu Ile₄₂₀ Ala Asn Ile Arg Ser₄₂₅ Trp Phe Thr Arg Gly₄₃₀ Leu Thr

Pro Ile Ser₄₃₅ Ala Ala Gln Ala Leu₄₄₀ Glu Tyr Ser Ser Asn₄₄₅ Thr Tyr Met

Val Gln Val Ala Leu Arg₄₅₅ Leu Met Gly Gln Asp Tyr₄₆₀ Asn Thr Gly Asp

Ala Leu Thr Asp Arg Gly₄₇₀ Tyr Gln Glu Ala Met₄₇₅ Ala Lys Leu Arg Lys₄₈₀

Thr Tyr Gly Glu Tyr₄₈₅ Gly Leu Gly Val Ser₄₉₀ Thr Gly Leu Asp Leu₄₉₅ Pro

Glu Ser Glu Gly₅₀₀ Tyr Val Pro Gly Lys₅₀₅ Tyr Ser Leu Gly Thr₅₁₀ Thr Leu

Met Glu Ser₅₁₅ Phe Gly Gln Tyr Asp₅₂₀ Ala Tyr Thr Pro Met₅₂₅ Gln Leu Gly

Gln Tyr₅₃₀ Ile Ser Thr Ile Ala₅₃₅ Asn Asn Gly Asn Arg₅₄₀ Leu Ala Pro His

Val Val Ser Asp Ile Tyr₅₅₀ Glu Gly Asn Asp Ser₅₅₅ Asn Lys Phe Ala Gln₅₆₀

Leu Val Arg Ser Ile₅₆₅ Thr Pro Lys Thr Leu₅₇₀ Asn Lys Ile Ala Ile₅₇₅ Ser

Asp Gln Glu Leu₅₈₀ Ala Ile Ile Gln Glu₅₈₅ Gly Phe Tyr Asn Val₅₉₀ Val Asn

Ser Gly Ser₅₉₅ Gly Tyr Ala Thr Gly₆₀₀ Thr Ser Met Arg Gly₆₀₅ Asn Val Thr

GBS patentin.ST25

Thr Ile Ser Gly Lys Thr Gly Thr Ala Glu Thr Phe Ala Lys Asn Val
610 615 620

Asn Gly Gln Thr Val Ser Thr Tyr Asn Leu Asn Ala Ile Ala Tyr Asp
625 630 635 640

Thr Asn Arg Lys Ile Ala Val Ala Val Met Tyr Pro His Val Thr Thr
645 650 655

Asp Thr Thr Lys Ser His Gln Leu Val Ala Arg Asp Met Ile Asp Gln
660 665 670

Tyr Ile Ser Gln Phe Thr Gly Gln
675 680

<210> 261

<211> 475

<212> PRT

<213> streptococcus agalactiae

<400> 261

Met Thr Val Phe Pro Lys His Phe Leu Trp Gly Gly Ala Val Ala Ala
1 5 10 15

Asn Gln Val Glu Gly Ala Phe Arg Thr Asp Gly Lys Gly Leu Ser Val
20 25 30

Gln Asp Val Leu Pro Asn Gly Gly Leu Gly Asp Phe Thr Ala Lys Pro
35 40 45

Thr Pro Asp Asn Leu Lys Leu Glu Ala Ile Asp Phe Tyr His Asn Tyr
50 55 60

Lys Asn Asp Ile Lys Leu Phe Ala Glu Met Gly Phe Lys Val Phe Arg
65 70 75 80

Thr Ser Ile Ala Trp Ser Arg Ile Phe Pro Asn Gly Asp Asp Ser Ala
85 90 95

Pro Asn Glu Ala Gly Leu Gln Phe Tyr Asp Asn Leu Phe Asp Glu Leu
100 105 110

Leu Lys Tyr Asn Ile Glu Pro Leu Val Thr Leu Ser His Tyr Glu Thr
115 120 125

Pro Leu His Leu Ala Lys Thr Tyr Asn Gly Trp Ala Asp Arg Arg Leu
130 135 140

GBS patentin.ST25

Ile Ala Phe Phe Glu Lys Phe Ala Gln Thr Val Met Glu Arg Tyr Lys
145 150 155 160

Asp Lys Val Lys Tyr Trp Leu Thr Phe Asn Glu Val Asn Ser Ile Leu
165 170 175

His Met Pro Phe Thr Ser Gly Ala Ile Met Thr Asp Lys Ser Gln Leu
180 185 190

Ser Pro Gln Glu Leu Tyr Gln Ala Ile His His Glu Leu Val Ala Ser
195 200 205

Ala Arg Val Thr Lys Leu Gly Arg Ser Ile Asn Pro Asn Phe Lys Ile
210 215 220

Gly Cys Met Ile Leu Ala Met Pro Ala Tyr Pro Met Thr Ser Asp Pro
225 230 235 240

Arg Asp Val Leu Ala Ala Arg Gln Phe Glu Gln His Asn Leu Leu Phe
245 250 255

Ser Asp Ile His Val Arg Gly Lys Tyr Pro Thr Tyr Ile Gln Ser Tyr
260 265 270

Phe Lys Asn Asn Gly Ile Lys Ile Lys Phe Glu Glu Gly Asp Glu Glu
275 280 285

Val Leu Ala Gln Asn Thr Val Asp Phe Leu Ser Phe Ser Tyr Tyr Met
290 295 300

Ser Val Thr Gln Ala Tyr Asp Phe Glu Asn Tyr Gln Ser Gly Gln Gly
305 310 315 320

Asn Ile Leu Gly Gly Leu Thr Asn Pro His Leu Thr Thr Ser Glu Trp
325 330 335

Gly Trp Gln Ile Asp Pro Ile Gly Leu Arg Leu Val Leu Asn Gln Tyr
340 345 350

Tyr Glu Arg Tyr Gln Ile Pro Leu Phe Ile Val Glu Asn Gly Leu Gly
355 360 365

Ala Lys Asp Gln Leu Ile Glu Thr Leu Asp Gly Asp Tyr Thr Val Glu
370 375 380

Asp Asp Tyr Arg Ile Asp Tyr Met Asn Gln His Leu Val Gln Val Ala
385 390 395 400

Lys Ala Ile Glu Asp Gly Val Glu Ile Met Gly Tyr Thr Ser Trp Gly
405 410 415

GBS patentin.ST25

Cys Ile Asp Cys Val Ser Met Ser Thr Ala Gln Leu Ser Lys Arg Tyr
420 425 430

Gly Leu Ile Tyr Val Asp Arg Asn Asp Asp Gly Thr Gly Ser Leu Gln
435 440 445

Arg Tyr Lys Lys Lys Ser Phe Gly Trp Tyr Gln Lys Val Ile Lys Thr
450 455 460

Asn Gly Gln Ser Leu Phe Glu His His Asn Arg
465 470 475

<210> 262

<211> 161

<212> PRT

<213> Streptococcus agalactiae

<400> 262

Met Ala Thr Phe Gln Ile Lys Glu Lys Met Phe Ser Leu Gly Gly Lys
1 5 10 15

Phe Thr Ile Thr Asp Gln Thr Gly Leu Pro Cys Tyr His Val Glu Gly
20 25 30

Ser Leu Phe Pro Leu Pro Lys Thr Phe Lys Val Phe Asp Glu Glu Gly
35 40 45

His Leu Ile Ser Gln Ile Glu Lys Lys Val Leu Ser Phe Leu Pro Lys
50 55 60

Phe Asn Val Thr Leu Ala Asn Gly Asn His Phe Thr Ile Lys Lys Asp
65 70 75 80

Phe Ser Phe Leu Lys Pro His Tyr Thr Ile Glu Asp Leu Asp Met Glu
85 90 95

Val Lys Gly Asn Phe Trp Asp Ile Asp Phe Gln Leu Leu Lys Asp Asn
100 105 110

Gln Val Ile Ala Asn Ile Ser Gln Gln Trp Phe Arg Met Thr Ser Thr
115 120 125

Tyr Gln Val Glu Val Tyr Asn Glu Thr Tyr Asn Asp Leu Thr Ile Ser
130 135 140

Leu Val Ile Ala Ile Asp Tyr Val Lys Glu Leu Glu Lys Asn Ala Ser
145 150 155 160

Asn

<210> 263

<211> 181

<212> PRT

<213> Streptococcus agalactiae

<400> 263

Met Lys Lys Ile Thr Thr Leu Ile Leu Ala Ser Ser Leu Leu Leu Val
 1 5 10 15

Ala Thr Thr Ser Val Lys Ala Asp Asp Asn Phe Glu Met Pro Thr Arg
 20 25 30

Tyr Val Lys Met Ser Glu Lys Ser Lys Ala Phe Tyr Gln Arg Leu Gln
 35 40 45

Glu Lys Gln Arg Lys Ala His Thr Thr Val Lys Thr Phe Asn Asn Ser
 50 55 60

Glu Ile Arg His Gln Leu Pro Leu Lys Gln Glu Lys Ala Arg Asn Asp
 65 70 75 80

Ile Tyr Asn Leu Gly Ile Leu Ile Ser Gln Glu Ser Lys Gly Phe Ile
 85 90 95

Gln Arg Ile Asp Asn Ala Tyr Ser Leu Glu Asn Val Ser Asp Ile Val
 100 105 110

Asn Glu Ala Gln Ala Leu Tyr Lys Arg Asn Tyr Asp Leu Phe Glu Lys
 115 120 125

Ile Lys Ser Thr Arg Asp Lys Val Gln Val Leu Leu Ala Ser His Gln
 130 135 140

Asp Asn Thr Asp Leu Lys Asn Phe Tyr Ala Glu Leu Asp Asp Met Tyr
 145 150 155 160

Glu His Val Tyr Leu Asn Glu Ser Arg Val Glu Ala Ile Asn Arg Asn
 165 170 175

Ile Gln Lys Tyr Asn
 180

<210> 264

GBS patentin.ST25

<211> 306

<212> PRT

<213> Streptococcus agalactiae

<400> 264

Met Lys Leu Lys Lys Phe Phe Glu Asp Leu Leu Ala Lys Leu Glu Tyr
 1 5 10 15

Arg Pro Ile Gln Val Phe Met Arg His Phe Gln Ser Ala Glu Met Asp
 20 25 30

Leu Ser Ala Ile Ala Val Ala Tyr Tyr Leu Leu Val Thr Ala Phe Pro
 35 40 45

Leu Leu Val Ile Ala Ala Asn Ile Phe Pro Tyr Phe His Ile Asn Val
 50 55 60

Ser Asp Leu Leu Ser Leu Met Gln Lys Asn Leu Pro Lys Asn Ile Tyr
 65 70 75 80

Glu Pro Ala Ser Arg Leu Ala Val Asp Ala Phe Ser Lys Pro Ser Thr
 85 90 95

Gly Ile Leu Gly Phe Ala Ser Leu Thr Ala Phe Trp Thr Met Ser Lys
 100 105 110

Ser Leu Thr Ser Leu Gln Lys Ala Ile Asn Lys Ala Tyr Gly Val Asp
 115 120 125

Gln His Arg Asp Phe Val Ile Ser Arg Leu Val Gly Val Gly Thr Gly
 130 135 140

Leu Ile Ile Leu Phe Leu Leu Thr Phe Val Leu Ile Phe Ser Thr Phe
 145 150 155 160

Ser Lys Pro Val Leu Gln Ile Ile Val Asn Met Tyr Asp Leu Gly Asp
 165 170 175

Thr Leu Thr Ala Trp Leu Leu Asn Leu Ala Gln Pro Val Thr Phe Leu
 180 185 190

Thr Ile Phe Leu Gly Ile Gly Ile Leu Tyr Phe Ile Leu Pro Asn Ala
 195 200 205

Arg Ile Arg Lys Val Arg Tyr Val Ile Pro Gly Thr Leu Phe Ser Thr
 210 215 220

Phe Val Ile Gly Phe Phe Ser Asn Leu Ile Ser Gln Tyr Val Leu Asn
 225 230 235 240

GBS patentin.ST25

Arg Val Glu Lys Met Val Asp Ile Lys Thr Phe Gly Ser Val Val Ile
245 250 255

Phe Ile Leu Met Leu Trp Phe Ile Phe Leu Ala His Ile Met Ile Leu
260 265 270

Gly Ala Ile Leu Asn Ala Ser Val Gln Glu Ile Ala Thr Gly Lys Ile
275 280 285

Glu Ser Arg Arg Gly Asp Ile Met Ser Leu Ile Gln Lys Ser Lys Glu
290 295 300

Glu Lys
305

<210> 265

<211> 1077

<212> PRT

<213> streptococcus agalactiae

<400> 265

Met Lys Leu Leu Tyr Thr Asp Ile Asn His Asp Met Thr Glu Ile Leu
1 5 10 15

Val Asn Gln Ala Ala His Ala Ala Glu Ala Gly Trp Arg Ile Phe Tyr
20 25 30

Ile Ala Pro Asn Ser Leu Ser Phe Glu Lys Glu Arg Ala Val Leu Glu
35 40 45

Asn Leu Pro Gln Glu Ala Ser Phe Ala Ile Thr Ile Thr Arg Phe Ala
50 55 60

Gln Leu Ala Arg Tyr Phe Thr Leu Asn Gln Pro Asn Gln Lys Glu Ser
65 70 75 80

Leu Asn Asp Ile Gly Leu Ala Met Ile Phe Tyr Arg Ala Leu Ala Ser
85 90 95

Phe Glu Asp Gly Gln Leu Lys Val Phe Gly Arg Leu Lys Gln Asp Ala
100 105 110

Ser Phe Ile Ser Gln Leu Val Asp Leu Tyr Lys Glu Leu Gln Thr Ala
115 120 125

Asn Leu Ser Ile Leu Asp Leu Lys Tyr Leu His Ser Pro Glu Lys Phe
130 135 140

GBS patentin.ST25

Glu Asp Leu Leu Ala Ile Phe Leu Val Val Ser Asp Leu Leu Arg Glu
 145 150 155 160
 Gly Glu Tyr Asp Asn Gln Ser Lys Ile Ala Phe Phe Thr Glu Gln Val
 165 170 175
 Arg Ser Gly Gln Leu Asp Val Asp Leu Lys Asn Thr Ile Leu Ile Val
 180 185 190
 Asp Gly Phe Thr Arg Phe Ser Ala Glu Glu Glu Ala Leu Ile Lys Ser
 195 200 205
 Leu Ser Ser Arg Cys Gln Glu Ile Ile Ile Gly Ala Tyr Ala Ser Gln
 210 215 220
 Lys Ala Tyr Lys Ala Asn Phe Thr Asn Gly Asn Ile Tyr Ser Ala Gly
 225 230 235 240
 Val Asp Phe Leu Arg Tyr Leu Ala Thr Thr Phe Gln Thr Lys Pro Glu
 245 250 255
 Phe Ile Leu Ser Lys Trp Glu Ser Lys Ser Gly Phe Glu Met Ile Ser
 260 265 270
 Lys Asn Ile Glu Gly Lys His Asp Phe Thr Asn Ser Ser His Ile Leu
 275 280 285
 Asp Asp Thr Ala Lys Asp Cys Ile Thr Ile Trp Glu Cys Ile Asn Gln
 290 295 300
 Lys Asp Glu Val Glu His Val Ala Arg Ala Ile Arg Gln Lys Leu Tyr
 305 310 315 320
 Gln Gly Tyr Arg Tyr Lys Asp Ile Leu Val Leu Leu Gly Asp Val Asp
 325 330 335
 Ser Tyr Lys Leu Gln Leu Ser Lys Ile Phe Glu Gln Tyr Asp Ile Pro
 340 345 350
 Tyr Tyr Phe Gly Lys Ala Glu Thr Met Ala Ala His Pro Leu Val His
 355 360 365
 Phe Met Asp Ser Leu Ser Arg Ile Lys Arg Tyr Arg Phe Arg Ala Glu
 370 375 380
 Asp Val Leu Asn Leu Phe Lys Thr Gly Ile Tyr Gly Glu Ile Ser Gln
 385 390 395 400
 Asp Asp Leu Asp Tyr Phe Glu Ala Tyr Ile Ser Tyr Ala Asp Ile Lys
 405 410 415

GBS patentin.ST25

Gly Pro Lys Lys Phe Phe Thr Asp Phe Val Val Gly Ala Lys Lys Phe
420 425 430

Asp Leu Gly Arg Leu Asn Thr Ile Arg Gln Ser Leu Leu Ala Pro Leu
435 440 445

Glu Ser Phe Val Lys Thr Lys Lys Gln Asp Gly Ile Lys Thr Leu Asn
450 455 460

Gln Phe Met Phe Phe Leu Thr Gln Val Gly Leu Ser Asp Asn Leu Ser
465 470 475 480

Arg Leu Val Gly Gln Met Ser Glu Asn Glu Gln Glu Lys His Gln Glu
485 490 495

Val Trp Lys Thr Phe Thr Asp Ile Leu Glu Gln Phe Gln Thr Ile Phe
500 505 510

Gly Gln Glu Lys Leu Asn Leu Asp Glu Phe Leu Ser Leu Leu Asn Ser
515 520 525

Gly Met Met Gln Ala Glu Tyr Arg Met Val Pro Ala Thr Val Asp Val
530 535 540

Val Thr Val Lys Ser Tyr Asp Leu Val Glu Pro His Ser Asn Gln Phe
545 550 555 560

Val Tyr Ala Leu Gly Met Thr Gln Ser His Phe Pro Lys Ile Ala Gln
565 570 575

Asn Lys Ser Leu Ile Ser Asp Ile Glu Arg Gln Leu Ile Asn Asp Ala
580 585 590

Asn Asp Thr Asp Gly His Phe Asp Ile Met Thr Arg Glu Asn Leu Lys
595 600 605

Lys Asn His Phe Ala Ala Leu Ser Leu Phe Asn Ala Ala Lys Gln Ala
610 615 620

Leu Val Leu Thr Ile Pro Gln Leu Leu Asn Glu Ser Glu Asp Gln Met
625 630 635 640

Ser Pro Tyr Leu Ile Glu Leu Arg Asp Ile Gly Val Pro Phe Asn His
645 650 655

Lys Gly Arg Gln Ser Leu Lys Glu Glu Ala Asp Asn Ile Gly Asn Tyr
660 665 670

Lys Ala Leu Leu Ser Arg Val Val Asp Leu Tyr Arg Ser Ala Ile Asp
675 680 685

GBS patentin.ST25

Lys Glu Met Thr Lys Glu Glu Gln Thr Phe Trp Ser Val Ala Val Arg
 690 695 700
 Tyr Leu Arg Arg Gln Leu Thr Ser Lys Gly Ile Glu Ile Pro Ile Ile
 705 710 715 720
 Thr Asp Ser Leu Asp Thr Val Thr Val Ser Ser Asp Val Met Thr Arg
 725 730 735
 Arg Phe Pro Glu Asp Asp Pro Leu Lys Leu Ser Ser Ser Ala Leu Thr
 740 745 750
 Thr Phe Tyr Asn Asn Gln Tyr Lys Tyr Phe Leu Gln Tyr Val Leu Gly
 755 760 765
 Leu Glu Glu Gln Asp Ser Ile His Pro Asp Met Arg His His Gly Thr
 770 775 780
 Tyr Leu His Arg Val Phe Glu Ile Leu Met Lys Asn Gln Gly Ile Glu
 785 790 795 800
 Ser Phe Glu Glu Lys Leu Asn Ser Ala Ile Asn Lys Thr Asn Gln Glu
 805 810 815
 Asp Val Phe Lys Ser Leu Tyr Ser Glu Asp Ala Glu Ser Arg Tyr Ser
 820 825 830
 Leu Glu Ile Leu Glu Asp Ile Ala Arg Ala Thr Ala Thr Ile Leu Arg
 835 840 845
 Gln Asp Ser Gln Met Thr Val Glu Ser Glu Glu Glu Arg Phe Glu Leu
 850 855 860
 Met Ile Asp Asn Thr Ile Lys Ile Asn Gly Ile Ile Asp Arg Ile Asp
 865 870 875 880
 Arg Leu Ser Asp Gly Ser Leu Gly Val Val Asp Tyr Lys Ser Ser Ala
 885 890 895
 Gln Lys Phe Asp Ile Gln Lys Phe Tyr Asn Gly Leu Ser Pro Gln Leu
 900 905 910
 Val Thr Tyr Ile Asp Ala Ile Ser Arg Asp Lys Glu Val Glu Gln Lys
 915 920 925
 Pro Pro Ile Phe Gly Ala Met Tyr Leu His Met Gln Glu Pro Lys Gln
 930 935 940
 Asp Leu Ser Lys Ile Lys Asn Leu Asp Asp Leu Val Thr Lys Asn His
 945 950 955 960

GBS patentin.ST25

Gln Ala Leu Thr Tyr Lys Gly Leu Phe Ser Glu Ala Glu Lys Glu Phe
965 970 975

Leu Ala Asn Gly Lys Tyr His Leu Lys Asp Ser Leu Tyr Ser Glu Ala
980 985 990

Glu Ile Ala Ile Leu Gln Ala His Asn Gln Leu Leu Tyr Lys Lys Ala
995 1000 1005

Ser Glu Thr Ile Lys Ser Gly Lys Phe Leu Ile Asn Pro Tyr Thr
1010 1015 1020

Glu Asp Ala Lys Thr Val Asp Gly Asp Gln Phe Lys Ser Ile Thr
1025 1030 1035

Gly Phe Glu Ala Asp Arg His Met Ala Arg Ala Arg Ala Leu Tyr
1040 1045 1050

Lys Leu Pro Ala Lys Glu Lys Arg Gln Gly Phe Leu Thr Leu Met
1055 1060 1065

Gln Gln Glu Glu Glu Asn Asp Asp Leu
1070 1075

<210> 266

<211> 332

<212> PRT

<213> Streptococcus agalactiae

<400> 266

Met Ser Glu Thr Lys Val Met Ala Leu Arg Glu Ala Ile Asn Val Ala
1 5 10 15

Met Ser Glu Glu Met Arg Lys Asp Glu Lys Val Phe Leu Met Gly Glu
20 25 30

Asp Val Gly Val Tyr Gly Gly Asp Phe Gly Thr Ser Val Gly Met Leu
35 40 45

Glu Glu Phe Gly Ala Lys Arg Val Arg Asp Thr Pro Ile Ser Glu Ala
50 55 60

Ala Ile Ala Gly Ser Ala Ile Gly Ala Ala Gln Thr Gly Leu Arg Pro
65 70 75 80

Ile Val Asp Leu Thr Phe Met Asp Phe Val Thr Ile Ala Met Asp Ala
85 90 95

GBS patentin.ST25

Ile Val Asn Gln Gly Ala Lys Thr Asn Tyr Met Phe Gly Gly Gly Leu
100 105 110

Ser Thr Pro Val Thr Phe Arg Val Ala Ser Gly Ser Gly Ile Gly Ser
115 120 125

Ala Ala Gln His Ser Gln Ser Leu Glu Ala Trp Leu Thr His Ile Pro
130 135 140

Gly Leu Lys Val Val Ala Pro Gly Thr Val Asn Glu Ser Lys Ala Leu
145 150 155 160

Leu Lys Ser Ser Ile Leu Asp Asn Asn Pro Val Ile Phe Leu Glu Pro
165 170 175

Lys Ala Leu Tyr Gly Lys Lys Glu Glu Val Asn Met Asp Pro Asp Phe
180 185 190

Tyr Ile Pro Leu Gly Lys Gly Asp Ile Lys Arg Glu Gly Thr Asp Leu
195 200 205

Thr Ile Val Ser Tyr Gly Arg Met Leu Glu Arg Val Met Gln Ala Ala
210 215 220

Glu Glu Val Ala Glu Glu Gly Ile Asn Val Glu Val Val Asp Pro Arg
225 230 235 240

Thr Leu Ile Pro Leu Asp Lys Glu Leu Ile Ile Asp Ser Val Lys Lys
245 250 255

Thr Gly Lys Leu Ile Leu Val Asn Asp Ala Tyr Lys Thr Gly Gly Phe
260 265 270

Thr Gly Glu Ile Ala Thr Met Val Ala Glu Ser Glu Ala Phe Asp Tyr
275 280 285

Leu Asp His Pro Ile Val Arg Leu Ala Ser Glu Asp Val Pro Val Pro
290 295 300

Tyr Ser Arg Val Leu Glu Gln Gly Ile Leu Pro Asp Val Ala Lys Ile
305 310 315 320

Lys Asp Ala Ile Tyr Lys Val Val Asn Lys Gly Lys
325 330

<210> 267

<211> 585

<212> PRT

<213> Streptococcus agalactiae

<400> 267

Met Ala Phe Asp Val Ile Met Pro Lys Leu Gly Val Asp Met Gln Glu
 1 5 10 15

Gly Glu Ile Leu Glu Trp Lys Lys Asn Glu Gly Asp Thr Val Asn Glu
 20 25 30

Gly Asp Val Leu Leu Glu Ile Met Ser Asp Lys Thr Asn Met Glu Ile
 35 40 45

Glu Ala Glu Asp Thr Gly Val Leu Leu Lys Ile Val His Gln Ala Gly
 50 55 60

Asp Val Val Pro Val Thr Glu Val Ile Ala Tyr Ile Gly Glu Glu Gly
 65 70 75 80

Glu Glu Val Gly Thr Ser Ser Pro Ser Ala Asp Ala Thr Ile Thr Ala
 85 90 95

Glu Asp Gly Gln Ser Val Ser Gly Pro Ala Ala Pro Ser Gln Glu Thr
 100 105 110

Val Ala Ala Ala Thr Pro Lys Glu Glu Leu Ala Ala Asp Glu Tyr Asp
 115 120 125

Ile Val Val Val Gly Gly Gly Pro Ala Gly Tyr Tyr Ala Ala Ile Arg
 130 135 140

Gly Ala Gln Leu Gly Gly Lys Ile Ala Ile Val Glu Lys Thr Glu Phe
 145 150 155 160

Gly Gly Thr Cys Leu Asn Val Gly Cys Ile Pro Thr Lys Thr Tyr Leu
 165 170 175

Lys Asn Ala Glu Ile Leu Asp Gly Leu Lys Val Ala Ala Gly Arg Gly
 180 185 190

Ile Asn Leu Ala Ser Thr Asn Tyr Ala Ile Asp Met Asp Lys Thr Val
 195 200 205

Ala Phe Lys Asn Ser Val Val Lys Thr Leu Thr Gly Gly Val Arg Gly
 210 215 220

Leu Leu Lys Ala Asn Lys Val Glu Ile Phe Asn Gly Leu Gly Gln Val
 225 230 235 240

Asn Pro Asp Lys Ser Val Val Ile Gly Asp Lys Val Ile Lys Gly Arg
 245 250 255

GBS patentin.ST25

Asn Val Val Leu Ala Thr Gly Ser Lys Val Ser Arg Ile Asn Ile Pro
 260 265 270
 Gly Ile Glu Ser Pro Leu Val Leu Thr Ser Asp Asp Ile Leu Asp Leu
 275 280 285
 Arg Glu Ile Pro Lys Ser Leu Ala Val Met Gly Gly Gly Val Val Gly
 290 295 300
 Ile Glu Leu Gly Leu Val Trp Ala Ser Tyr Gly Val Asp Val Thr Val
 305 310 315 320
 Ile Glu Met Ala Asp Arg Ile Ile Pro Ala Met Asp Lys Glu Val Ser
 325 330 335
 Leu Glu Leu Gln Lys Ile Leu Ala Lys Lys Gly Met Lys Ile Lys Thr
 340 345 350
 Ser Val Gly Val Ser Glu Ile Val Glu Ala Asn Asn Gln Leu Thr Leu
 355 360 365
 Lys Leu Asn Asn Gly Glu Glu Val Val Ala Asp Lys Ala Leu Leu Ser
 370 375 380
 Ile Gly Arg Val Pro Gln Met Asn Gly Leu Glu Asn Leu Glu Pro Glu
 385 390 395 400
 Leu Glu Met Glu Arg Gly Arg Ile Lys Val Asn Ala Tyr Gln Glu Thr
 405 410 415
 Ser Ile Pro Gly Ile Tyr Ala Pro Gly Asp Val Asn Gly Thr Arg Met
 420 425 430
 Leu Ala His Ala Ala Tyr Arg Met Gly Glu Val Ala Ala Glu Asn Ala
 435 440 445
 Leu Gly Gly Asn Lys Arg Lys Ala His Leu Asp Phe Thr Pro Ala Ala
 450 455 460
 Val Tyr Thr His Pro Glu Val Ala Met Val Gly Met Thr Glu Glu Gln
 465 470 475 480
 Ala Arg Glu Gln Tyr Gly Asp Ile Leu Val Gly Lys Asn Ser Phe Thr
 485 490 495
 Gly Asn Gly Arg Ala Ile Ala Ser Asn Glu Ala His Gly Phe Val Lys
 500 505 510
 Val Ile Ala Glu Pro Lys Tyr Lys Glu Ile Leu Gly Val His Ile Ile
 515 520 525

GBS patentin.ST25

Gly Pro Ala Ala Ala Glu Leu Ile Asn Glu Ala Ser Thr Ile Met Glu
530 535 540

Asn Glu Leu Thr Val Tyr Asp Val Ala Gln Ser Ile His Gly His Pro
545 550 555 560

Thr Phe Ser Glu Val Met Tyr Glu Ala Phe Leu Asp Val Leu Gly Glu
565 570 575

Ala Ile His Asn Pro Pro Lys Arg Lys
580 585

<210> 268

<211> 450

<212> PRT

<213> streptococcus agalactiae

<400> 268

Met Gly Lys Tyr Phe Gly Thr Asp Gly Val Arg Gly Glu Ala Asn Val
1 5 10 15

Glu Leu Thr Pro Glu Leu Ala Phe Lys Leu Gly Arg Phe Gly Gly Tyr
20 25 30

Val Leu Ser Gln His Glu Thr Asp Arg Pro Arg Val Phe Val Ala Arg
35 40 45

Asp Thr Arg Ile Ser Gly Glu Met Leu Glu Ser Ala Leu Ile Ala Gly
50 55 60

Leu Leu Ser Val Gly Ile Glu Val Tyr Lys Leu Gly Val Leu Ala Thr
65 70 75 80

Pro Gly Val Ser Tyr Leu Val Arg Thr Glu Lys Ala Ser Ala Gly Val
85 90 95

Met Ile Ser Ala Ser His Asn Pro Ala Leu Asp Asn Gly Ile Lys Phe
100 105 110

Phe Gly Ser Asp Gly Phe Lys Leu Asp Asp Asp Arg Glu Leu Glu Ile
115 120 125

Glu Ala Leu Leu Asp Ala Lys Glu Asp Thr Leu Pro Arg Pro Ser Ala
130 135 140

Gln Gly Leu Gly Thr Leu Val Asp Tyr Pro Glu Gly Leu Arg Lys Tyr
145 150 155 160

GBS patentin.ST25

Glu Lys Phe Met Glu Ser Thr Gly Ile Asp Leu Glu Gly Met Lys Val
165 170 175

Ala Leu Asp Thr Ala Asn Gly Ala Ala Thr Ala Ser Ala Arg Asn Ile
180 185 190

Phe Leu Asp Leu Asn Ala Asp Ile Ser Val Ile Gly Asp Gln Pro Asp
195 200 205

Gly Leu Asn Ile Asn Asp Gly Val Gly Ser Thr His Pro Glu Gln Leu
210 215 220

Gln Ser Leu Val Arg Glu Asn Gly Ser Asp Ile Gly Leu Ala Phe Asp
225 230 235 240

Gly Asp Ser Asp Arg Leu Ile Ala Val Asp Glu Asn Gly Glu Ile Val
245 250 255

Asp Gly Asp Lys Ile Met Phe Ile Ile Gly Lys Tyr Leu Ser Asp Lys
260 265 270

Gly Gln Leu Ala Gln Asn Thr Ile Val Thr Thr Val Met Ser Asn Leu
275 280 285

Gly Phe His Lys Ala Leu Asp Arg Glu Gly Ile His Lys Ala Ile Thr
290 295 300

Ala Val Gly Asp Arg Tyr Val Val Glu Glu Met Arg Lys Ser Gly Tyr
305 310 315 320

Asn Leu Gly Gly Glu Gln Ser Gly His Val Ile Ile Met Asp Tyr Asn
325 330 335

Thr Thr Gly Asp Gly Gln Leu Thr Ala Ile Gln Leu Thr Lys Val Met
340 345 350

Lys Glu Thr Gly Lys Lys Leu Ser Glu Leu Ala Ser Glu Val Thr Ile
355 360 365

Tyr Pro Gln Lys Leu Val Asn Ile Arg Val Glu Asn Asn Met Lys Asp
370 375 380

Lys Ala Met Glu Val Pro Ala Ile Ala Glu Ile Ile Ala Lys Met Glu
385 390 395 400

Glu Glu Met Asp Gly Asn Gly Arg Ile Leu Val Arg Pro Ser Gly Thr
405 410 415

Glu Pro Leu Leu Arg Val Met Ala Glu Ala Pro Thr Asn Glu Ala Val
420 425 430

GBS patentin.ST25

Asp Tyr Tyr Val Asp Thr Ile Ala Asp Val Val Arg Thr Glu Ile Gly
435 440 445

Leu Asp
450

<210> 269

<211> 877

<212> PRT

<213> streptococcus agalactiae

<400> 269

Met Lys Gly Gln Lys Ile Ile Ala Leu Ala Gly Leu Val Leu Ser Cys
1 5 10 15

His Phe Ala Leu Thr Ala Cys His Thr Gln Glu His Lys Asn Ser His
20 25 30

His Ile Lys Thr Lys Gln Val Ala Lys Lys Lys Ala Asn Lys Lys Lys
35 40 45

Val Ser Val Lys Glu Ser His Lys Lys Arg Lys Gly Val Ala Gly Val
50 55 60

Asp Phe Pro Thr Asp Asp Gly Phe Leu Leu Thr Lys Asp Ser Lys Ile
65 70 75 80

Leu Ser His Pro Asp Ser Gly Ile Val Val Ala His Gly Asn His Ser
85 90 95

His Phe Ile Phe Tyr Ser Asp Leu Lys Gly Ser Lys Phe Ser Tyr Leu
100 105 110

Ile Pro Asn Ala Asn Ala Lys Thr Asn Lys Lys Gln Ala Val Arg Asn
115 120 125

Phe Lys Ala Gly Ala Val Ala Val Asn Thr Leu Asn Asp Gly Tyr Val
130 135 140

Phe Asn Pro Ala Asp Ile Val Ser Glu Asp Ala Asn Gly Tyr Val Val
145 150 155 160

Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ala Ser Leu Ser Gln
165 170 175

Gln Lys Gln Val Gln Ala Ser Arg Ala Val Ser Arg Leu Gly Asn Gln
180 185 190

GBS patentin.ST25

Asn Asn Ser His Tyr Arg Val Asn Ser Ser Lys Ile Ala Gly Leu His
 195 200 205
 His Pro Thr Ser Asp Gly Phe Leu Phe Asn Gly Gln Gly Ile Lys Gly
 210 215 220
 Thr Thr Pro Thr Gly Ile Leu Val Glu His His Asn His Leu His Phe
 225 230 235 240
 Ile Ser Phe Ala Asp Leu Arg Lys Gly Gly Trp Gly Ser Ile Ala Asp
 245 250 255
 Arg Tyr Gln Pro Gln Lys Lys Val Asp Ser Lys Lys Gln Ser Pro Ser
 260 265 270
 Ser Lys Lys Pro Arg Thr Glu Asn Thr Leu Pro Lys Asp Ile Lys Asp
 275 280 285
 Lys Leu Ala Tyr Leu Ala Arg Glu Leu His Leu Asp Ile Ser Arg Ile
 290 295 300
 Arg Val Leu Lys Thr Leu Asn Gly Glu Ile Gly Phe Glu Tyr Pro His
 305 310 315 320
 Asp Asp His Thr His Val Ile Met Ala Lys Asp Ile Asp Leu Ser Lys
 325 330 335
 Pro Ile Pro Asn Pro His His Asp Asp Glu Asp His His Lys Gly His
 340 345 350
 His His Asp Glu Ser Asp His Lys His Glu Glu His Glu His Thr Lys
 355 360 365
 Ser Asn Lys Leu Ser Asp Glu Asp Gln Lys Lys Leu Ile Tyr Leu Ala
 370 375 380
 Glu Lys Leu Gly Leu Asn Pro Asn Gln Ile Glu Val Leu Thr Ser Glu
 385 390 395 400
 Asp Gly Ser Ile Ile Phe Lys Tyr Pro His Asp Asp His Ser His Thr
 405 410 415
 Ile Ala Ser Lys Asp Ile Glu Ile Gly Lys Pro Ile Pro Asp Gly His
 420 425 430
 His Asp His Ser His Ala Lys Asp Lys Val Gly Met Ala Thr Leu Lys
 435 440 445
 Gln Ile Gly Phe Asp Asp Glu Ile Ile Gln Asp Ile Leu His Ala Asp
 450 455 460

GBS patentin.ST25

Ala Pro Thr Pro Phe Pro Ser Asn Glu Thr Asn Pro Glu Lys Met Arg
465 470 475 480

Gln Trp Leu Ala Thr Val Thr Lys Ile Asn Ile Gly Gln Arg Thr Asn
485 490 495

Pro Phe Gln Arg Phe Gly Leu Ser Leu Met Pro Asn Ile Glu Val Leu
500 505 510

Gly Ile Gly Phe Thr Pro Ile Asn Asp Met Thr Pro Val Leu Gln Phe
515 520 525

Lys Lys Leu Lys Gln Leu Trp Met Thr Asn Thr Gly Ile Thr Asp Tyr
530 535 540

Ser Phe Leu Asp Lys Met Pro Leu Leu Glu Gly Leu Asp Ile Ser Gln
545 550 555 560

Asn Gly Ile Lys Asp Leu Ser Phe Leu Thr Lys Tyr Lys Gln Leu Ser
565 570 575

Leu Ile Ala Ala Ala Asn Asn Gly Ile Thr Ser Leu Lys Pro Leu Ala
580 585 590

Glu Leu Pro Asn Leu Gln Phe Leu Val Leu Ser His Asn Asn Ile Ser
595 600 605

Asp Leu Thr Pro Leu Ser Asn Leu Thr Lys Leu Gln Glu Leu His Leu
610 615 620

Asp His Asn Asn Val Lys Asn Leu Ser Ala Leu Ser Gly Lys Lys Asp
625 630 635 640

Leu Lys Val Leu Asp Leu Ser Asn Asn Lys Ser Ala Asp Leu Ser Thr
645 650 655

Leu Lys Thr Thr Ser Leu Glu Thr Leu Leu Leu Asn Glu Thr Asn Thr
660 665 670

Ser Asn Leu Ser Phe Leu Lys Gln Asn Pro Lys Val Ser Asn Leu Thr
675 680 685

Ile Asn Asn Ala Lys Leu Ala Ser Leu Asp Gly Ile Glu Glu Ser Asp
690 695 700

Glu Ile Val Lys Val Glu Ala Glu Gly Asn Gln Ile Lys Ser Leu Val
705 710 715 720

Leu Lys Asn Lys Gln Gly Ser Leu Lys Phe Leu Asn Val Thr Asn Asn
725 730 735

GBS patentin.ST25

Gln Leu Thr Ser₇₄₀ Leu Glu Gly Val₇₄₅ Asn Asn Tyr Thr Ser₇₅₀ Leu Glu Thr

Leu Ser Val₇₅₅ Ser Lys Asn Lys₇₆₀ Leu Glu Ser Leu Asp Ile₇₆₅ Lys Thr Pro

Asn Lys₇₇₀ Thr Val Thr Asn₇₇₅ Leu Asp Phe Ser His₇₈₀ Asn Asn Val Pro Thr

Ser Gln Leu Lys Leu₇₉₀ Asn Glu Lys Asn Ile₇₉₅ Pro Glu Ala Val Ala₈₀₀ Lys

Asn Phe Pro Ala₈₀₅ Val Val Glu Gly Ser₈₁₀ Met Val Gly Asn Gly₈₁₅ Ser Leu

Ala Glu Lys Ala₈₂₀ Ala Met Ala Ser₈₂₅ Lys Glu Asp Lys Gln Val₈₃₀ Ser Asp

Asn Thr₈₃₅ Asn His Gln Lys Asn₈₄₀ Thr Glu Lys Ser Ala₈₄₅ Gln Ala Asn Ala

Asp Ser₈₅₀ Lys Lys Glu Asn₈₅₅ Pro Lys Thr His Asp₈₆₀ Glu His His Asp His

Glu Glu Thr Asp His₈₆₅ Ala₈₇₀ His Val Gly His₈₇₅ His His His

<210> 270

<211> 500

<212> PRT

<213> Streptococcus agalactiae

<400> 270

Met Asn Lys Arg Val₅ Lys Ile Val Ala₁₀ Thr Leu Gly Pro Ala₁₅ Val Glu

Phe Arg Gly Gly₂₀ Lys Lys Phe Gly₂₅ Glu Ser Gly Tyr Trp₃₀ Gly Glu Ser

Leu Asp Val₃₅ Glu Ala Ser Ala₄₀ Glu Lys Ile Ala₄₅ Gln Leu Ile Lys Glu

Gly Ala Asn Val₅₀ Phe Arg₅₅ Phe Asn Phe Ser His₆₀ Gly Asp His Ala Glu

Gln Gly Ala Arg Met₆₅ Ala₇₀ Thr Val Arg Lys₇₅ Ala Glu Glu Ile Ala₈₀ Gly

GBS patentin.ST25

Gln Lys Val Gly Phe Leu Leu Asp Thr Lys Gly Pro Glu Ile Arg Thr
85 90 95

Glu Leu Phe Glu Asp Gly Ser Asp Phe His Ser Tyr Thr Thr Gly Thr
100 105 110

Lys Leu Arg Val Ala Thr Lys Gln Gly Ile Lys Ser Thr Pro Glu Val
115 120 125

Ile Ala Leu Asn Val Ala Gly Gly Leu Asp Ile Phe Asp Asp Val Glu
130 135 140

Val Gly Lys Gln Ile Leu Val Asp Asp Gly Lys Leu Gly Leu Thr Val
145 150 155 160

Phe Ala Lys Asp Lys Asp Thr Arg Glu Phe Glu Val Val Val Glu Asn
165 170 175

Asp Gly Leu Ile Gly Lys Gln Lys Gly Val Asn Ile Pro Tyr Thr Lys
180 185 190

Ile Pro Phe Pro Ala Leu Ala Glu Arg Asp Asn Ala Asp Ile Arg Phe
195 200 205

Gly Leu Glu Gln Gly Leu Asn Phe Ile Ala Ile Ser Phe Val Arg Thr
210 215 220

Ala Lys Asp Val Asn Glu Val Arg Ala Ile Cys Glu Glu Thr Gly Asn
225 230 235 240

Gly His Val Lys Leu Phe Ala Lys Ile Glu Asn Gln Gln Gly Ile Asp
245 250 255

Asn Ile Asp Glu Ile Ile Glu Ala Ala Asp Gly Ile Met Ile Ala Arg
260 265 270

Gly Asp Met Gly Ile Glu Val Pro Phe Glu Met Val Pro Val Tyr Gln
275 280 285

Lys Met Ile Ile Thr Lys Val Asn Ala Ala Gly Lys Ala Val Ile Thr
290 295 300

Ala Thr Asn Met Leu Glu Thr Met Thr Asp Lys Pro Arg Ala Thr Arg
305 310 315 320

Ser Glu Val Ser Asp Val Phe Asn Ala Val Ile Asp Gly Thr Asp Ala
325 330 335

Thr Met Leu Ser Gly Glu Ser Ala Asn Gly Lys Tyr Pro Val Glu Ser
340 345 350

GBS patentin.ST25

Val Arg Thr Met Ala Thr Ile Asp Lys Asn Ala Gln Thr Leu Leu Asn
355 360 365

Glu Tyr Gly Arg Leu Asp Ser Ser Ala Phe Pro Arg Asn Asn Lys Thr
370 375 380

Asp Val Ile Ala Ser Ala Val Lys Asp Ala Thr His Ser Met Asp Ile
385 390 395 400

Lys Leu Val Val Thr Ile Thr Glu Thr Gly Asn Thr Ala Arg Ala Ile
405 410 415

Ser Lys Phe Arg Pro Asp Ala Asp Ile Leu Ala Val Thr Phe Asp Glu
420 425 430

Lys Val Gln Arg Ser Leu Met Ile Asn Trp Gly Val Ile Pro Val Leu
435 440 445

Ala Asp Lys Pro Ala Ser Thr Asp Asp Met Phe Glu Val Ala Glu Arg
450 455 460

Val Ala Leu Glu Ala Gly Leu Val Glu Ser Gly Asp Asn Ile Val Ile
465 470 475 480

Val Ala Gly Val Pro Val Gly Thr Gly Gly Thr Asn Thr Met Arg Val
485 490 495

Arg Thr Val Lys
500

<210> 271

<211> 329

<212> PRT

<213> Streptococcus agalactiae

<400> 271

Met Thr Ala Thr Lys Gln His Lys Lys Val Ile Leu Val Gly Asp Gly
1 5 10 15

Ala Val Gly Ser Ser Tyr Ala Phe Ala Leu Val Asn Gln Gly Ile Ala
20 25 30

Gln Glu Leu Gly Ile Ile Glu Ile Pro Ala Leu Phe Asp Lys Ala Val
35 40 45

Gly Asp Ala Glu Asp Leu Ser His Ala Leu Ala Phe Thr Ser Pro Lys
50 55 60

GBS patentin.ST25

Lys Ile Tyr Ala Ala Thr Tyr Ala Asp Cys Ala Asp Ala Asp Leu Val
65 70 75 80

Val Ile Thr Ala Gly Ala Pro Gln Lys Pro Gly Glu Thr Arg Leu Asp
85 90 95

Leu Val Gly Lys Asn Leu Ala Ile Asn Lys Ser Ile Val Thr Gln Val
100 105 110

Val Glu Ser Gly Phe Asn Gly Ile Phe Leu Val Ala Ala Asn Pro Val
115 120 125

Asp Val Leu Thr Tyr Ser Thr Trp Lys Phe Ser Gly Phe Pro Lys Glu
130 135 140

Arg Val Ile Gly Ser Gly Thr Ser Leu Asp Ser Ala Arg Phe Arg Gln
145 150 155 160

Ala Leu Ala Asp Lys Ile Gly Val Asp Ala Arg Ser Val His Ala Tyr
165 170 175

Ile Met Gly Glu His Gly Asp Ser Glu Phe Ala Val Trp Ser His Ala
180 185 190

Asn Val Ala Gly Val Gln Leu Glu Gln Trp Leu Gln Glu Asn Arg Asp
195 200 205

Ile Asp Glu Gln Gly Leu Val Asp Leu Phe Ile Ser Val Arg Asp Ala
210 215 220

Ala Tyr Ser Ile Ile Asn Lys Lys Gly Ala Thr Tyr Tyr Gly Ile Ala
225 230 235 240

Val Ala Leu Ala Arg Ile Thr Lys Ala Ile Leu Asp Asp Glu Asn Ala
245 250 255

Val Leu Pro Leu Ser Val Tyr Gln Glu Gly Gln Tyr Gly Asp Val Lys
260 265 270

Asp Val Phe Ile Gly Gln Pro Ala Ile Val Gly Ala His Gly Ile Val
275 280 285

Arg Pro Val Asn Ile Pro Leu Asn Asp Ala Glu Leu Gln Lys Met Gln
290 295 300

Ala Ser Ala Glu Gln Leu Lys Asp Ile Ile Asp Glu Ala Trp Lys Asn
305 310 315 320

Pro Glu Phe Gln Glu Ala Ser Lys Asn
325

GBS patentin.ST25

<210> 272

<211> 819

<212> PRT

<213> Streptococcus agalactiae

<400> 272

Met Gln Asp Lys Asn Leu Val Asp Val Asn Leu Thr Ser Glu Met Lys
1 5 10 15

Thr Ser Phe Ile Asp Tyr Ala Met Ser Val Ile Val Ala Arg Ala Leu
20 25 30

Pro Asp Val Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr
35 40 45

Gly Met Asn Glu Leu Gly Val Thr Pro Asp Lys Pro His Lys Lys Ser
50 55 60

Ala Arg Ile Thr Gly Asp Val Met Gly Lys Tyr His Pro His Gly Asp
65 70 75 80

Ser Ser Ile Tyr Glu Ala Met Val Arg Met Ala Gln Trp Trp Ser Tyr
85 90 95

Arg His Met Leu Val Asp Gly His Gly Asn Phe Gly Ser Met Asp Gly
100 105 110

Asp Gly Ala Ala Ala Gln Arg Tyr Thr Glu Ala Arg Met Ser Lys Ile
115 120 125

Ala Leu Glu Met Leu Arg Asp Ile Asn Lys Asn Thr Val Asp Phe Gln
130 135 140

Asp Asn Tyr Asp Gly Ser Glu Arg Glu Pro Leu Val Leu Pro Ala Arg
145 150 155 160

Phe Pro Asn Leu Leu Val Asn Gly Ala Thr Gly Ile Ala Val Gly Met
165 170 175

Ala Thr Asn Ile Pro Pro His Asn Leu Gly Glu Ser Ile Asp Ala Val
180 185 190

Lys Leu Val Met Asp Asn Pro Asp Val Thr Thr Arg Glu Leu Met Glu
195 200 205

Val Ile Pro Gly Pro Asp Phe Pro Thr Gly Ala Leu Val Met Gly Arg
210 215 220

GBS patentin.ST25

Ser Gly Ile His Arg Ala Tyr Glu Thr Gly Lys Gly Ser Ile Val Leu
225 230 235 240

Arg Ser Arg Thr Glu Ile Glu Thr Thr Ser Asn Gly Lys Glu Arg Ile
245 250 255

Val Val Thr Glu Phe Pro Tyr Gly Val Asn Lys Thr Lys Val His Glu
260 265 270

His Ile Val Arg Leu Ala Gln Glu Lys Arg Ile Glu Gly Ile Thr Ala
275 280 285

Val Arg Asp Glu Ser Ser Arg Glu Gly Val Arg Phe Val Ile Glu Val
290 295 300

Arg Arg Asp Ala Ser Ala Asn Val Ile Leu Asn Asn Leu Phe Lys Leu
305 310 315 320

Thr Ser Leu Gln Thr Asn Phe Ser Phe Asn Met Leu Ala Ile Glu Lys
325 330 335

Gly Val Pro Lys Ile Leu Ser Leu Arg Gln Ile Ile Asp Asn Tyr Ile
340 345 350

Glu His Gln Lys Glu Val Ile Val Arg Arg Thr Gln Phe Asp Lys Ala
355 360 365

Lys Ala Glu Ala Arg Ala His Ile Leu Glu Gly Leu Leu Val Ala Leu
370 375 380

Asp His Leu Asp Glu Val Ile Thr Ile Ile Arg Asn Ser Glu Thr Asp
385 390 395 400

Thr Ile Ala Gln Ala Glu Leu Met Ser Arg Phe Glu Leu Ser Glu Arg
405 410 415

Gln Ser Gln Ala Ile Leu Asp Met Arg Leu Arg Arg Leu Thr Gly Leu
420 425 430

Glu Arg Asp Lys Ile Gln Ser Glu Tyr Asn Asp Leu Leu Ala Leu Ile
435 440 445

Ala Asp Leu Ala Asp Ile Leu Ala Lys Pro Glu Arg Val Val Thr Ile
450 455 460

Ile Lys Glu Glu Met Asp Glu Val Lys Arg Lys Tyr Ala Asp Ala Arg
465 470 475 480

Arg Thr Glu Leu Met Ile Gly Glu Val Leu Ser Leu Glu Asp Glu Asp
485 490 495

GBS patentin.ST25

Leu Ile Glu Glu Glu Asp Val Leu Ile Thr Leu Ser Asn Lys Gly Tyr
 500 505 510
 Ile Lys Arg Leu Ala Gln Asp Glu Phe Arg Ala Gln Lys Arg Gly Gly
 515 520 525
 Arg Gly Ile Gln Gly Thr Gly Val Asn Asn Asp Asp Phe Val Arg Glu
 530 535 540
 Leu Val Ser Thr Ser Thr His Asp Thr Val Leu Phe Phe Thr Asn Leu
 545 550 555 560
 Gly Arg Val Tyr Arg Leu Lys Ala Tyr Glu Ile Pro Glu Tyr Gly Arg
 565 570 575
 Thr Ala Lys Gly Leu Pro Ile Val Asn Leu Leu Lys Leu Asp Glu Gly
 580 585 590
 Glu Thr Ile Gln Thr Ile Ile Asn Ala Arg Lys Glu Asp Val Ala Asn
 595 600 605
 Lys Tyr Phe Phe Phe Thr Thr Gln Gln Gly Ile Val Lys Arg Thr Ser
 610 615 620
 Val Ser Glu Phe Ser Asn Ile Arg Gln Asn Gly Leu Arg Ala Ile Asn
 625 630 635 640
 Leu Lys Glu Asn Asp Glu Leu Ile Asn Val Leu Leu Ile Asp Glu Asn
 645 650 655
 Glu Asp Val Ile Ile Gly Thr Arg Thr Gly Tyr Ser Val Arg Phe Lys
 660 665 670
 Val Asn Ala Val Arg Asn Met Gly Arg Thr Ala Thr Gly Val Arg Gly
 675 680 685
 Val Asn Leu Arg Glu Gly Asp Lys Val Val Gly Ala Ser Arg Ile Val
 690 695 700
 Asn Gly Gln Glu Val Leu Ile Ile Thr Glu Lys Gly Tyr Gly Lys Arg
 705 710 715 720
 Thr Glu Ala Ser Glu Tyr Pro Thr Lys Gly Arg Gly Gly Lys Gly Ile
 725 730 735
 Lys Thr Ala Asn Ile Thr Ala Lys Asn Gly Pro Leu Ala Arg Leu Val
 740 745 750
 Thr Ile Asn Gly Asn Glu Asp Ile Met Val Ile Thr Asp Thr Gly Val
 755 760 765

GBS patentin.ST25

Ile Ile Arg Thr Asn Val Ala Asn Ile Ser Gln Thr Gly Arg Ser Thr
770 775 780

Met Gly Val Lys Val Met Arg Leu Asp Gln Glu Ala Lys Ile Val Thr
785 790 795 800

Val Ala Leu Val Glu Gln Glu Ile Glu Asp Lys Ser Asn Ile Glu Asp
805 810 815

Thr Lys Glu

<210> 273

<211> 442

<212> PRT

<213> Streptococcus agalactiae

<400> 273

Met Thr Ile Phe Asp Glu Arg Glu Leu Lys Glu Arg Phe Thr His Glu
1 5 10 15

Asn Arg Val Ser Phe Tyr Glu Phe Val Ala Lys Tyr Asp Ala Gln Met
20 25 30

Val Pro Val Met Lys Ala Lys Gly Tyr Arg Cys Ile His Ser Met Glu
35 40 45

Arg Thr Val Val Phe Thr Phe Gly Glu Phe Thr Ile Arg Arg Arg Arg
50 55 60

Trp Gln Lys Gly Glu His Trp Val Val Pro Val Asp Glu Lys Leu Gly
65 70 75 80

Leu Lys Lys Asn Val Arg Tyr Ser Leu Glu Phe Met Tyr Gln Ile Ala
85 90 95

Ser Leu Ala Thr Met Met Pro Tyr Glu Lys Val Ile Lys Val Val Gln
100 105 110

Met Met Tyr Cys Ile Val Ile Thr Lys Pro Thr Val Val Lys Ala Val
115 120 125

Lys Ile Ser Arg Glu Leu Leu Lys Glu Lys Glu Ala Tyr Arg Phe Phe
130 135 140

Asp Glu Asp Ile Pro Val Asp Lys Glu Pro Val Asp Met Ile Tyr Leu
145 150 155 160

GBS patentin.ST25

Glu Gly Asp Gly Val Met Val Lys Ala Arg Glu Glu Gly Leu Asp Asn
 165 170 175
 Arg Asn Val Asp Leu Ser His Phe Val Val His Thr Gly Ser Gln Lys
 180 185 190
 Val Gly Ser Asn Arg Phe Val Leu Gln Asn Lys Lys Glu Phe Val Ser
 195 200 205
 Leu Asp Asn Arg Gln Thr Arg Gln Lys Ile Leu Asp Tyr Leu Tyr Asn
 210 215 220
 His Phe Tyr Ile Ala Pro Asn Thr Leu Leu Ile Thr Asn Ser Asp Gly
 225 230 235 240
 Gly His Gly Tyr Thr Pro Tyr Val Phe Lys Glu Ile Ala Lys Ala Leu
 245 250 255
 Lys Val Lys Gln His Glu His Phe Trp Asp Arg Tyr His Val Asn Glu
 260 265 270
 Lys Ile Lys Ser Phe Phe Lys Leu Tyr Pro Val Glu Leu Met Thr Gly
 275 280 285
 Ala Phe Gln Ser Ile Lys Gln His Asp Lys Glu Lys Leu Arg Thr Val
 290 295 300
 Leu Asp Thr Thr Glu Ala Leu Ile Leu Met Glu Glu Glu Met Glu Gly
 305 310 315 320
 Phe Asn Gln Phe Lys Arg Lys Leu Leu Asn Asn Phe Gln Tyr Thr Lys
 325 330 335
 Ser Ala Glu Leu Arg Gly Phe Ser Arg Ala Gly Ile Gly Val Met Glu
 340 345 350
 Ser Gln His Arg Lys Ile Thr Tyr Arg Met Lys Lys Arg Gly Met Tyr
 355 360 365
 Trp Thr Ile Gln Gly Ala Glu Thr Met Ser Gln Leu Ile Val Leu Ser
 370 375 380
 Tyr Glu Gly Gln Leu Arg Asp Leu Phe Phe Gly Ser Trp Arg Glu Asp
 385 390 395 400
 Tyr Gln Lys Tyr Gln Glu Leu Glu Asn Leu Ser Ala Gly Lys Ile Lys
 405 410 415
 His Glu Gln Asn Lys Ile Asn Lys Arg Tyr Asp Leu Gln Thr Leu Gly
 420 425 430

GBS patentin.ST25

Arg Leu Arg Tyr Gly Arg His Arg Asn Leu
435 440

<210> 274

<211> 127

<212> PRT

<213> Streptococcus agalactiae

<400> 274

Met Ala Tyr Leu Ser Lys Leu Ser Asp Leu Asp Pro Ser Leu Met Asp
1 5 10 15

Ala Asp Ser Glu Gln Ile Tyr Ile Pro Lys Val Leu Phe Glu His Asn
20 25 30

Asp Phe Lys Gly Leu Thr Tyr Lys Glu Ile Leu Leu Tyr Ser Phe Leu
35 40 45

Leu Asn Arg Leu Arg Glu Pro Leu Asp Phe Ile Gln Lys Gly Tyr Asp
50 55 60

Asp Asn Glu Asp Thr Tyr Val His Phe Lys Val Glu Asp Leu Cys Glu
65 70 75 80

Leu Leu Asn Gln Ser Lys Thr Thr Val Ile Ser Leu Lys Lys Arg Leu
85 90 95

Ala Gln Tyr Gly Leu Ile Glu Glu Val Lys Ala Gly Ser His Gln Pro
100 105 110

Asn Arg Ile Tyr Leu Thr Asp Lys Leu Val Pro Tyr Ile Lys Gly
115 120 125

<210> 275

<211> 92

<212> PRT

<213> Streptococcus agalactiae

<400> 275

Met Thr Asp Asn Arg Phe Ala Gln Leu Lys Glu Asn Phe Glu Lys Gly
1 5 10 15

Ser Pro Lys Arg Arg Val Pro Thr Ser Arg Pro Ile Ala Ala Gln Lys
20 25 30

GBS patentin.ST25

Ala Pro Glu Ser Tyr Asn Lys Lys Gly Arg Tyr Pro Phe Ser Leu His
35 40 45

Gln Asp Val Arg Tyr Asp Lys Leu Glu Ala Leu Val Ala Tyr His Gly
50 55 60

Ala Lys Ser Ala Ser Asp Tyr Leu Glu Arg Leu Ile Val Gln Glu Trp
65 70 75 80

Glu Lys Met Gln Arg Lys Leu Lys Asn Lys Glu Lys
85 90

<210> 276

<211> 1049

<212> PRT

<213> Streptococcus agalactiae

<400> 276

Met Phe Ser Trp Leu Glu Ala Leu Tyr Tyr Thr Leu Ile Gln Leu Ala
1 5 10 15

Lys Val Asn Arg Leu Asn Ala Leu Phe Leu Val Ser Val Val Gly Tyr
20 25 30

Leu Cys Tyr Gln Gly Ile Lys Leu Val Arg Lys Thr Ile Arg Asn Phe
35 40 45

Phe Gln Leu Met Lys Gly Phe Ile Gly Asp Arg Glu Asn Ile Lys Lys
50 55 60

Cys Ile Lys Asn Lys Lys Glu Ala Leu Val His Ser Trp Lys His Arg
65 70 75 80

Gln Asp Ile Asp Trp Lys Ser Thr Gly Lys Asp Lys Ser Lys Gln Leu
85 90 95

Trp Asn Leu Met Lys Arg Leu Ala Thr Val Ala Pro Ser Phe Leu Phe
100 105 110

Leu Leu Leu Gly Asn Val Leu Phe Arg Leu Ile Tyr Gln Leu Pro Phe
115 120 125

Val Lys Gln Asp Arg Lys Arg Phe Asp Lys Glu Met Lys Pro Leu Leu
130 135 140

Tyr Phe Lys Asn Tyr Arg Ser Phe Val Phe Met Gly Ile Gly Phe Ser
145 150 155 160

GBS patentin.ST25

Phe Ile Ala Phe Ile Leu Thr Asn Tyr Phe Val Thr Val Leu Arg Ala
 165 170 175
 Ala Ile Arg Phe Leu Tyr Phe Ser Ile Met Thr Leu Arg Asp Asn Ser
 180 185 190
 Gln Val Val Ser Phe Asn Val Asp Ser Leu Leu Ile Gln Asn Leu Phe
 195 200 205
 Asn Ala Arg Val Phe Val Ile Ala Pro Ile Leu Ala Val Pro Ile Phe
 210 215 220
 Leu Ile Gly Leu Val Val Ala Trp Arg Ser Ala Trp Val Asn Phe Glu
 225 230 235 240
 Gln Tyr Arg Asp Tyr Asn His Asn Glu Glu Gly Asp Asp Arg Phe Ala
 245 250 255
 Thr Val Lys Glu Ile His Gln Gln Tyr Lys Lys Val Pro Asn Lys Thr
 260 265 270
 Glu Thr Tyr Pro Gly Glu Gly Gly Val Pro Val Leu His Glu Thr Arg
 275 280 285
 Lys Asn Leu Thr Gly Leu Thr Leu Lys Ser Gln Met Leu Trp Gln Asn
 290 295 300
 Arg Thr Phe Ser Arg Tyr Leu Thr Asn Ala Glu Arg Ile Leu Gly Leu
 305 310 315 320
 Leu Ser Thr Pro Ser Gly Asp Tyr Tyr Ile Asp Asp Ser Thr Thr Asn
 325 330 335
 Leu Ile Thr Met Gly Ile Thr Arg Ser Gly Lys Gly Glu Ala His Ile
 340 345 350
 Ala Pro Ile Ile Asp Ile Asn Ser Arg Ala Glu Ile Gln Pro Ser Leu
 355 360 365
 Ile Ile Ala Asp Pro Lys Gly Glu His Tyr Gln Ser Ser Tyr Lys Thr
 370 375 380
 Met Arg Arg Arg Gly Tyr Asp Val Asn Val Leu Ser Phe Gln Asn Met
 385 390 395 400
 Asp Trp Ser Met Ser Tyr Asn Pro Leu Ala Leu Ala Ile Ala Ala Ala
 405 410 415
 Lys Lys Gly Tyr Tyr Glu Met Thr Gln Thr Arg Val Asn Ala Val Ala
 420 425 430

GBS patentin.ST25

Glu Ala Ile Tyr Arg Lys Thr Lys Pro Gly Ser Gly Asn Gly Asn Ala
 435 440 445
 Lys Tyr Trp Glu Asp Thr Ser Ile Ser Leu Phe Asn Ala Ile Ala Met
 450 455 460
 Ala Leu Met Asp Arg Ala Asn Glu Thr Val Arg Asn Gly Glu Thr Asp
 465 470 475 480
 Ala Trp Asp Thr Val Thr Val Arg Asn Ile Ala Lys Phe Leu Thr Asp
 485 490 495
 Leu Gly Ser Glu Glu Val Phe Val Asn Asp Phe Gly Glu Ile Val Glu
 500 505 510
 Asn Pro Asp Lys Asn Gln Gln Val Lys Lys Lys Ser Lys Ile Thr Val
 515 520 525
 Tyr Phe Asp Asn Leu Arg Lys Ile Asn Gln Glu Gln Phe Ser Lys Phe
 530 535 540
 Arg Asp Met Ala Asp Leu Asn Phe Arg Ser Ser Asp Phe Ala Ser Glu
 545 550 555 560
 Glu Thr Lys Gly Asn Val Phe Ser Ser Met Met Ser Gly Ile Asn Leu
 565 570 575
 Phe Leu Gln Asp Asn Ile Ala Lys Leu Thr Ser Lys Asn Ser Ile Asp
 580 585 590
 Leu Glu Ser Val Gly Phe Pro Arg Arg Leu Ser Ile Lys Phe Arg Ser
 595 600 605
 Ser Ser Asn Val Ala Met Arg Asn Glu Tyr Thr His Lys Thr Ala Lys
 610 615 620
 Val Thr Ile Thr Ser Gln Ala Val Trp Gly Lys Thr Thr Lys Gln Val
 625 630 635 640
 Ile His Val Asp Ala Ala Thr Ala Leu Ile Asp Gly Glu Gly Tyr Leu
 645 650 655
 Thr Tyr Val Ile Glu Pro Gln Leu Pro Asp Gln Phe Leu Val Thr Ile
 660 665 670
 Asp Phe Asn His Glu Asn Asn Gly Gly Ser Ala Ile Arg His Lys Thr
 675 680 685
 Phe Gln Phe Ser Ala Glu Lys Val Tyr Lys Lys Arg Gly Asn Val Ile
 690 695 700

GBS patentin.ST25

Thr Leu Asp Asp Tyr Thr Lys Lys Pro Val Leu Asp His Ile Lys Val
705 710 715 720

Thr Val Leu Asn Lys Gln Asp Asp Asn Leu Leu Gln Lys Glu Asp Ile
725 730 735

Asp Leu Ile Tyr Ser Asp Asn Pro Lys Val Ile Tyr Leu Val Thr Pro
740 745 750

Pro Asn Arg Thr Glu Tyr Asn Ser Ile Val Ser Leu Phe Leu Asp Gln
755 760 765

Leu Phe Asn Ala Asn Tyr Glu Leu Ala Leu Ser Asn Gly Arg Lys Cys
770 775 780

Val Asn Arg Ile Leu His Ile Leu Asp Glu Phe Thr Asn Ile Pro Ala
785 790 795 800

Ile Pro His Met Asp Thr Lys Ile Ser Ile Gly Leu Gly Gln Asn Ile
805 810 815

Leu Tyr Tyr Leu Trp Ile Gln Asn Leu Lys Gln Leu Val Ser Glu Tyr
820 825 830

Gly Glu Asn Thr Ala Glu Thr Ile Arg Glu Asn Cys Ser Leu Lys Val
835 840 845

Tyr Ile Lys Ser Thr Ala Pro Ala Thr Asn Glu Tyr Phe Ser Lys Glu
850 855 860

Leu Gly Thr Arg Thr Ile Thr Arg Arg Arg Arg Ser Ser Asn Ile Leu
865 870 875

Asp Glu Ala Asn Pro Asn Val Ser Ile Glu Asn Pro Arg Gln Glu Leu
885 890 895

Leu Thr Pro Thr Gln Leu Ser Lys Leu Gln Glu Gly Glu Ala Val Ile
900 905 910

Leu Arg Gly Val Lys Gly Arg Asp Asn Ala Gly Arg Lys Ile Thr Thr
915 920 925

Asp Pro Ile Phe Leu His Glu Lys Thr Ser Leu Pro Tyr Arg Tyr Met
930 935 940

Phe Leu Gln Glu Glu Phe Asp Gln Ser Met Ala Leu Ala Asp Ile Pro
945 950 955 960

Val Glu Ser Gly His Arg Asp Leu Asp Leu Gln Asp Ile Ala Val Gly
965 970 975

GBS patentin.ST25

Ala Gln Ser Thr Phe Asn Lys Ile Ile Asp Trp Arg Met Ala Leu Thr
980 985 990

Asp Arg Met Arg Thr Asn Gly Lys Ile Pro Gln Leu Ala Ser Arg Lys
995 1000 1005

Gln Thr Ile Lys Ala Leu Ser Gln Ser Gln Phe Thr Ser Pro Ala
1010 1015 1020

Asp Leu Thr Gln Ala Val Ile Ala Glu Val Phe Asp Glu Glu Asp
1025 1030 1035

Asp Asp Asp Leu Phe Phe Val Asp Asp Val Met
1040 1045

<210> 277

<211> 933

<212> PRT

<213> Streptococcus agalactiae

<400> 277

Met Asn Ser Asn Thr Lys Gly His Gly Phe Phe Arg Lys Ser Lys Ala
1 5 10 15

Tyr Gly Leu Val Cys Ala Ile Ala Leu Ala Gly Ala Phe Thr Leu Ala
20 25 30

Thr Ser Gln Val Ser Ala Asp Gln Val Thr Thr Gln Ala Thr Thr Gln
35 40 45

Thr Val Thr Gln Asn Gln Ala Glu Thr Val Thr Ser Thr Gln Leu Asp
50 55 60

Lys Ala Val Ala Thr Ala Lys Lys Ala Ala Val Ala Val Thr Thr Thr
65 70 75 80

Pro Ala Val Asn His Ala Thr Thr Thr Asp Ala Gln Ala Asp Leu Ala
85 90 95

Asn Gln Thr Gln Ala Val Lys Asp Val Thr Ala Lys Ala Gln Ala Asn
100 105 110

Thr Gln Ala Ile Lys Asp Ala Thr Ala Glu Asn Ala Lys Ile Asp Ala
115 120 125

Glu Asn Lys Ala Glu Ala Glu Arg Val Ala Lys Glu Asn Lys Glu Gly
130 135 140

GBS patentin.ST25

Gln Ala Ala Val Asp Ala Arg Asn Lys Ala Gly Gln Ala Ala Val Asp
145 150 155 160

Ala Arg Asn Lys Ala Lys Gln Gln Ala Gln Asp Asp Gln Lys Ala Lys
165 170 175

Ile Asp Ala Glu Asn Lys Ala Glu Ser Gln Arg Val Ser Gln Leu Asn
180 185 190

Ala Gln Asn Lys Ala Lys Ile Asp Ala Glu Asn Lys Asp Ala Gln Ala
195 200 205

Lys Ala Asn Ala Thr Asn Ala Gln Leu Gln Lys Asp Tyr Gln Ala Lys
210 215 220

Leu Ala Glu Ile Lys Ser Val Glu Ala Tyr Asn Ala Gly Val Arg Gln
225 230 235 240

Arg Asn Lys Asp Ala Gln Ala Lys Ala Asp Ala Thr Asn Ala Gln Leu
245 250 255

Gln Lys Asp Tyr Gln Ala Lys Leu Ala Leu Tyr Asn Gln Ala Leu Lys
260 265 270

Ala Lys Ala Glu Ala Asp Lys Gln Ser Ile Asn Asn Val Ala Phe Asp
275 280 285

Ile Lys Ala Gln Ala Lys Gly Val Asp Asn Ala Glu Tyr Gly Asn Ser
290 295 300

Ile Met Thr Ala Lys Thr Lys Pro Asp Gly Ser Phe Glu Phe Asn His
305 310 315 320

Asp Met Ile Asp Gly Val Lys Thr Ile Gly Tyr Gly Lys Leu Thr Gly
325 330 335

Lys Val Asn His His Tyr Val Ala Asn Lys Asp Gly Ser Val Thr Ala
340 345 350

Phe Val Asp Ser Val Thr Leu Tyr Lys Tyr Glu Tyr Arg Asn Val Ala
355 360 365

Gln Asn Ala Ala Val Asn Gln Asn Ile Val Phe Arg Val Leu Thr Lys
370 375 380

Asp Gly Arg Pro Ile Phe Glu Lys Ala His Asn Gly Asn Lys Thr Phe
385 390 395 400

Ala Glu Thr Leu Asn Lys Thr Leu Gln Leu Asn Leu Lys Tyr Glu Leu
405 410 415

GBS patentin.ST25

Lys Pro His Ala Ser Ser Gly Asn Val Glu Val Phe Lys Ile His Asp
 420 425 430
 Asp Trp Val His Asp Thr His Gly Ser Ala Leu Val Ser Tyr Val Asn
 435 440 445
 Asn Asn Asp Ala Val Pro Asn Val Val Ile Pro Glu Arg Pro Thr Pro
 450 455 460
 Pro Lys Pro Val Lys Val Thr Pro Glu Ala Glu Lys Pro Val Pro Glu
 465 470 475 480
 Lys Pro Val Glu Pro Lys Leu Val Thr Pro Thr Leu Lys Thr Tyr Thr
 485 490 495
 Pro Val Lys Phe Ile Pro Arg Glu Tyr Lys Pro Glu Pro Ile Thr Pro
 500 505 510
 Glu Thr Phe Thr Pro Glu Lys Phe Thr Pro Ala Gln Pro Lys Val Lys
 515 520 525
 Pro His Val Ser Ile Pro Glu Lys Ile Asn Tyr Ser Val Ser Val His
 530 535 540
 Pro Val Leu Val Pro Ala Ala Asn Pro Ser Lys Ala Val Ile Asp Glu
 545 550 555 560
 Ala Gly Gln Ser Val Asn Gly Lys Thr Val Leu Pro Asn Ala Thr Leu
 565 570 575
 Asp Tyr Val Ala Lys Gln Asn Phe Ser Gln Tyr Lys Gly Ile Lys Ala
 580 585 590
 Ser Ala Glu Ala Ile Ala Lys Gly Phe Ala Phe Val Asp Gln Pro Asn
 595 600 605
 Glu Ala Leu Ala Glu Leu Thr Val Lys Ser Ile Lys Ala Ser Asn Gly
 610 615 620
 Asp Asp Val Ser Ser Leu Leu Glu Met Arg His Val Leu Ser Lys Asp
 625 630 635 640
 Thr Leu Asp Gln Lys Leu Gln Ser Leu Ile Lys Glu Ala Gly Ile Ser
 645 650 655
 Pro Val Gly Glu Phe Tyr Met Trp Thr Ala Lys Asp Pro Gln Ala Phe
 660 665 670
 Tyr Lys Ala Tyr Val Gln Lys Gly Leu Asp Ile Thr Tyr Asn Leu Ser
 675 680 685

GBS patentin.ST25

Phe Lys Ile Lys Ala Asn Phe Thr Lys Gly Gln Ile Lys Asn Gly Val
690 695 700

Ala Gln Ile Asp Phe Gly Asn Gly Tyr Thr Gly Asn Ile Val Val Asn
705 710 715 720

Asp Val Thr Val Pro Glu Val His Lys Asp Ile Leu Asp Lys Glu Asp
725 730 735

Gly Lys Ser Ile Asn Asn Ser Thr Val Lys Leu Gly Asp Glu Val Thr
740 745 750

Tyr Lys Leu Glu Gly Trp Val Val Pro Ala Asn Arg Gly Tyr Asp Leu
755 760 765

Phe Glu Tyr Lys Phe Val Asp Gln Leu Gln His Thr His Asp Leu Tyr
770 775 780

Leu Arg Asp Lys Val Val Ala Lys Val Asp Val Thr Leu Lys Asp Gly
785 790 795 800

Thr Val Ile Lys Lys Gly Thr Asn Leu Gly Glu Tyr Thr Glu Thr Val
805 810 815

Tyr Asn Lys Thr Thr Gly His Tyr Glu Leu Ala Phe Lys Lys Glu Phe
820 825 830

Leu Ala Lys Val Ser Arg Glu Ser Glu Phe Gly Ala Asp Asp Phe Ile
835 840 845

Val Val Lys Arg Ile Lys Ala Gly Asp Val Tyr Asn Thr Ala Asp Leu
850 855 860

Tyr Val Asn Gly Tyr Lys Val Lys Ser Glu Ala Val Val Thr His Thr
865 870 875 880

Thr Glu Lys Ser Lys Pro Val Glu Pro Gln Lys Ala Thr Pro Lys Ala
885 890 895

Pro Ala Lys Gly Leu Pro Ser Thr Gly Glu Ala Ser Met Thr Pro Leu
900 905 910

Thr Ala Ile Gly Ala Ile Ile Leu Ser Ala Leu Gly Leu Ala Gly Phe
915 920 925

Lys Lys Arg Gln Lys
930

<210> 278

GBS patentin.ST25

<211> 753

<212> PRT

<213> Streptococcus agalactiae

<400> 278

Met Lys Gln Ile Lys Ile Ile Thr Gly Leu Thr Val Ala Thr Leu Ser
1 5 10 15

Ala Val Val Gly Asn Val Tyr Ala Glu Asp Ile Thr Pro Thr Ala Pro
20 25 30

Val Asn Glu Pro Gln Val Ser Ser Glu Thr Ala Lys Thr Pro Gln Val
35 40 45

Thr Glu Ser Gln Val Asn Ser Ala Lys Val Thr Ala Asp Gln Ala Ile
50 55 60

Ser Asp Val Asn Asn Gln Gln Ile Val Val Asp Glu Ala Gln Lys Gln
65 70 75 80

Lys Asp Gln Ser Gln Gln Asn Leu Val Lys Ala Thr Ser Thr Val Thr
85 90 95

Glu Ala Glu Lys Val Ala Ala Glu Ala Thr Pro Glu Val Val Lys Glu
100 105 110

Ala Ile Lys Ala Val Thr Glu Ala Lys Glu Ala Val Thr Asp Ala Glu
115 120 125

Ala Asn Val Val Asp Ala Gln Lys Thr Glu Gln Lys Ala Asn Gln Glu
130 135 140

Val Gln Ser Gln Ala Lys Thr Val Asp Glu Asn Val Lys Val Val Ala
145 150 155 160

Asp Lys Glu Ser Glu Val Lys Gln Ala Glu Gly Val Val Thr Thr Ala
165 170 175

Gln Glu Ala Ile Asp Ser Lys Thr Ala Asn Thr Asn Ala Ser Glu Ala
180 185 190

Glu Lys Ala Val Thr Glu Lys Gln Thr Lys Leu Glu Thr Ala Glu Thr
195 200 205

Asn Leu Thr Glu Ala Gln Lys Gln Asp Ala Lys Ile Ala Glu Glu Lys
210 215 220

Arg Leu Ala Glu Gln Glu Val Val Asn Lys Gln Leu Ala Val Thr Asp
225 230 235 240

GBS patentin.ST25

Thr Gln Thr Leu Leu Lys Lys Leu Val Thr Glu Ile Asn Asn Glu Lys
245 250 255

Val Ser Thr Ser Leu Glu Asn Gln Ala Tyr Phe Asn Gln Arg Asp Gly
260 265 270

Ser Trp Ala Gly Tyr Tyr Gly Asn Tyr Thr Phe Ala Ala Thr Gly Cys
275 280 285

Val Pro Ser Ser Leu Ala Met Val Phe Thr Glu Leu Ala Arg Arg Gln
290 295 300

Ile Thr Pro Thr Glu Ile Ala Asn Tyr Leu Trp Asn Asn Ser Asn Glu
305 310 315 320

Phe Asn Lys Asn Tyr Gly Gly Thr Ser Gly Lys Gly Leu Val Gln Ala
325 330 335

Thr Lys His Phe Gly Phe Val Pro Thr His Leu Ala Ser Gln Ser Ala
340 345 350

Ile Val Glu Ala Leu Gln Ala Gly His His Val Leu Ala Ala Val Gln
355 360 365

Gln Asp Lys Phe Ser Pro Trp Gly Ile Asn Tyr Ser His Glu Ile Val
370 375 380

Leu Arg Gly Tyr Ser Asn Gly Asn Thr Tyr Val Tyr Asp Pro Tyr Asn
385 390 395 400

Arg Ala Asn Ile Gly Trp Tyr Pro Val Ala Asn Leu Trp Asn Glu Gln
405 410 415

Ser Arg Asp Ala Ile Asp Thr Ser Ser Val Gly Val Pro Phe Phe Lys
420 425 430

Ile Thr Thr Gln Lys Met Ala Gln Leu Glu Ala Gln Lys Ala Gln Val
435 440 445

Gln Ser Ser Leu Asn Thr Ala Lys Asn Gln Leu Ala Lys Thr Gln Asp
450 455 460

Val Leu Arg Thr Leu Glu Ala Thr Pro Leu Lys Thr Pro Glu Ala Gln
465 470 475 480

Ala Lys Leu Asn Gln Ala Lys Glu Ala Leu Ala Leu Ala Gln Ala Asp
485 490 495

Tyr Thr Lys Ala Gln Glu Ala Val Lys Leu Ala Ser Gln Asp Leu Ala
500 505 510

GBS patentin.ST25

Val Lys Glu Glu Thr Leu Lys Asn Ala Gln Ala Asp Leu Leu Thr Lys
515 520 525

Gln Thr Ala Leu Lys Asp Ala Gln Thr Val Leu Val Ala Ser Gln Val
530 535 540

Lys Leu Ala Asp Leu Lys Ala Thr Leu Ala Thr Val Glu Asn Asn Val
545 550 555 560

Lys Lys Ala Gln Ala Thr Leu Thr Asp Ala Lys Ala Ile Val Gly Gln
565 570 575

Lys Gln Ala Lys Leu Leu Ala Leu Gln Asn Ala Pro Lys Ile Leu Ala
580 585 590

Asp Ala Gln Ala Lys Leu Val Thr Ala Lys Asn Asp Leu Ala Asn Lys
595 600 605

Met Ala Ile Leu Asp Glu Ala Val Ala Lys Leu Lys Ser Leu Gln Ala
610 615 620

Val Gln Ala Glu Ala Gln Lys Gln Tyr His Val Val Phe Glu Ala Tyr
625 630 635 640

Lys Ala Val Arg Asp Ala Lys Glu Gln Ala Lys Leu Ala Glu Ser Tyr
645 650 655

Asn His Ile Ile Ala Arg Gly Gly Glu Ala Ile Pro Val Val Asp Glu
660 665 670

Thr Asp Lys Ile Thr Gly Tyr Val Asp Gly Ser Gln Lys Ala Val Ala
675 680 685

Asn Glu Val Thr Leu Ala Leu Thr Ser Asn Gly Ala Pro Leu Glu Ser
690 695 700

Pro Val Asn Lys Glu Asn Gln Asn Val Thr Lys Ser Ser Gln Ala Leu
705 710 715 720

Pro His Thr Gly Glu Ala Gly Leu Ser Ile Leu Ser Val Leu Gly Val
725 730 735

Gly Leu Ile Ser Thr Leu Gly Leu Thr Ser Leu Lys Lys Arg Arg Pro
740 745 750

His

<210> 279

<211> 639

<212> PRT

<213> Streptococcus agalactiae

<400> 279

Val Arg Leu Thr His Val Ser Leu Trp Met Pro Ser Lys Arg Ser Trp
 1 5 10 15

Pro Leu Lys Leu Gln Leu Leu Arg Lys Gly Val Ile Glu Leu Glu Asp
 20 25 30

Glu Leu Lys Thr Pro Tyr Leu Asp Gln Tyr Thr Asp Asn Leu Thr Ala
 35 40 45

Lys Val Thr Lys Lys Ser Asp Asp Tyr Gln Val Tyr Gly Arg Asn Lys
 50 55 60

Glu Val Gln Ser Val Ile Ile Ser Leu Leu Arg Arg Thr Lys Asn Asn
 65 70 75 80

Pro Ile Leu Val Gly Glu Ala Gly Val Gly Lys Ser Ala Ile Val Glu
 85 90 95

Gly Ile Thr Leu Ala Ile Leu Arg Gly Gln Val Pro Glu Pro Leu Lys
 100 105 110

Gly Leu Thr Val Arg Ser Leu Glu Leu Ser Ser Leu Met Ser Glu Asp
 115 120 125

Asp Glu Gly Phe Ile Ala Lys Phe Lys Lys Ile Ile Glu Glu Met Val
 130 135 140

Ala Thr Arg Gly His Asn Leu Leu Phe Val Asp Glu Phe His Thr Ile
 145 150 155 160

Ile Gly Ala Gly Ser Gln Asn Gly Gln Ala Leu Asp Ala Gly Asn Val
 165 170 175

Ile Lys Pro Val Leu Ala Arg Gly Asp Ile Gln Leu Ile Gly Ala Thr
 180 185 190

Thr Leu Asp Glu Phe His Glu Tyr Ile Glu Thr Asp Arg Ala Leu Glu
 195 200 205

Arg Arg Met Gln Pro Val Met Val Glu Glu Pro Thr Ile Ser Gln Ala
 210 215 220

Ile Thr Ile Ile Glu Gln Ala Lys Val Ile Tyr Glu Lys Phe His Gly
 225 230 235 240

GBS patentin.ST25

Ile Gln Ile Ser Ser Asp Ala Val His Gln Ala Ile Arg Leu Ser Val
245 250 255

Arg Tyr Leu Thr Asp Arg Phe Leu Pro Asp Lys Ala Phe Asp Leu Ile
260 265 270

Asp Glu Ala Ala Thr Ile Ala Ser Val Glu Gly Lys Ser Lys Val Thr
275 280 285

Glu Lys Asp Ile Ala Gln Val Leu Lys Asp Lys Thr Gly Ile Pro Val
290 295 300

Thr Thr Ile Leu Lys Gly Asp Gln Glu Arg Leu Glu Gly Phe Lys Glu
305 310 315 320

Arg Leu Met Asn Arg Val Lys Gly Gln Glu Asp Ala Ile Glu Ala Val
325 330 335

Val Asp Ala Val Thr Ile Ala Gln Ala Gly Leu Gln Asn Glu Lys Arg
340 345 350

Pro Leu Ala Ser Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr
355 360 365

Glu Leu Ala Lys Ala Ile Ala Glu Ala Leu Phe Asp Asp Glu Ala Ala
370 375 380

Met Ile Arg Phe Asp Met Ser Glu Tyr Lys Gln Lys Glu Asp Val Thr
385 390 395 400

Lys Leu Ile Gly Asn Arg Ala Thr Arg Ile Lys Gly Gln Leu Thr Glu
405 410 415

Gly Val Lys Gln Lys Pro Tyr Cys Val Leu Leu Leu Asp Glu Ile Glu
420 425 430

Lys Ala His Ser Glu Val Met Asp Leu Phe Leu Gln Val Leu Asp Asp
435 440 445

Gly Arg Leu Thr Asp Ser Ser Gly Arg Leu Ile Ser Phe Lys Asn Thr
450 455 460

Ile Val Ile Met Thr Thr Asn Ile Gly Ala Lys Lys Ile Ile Asn Lys
465 470 475 480

Trp Glu Leu Lys Gly Asn Phe Lys Asp Leu Thr Asp Arg Asp Arg Lys
485 490 495

Gln Phe Glu Lys Ser Met Asp Ser Glu Leu Gln Asn Glu Phe Arg Pro
500 505 510

GBS patentin.ST25

Glu Phe Leu Asn Arg Ile Glu Asn Lys Leu Ile Phe Asn Leu Leu Glu
515 520 525

Arg Asp Val Ile Glu Lys Ile Ala Glu Lys Asn Leu Ser Glu Ile Ala
530 535 540

Asp Arg Met Lys Arg Gln Asn Leu Thr Leu Ser Tyr Glu Pro Ser Leu
545 550 555 560

Ile Gln Tyr Leu Ser Asp Val Gly Thr Asp Val Lys Asn Gly Ala Arg
565 570 575

Pro Leu Glu Arg Leu Met Lys Arg Lys Val Leu Ala Pro Ile Ser Val
580 585 590

Lys Ser Leu Gln Leu Asp Lys Ser Lys Gln Gly Tyr Asn Val His Leu
595 600 605

Trp Val Glu Gly Arg Ala Pro Asp Gly Asn His Arg Gln Glu Gln Arg
610 615 620

Gln Ile His Met Glu Ile Glu Gly Glu Arg Asp Asn Phe Phe Ser
625 630 635

<210> 280

<211> 1576

<212> PRT

<213> Streptococcus agalactiae

<400> 280

Met Ala Glu Glu Asn Ala Gln Gln Pro Ser Leu Arg Gly Lys Ser Arg
1 5 10 15

Arg Glu Arg Val Glu Phe Ala Arg Ser Arg Asp Ile Leu Asp Val Ala
20 25 30

His Glu Leu Asn Met Glu Leu Phe Arg Asp Gly Lys Asn Tyr Arg Trp
35 40 45

Lys Glu His Asp Ser Met Val Ile Thr Pro Ala Thr Asn Gln Trp Tyr
50 55 60

Trp Phe Ser Gln Arg Gln Gly Gly Asp Val Ile Ala Leu Val Glu Thr
65 70 75 80

Ile Lys Glu Ile Gly Phe Asn Gln Ala Phe Glu Tyr Leu Asn Glu Gly
85 90 95

GBS patentin.ST25

Thr Phe Lys Glu Phe Thr Val Val Asn Gln Val Lys Glu Pro Phe Ser
100 105 110

Tyr Tyr Leu Glu Pro Tyr Glu Gln Leu Phe Val Glu Ala Arg Arg Tyr
115 120 125

Leu Lys Glu Asn Arg Gly Leu Ser Asp Asp Thr Ile Asp Phe Phe Tyr
130 135 140

Asp Lys Gly Val Leu Ala Gln Ala Asn Ala Lys Val Gly Asp Met Ile
145 150 155 160

Glu Pro Val Leu Val Phe Lys Asn Leu Asp Lys Asn Gly Gln Val Val
165 170 175

Gly Ala Ala Leu Gln Gly Leu Val Ala Ala Pro Asp Lys Tyr Phe Gly
180 185 190

Arg Gly Tyr Leu Lys Gln Ile Met Lys Asn Ser Gln Pro Tyr Asn Gly
195 200 205

Met His Val Asp Ile Gly Thr Pro Asn Arg Leu Val Phe Ala Glu Ser
210 215 220

Ser Ile Asp Leu Met Ser Tyr Tyr Glu Ile His Lys Asp Ser Leu Ser
225 230 235 240

Asp Val Arg Leu Val Ser Leu Glu Gly Leu Lys Thr Gly Thr Ile Gly
245 250 255

Arg His Leu Ile Gln Leu Arg Ala Glu Met Glu Arg Arg Pro Leu Ser
260 265 270

Ser Ser Trp Thr Asp Glu Ile Leu Ala Gln Gly Leu Asp Glu Ala Val
275 280 285

Lys Gln Gly Tyr Phe Lys Asp Gly Lys Asn Ser His Leu Leu Thr Leu
290 295 300

Ala Val Asp Asn Asp Val Lys Gly Lys Gln Leu Ile Glu Glu Leu Lys
305 310 315 320

Asp Lys Ser Ile Pro Val Ile Asp Ala Thr Pro Pro Lys Ala Glu Gly
325 330 335

Gln Ser Lys Met Asp Trp Asn Ala Tyr Leu Gln Glu Thr Lys Ala Thr
340 345 350

Phe Ser Thr Glu Lys Tyr Gln Glu Lys Ile Asp His Leu Ile Ser Asp
355 360 365

GBS patentin.ST25

Val Ile Leu Gly Asp Glu Thr Tyr Tyr Leu Trp His Asp Asp Glu Leu
370 375 380

Val Asn Leu Gly Ala Gly Asp Ser Ile Ile Gln Ala Phe His His Gln
385 390 395 400

Leu Glu Asp Arg Arg Tyr Val Ile Asn Gln Ala Glu Leu Tyr Val Glu
405 410 415

Glu Ser Ser Asn Asp Gly Ala Thr Gly Tyr Leu Ser Ile Glu Gly His
420 425 430

Val Leu Asp Lys Asp Gly Ile Ser Asp Tyr Leu Ser Asp Gln Ala Leu
435 440 445

Thr Asp Ala Glu Lys Val Ala Phe Leu Glu Thr Leu Gln Thr Glu Leu
450 455 460

Pro Asp Ile Trp Asp Glu Ile Val Asn His Tyr Asp Lys Val Phe Glu
465 470 475 480

Glu Val Val Val Lys Tyr Gly Leu Arg Glu Lys His Ala Asp Ile Ile
485 490 495

Gln Glu Gln Glu Leu Asp Leu Asp Pro Leu Val Val Pro Glu Ala Lys
500 505 510

Glu Lys Ser Leu Glu Met Asn Gln Glu Thr Asn Thr Gly Gly Glu Leu
515 520 525

Phe Asn Arg Asn Ser Ser Phe Leu Gly Glu Asp Ser Pro Gly Thr Ala
530 535 540

Pro Gln Pro Val Glu Pro Thr Ala Gln Pro Asp Phe Pro Thr Asn Val
545 550 555 560

Arg Leu His Phe Thr Thr Asp Asp Gly Asn Met Ser Asn Lys Ala Phe
565 570 575

Arg Lys Asn Met Arg Thr Leu Asn Leu Tyr Ala Asn Thr Met Arg Asp
580 585 590

Ser Ala Gln Trp Tyr Leu Ser Glu Ile Ala Asp Thr Thr Met Ser Tyr
595 600 605

Val Tyr Lys Thr Pro His Glu Glu Gly Val Gln Val Leu Ser Val His
610 615 620

Phe Gly Lys Lys Asn Trp Met His Leu Thr Gly Val Thr Pro Val Tyr
625 630 635 640

GBS patentin.ST25

Glu Asn Trp Val Asp Ser Leu Ser Glu Gln Phe Ile Asp Asp Ile Ala
645 650 655

Asn Ser Lys Gly His Phe Lys Asn Leu Lys Phe Ala Leu Gly Thr Pro
660 665 670

Asp Lys Leu Lys Val Leu Asn Leu Leu Pro Glu Ile Ile Glu Ser Asp
675 680 685

Thr Phe Val Phe Asn Asp Leu Ser Ser Val Gln Lys Leu Asn Asn Leu
690 695 700

Asp Leu Ser Gln Ala Leu Asn Pro Glu Asp Ser Asp Leu Leu Leu Leu
705 710 715 720

Phe Arg Asp Glu Gly Leu His Gln Val Pro Ala Ser Leu Met Arg Ile
725 730 735

Lys Gly Asp Leu Glu Glu Arg Leu Ser His Ile Asp Ser Gly Thr Val
740 745 750

Leu Gly Val Tyr Arg Glu Arg Asn Gly Gln Leu Glu Gln Val Ser Val
755 760 765

Asn Glu Glu Tyr Val Lys Asp Ser Gly Gln Glu Met Leu Ser Ile Leu
770 775 780

Gln Asn Lys His Tyr Glu Glu Ala Leu Asp Ser Gly Gln Glu Met Val
785 790 795 800

Gln Thr Asp Gly Phe Ser Ala Glu Asp Phe Thr Lys Val Leu Asp Ala
805 810 815

Val Tyr His Val Gly Val Pro Asp Asp Leu Ala Arg Val Pro Glu Gly
820 825 830

Val Leu Pro Val Trp Gln Lys Tyr Leu Glu Val Ser Glu Glu Asn Gln
835 840 845

Trp Asp Leu Glu Gln Met Ile Asp Tyr Ala Asp Lys Asn Ser Leu Leu
850 855 860

Val Lys Asp Ser Ala Phe Tyr Lys Glu Trp Lys Glu Asp Met Ile Tyr
865 870 875 880

Lys Asn Asp Tyr His Val Arg Leu Gln Phe Ala Glu Asn Trp Asp Asn
885 890 895

Gly Val Glu Leu Pro Phe Arg Thr Glu Gln Leu Ile Asp Tyr Lys Thr
900 905 910

GBS patentin.ST25

Phe Val Thr Gly Leu Tyr Glu Ala Asn Gln Ala His His Gln Arg Arg
915 920 925

Gln Glu Ser Gln Leu Pro Tyr Thr Lys Thr Glu Phe Asp Ile Tyr Ala
930 935 940

Pro Gly Gly Gln Leu Ile Lys Asp Asn Val His Tyr Ala Ile Gly Asp
945 950 955 960

Glu Thr Arg Pro Val Ser Gln Leu Met Gly Leu Gly Tyr Arg Arg Leu
965 970 975

Pro Gly Tyr Gln Glu Leu Ala Val Ile Asp Asn Ser Ile Leu Ser Gln
980 985 990

Leu Glu Asn Lys Glu Leu Asn Gln Glu Ile Ala Ser Glu Ala Asn Glu
995 1000 1005

His Ser Leu Asn Ser Gln Glu Ile Pro Lys Glu Asp Asn Tyr Pro
1010 1015 1020

Arg Glu Ala Phe Thr Ser Pro Lys Gln Asp Ile Lys Lys Gly Leu
1025 1030 1035

Ala Gln Arg Val Glu Glu Ile Val Ala Glu Asp Ala Thr Lys Ile
1040 1045 1050

Leu Val Ser Ser Ile Pro Gln Val Gln Glu Asn Leu Ser Val Glu
1055 1060 1065

Gly Asn Leu Val Gly Thr Pro Gln Ala Asp Asn Arg Met Leu Tyr
1070 1075 1080

Thr Asn Leu Glu Asp Phe Gly Gln Asp Tyr Gln Leu Glu Leu Ala
1085 1090 1095

Val Tyr Ser Pro Lys Arg Val Asp Phe Leu Glu Asp Val Gln Ala
1100 1105 1110

Pro Trp Thr Leu Ala Leu Ile Arg Lys Glu Lys Lys Ile Gly Tyr
1115 1120 1125

Leu Ala Tyr Gly Ser Asp Trp Ala Lys Glu Phe Gln Ile Glu Glu
1130 1135 1140

Glu Leu Glu His Leu Ala Ala Gln Ile Gly Asp Glu Lys Val Pro
1145 1150 1155

Glu Gly Leu Tyr Lys Gln Ala Glu Val Glu Ala Phe Ile Ala Ser
1160 1165 1170

GBS patentin.ST25

His Gln Gly Asn Glu Ser Leu Gln Glu Pro Ile Pro Thr Ile Val
 1175 1180 1185
 Ala Glu Pro Phe Asp Tyr Thr Ser Ala Ser Ala Tyr Glu Ile Ser
 1190 1195 1200
 Glu His Ala Phe Gln Lys Ile Arg Glu Tyr Thr Gln Ser Pro Glu
 1205 1210 1215
 Asp Leu Leu Glu Tyr Met Asp Phe Met Ser Lys Phe Pro Gln Leu
 1220 1225 1230
 Ser Pro Arg Asn Val Ala Leu Ile His Glu Gln Trp Arg Gly Ala
 1235 1240 1245
 Asn Ala Val Ala Thr Tyr Glu Gln Trp Lys Ala Met Gly Glu Ala
 1250 1255 1260
 Leu Gly Ile Lys Pro Asp Asp Val Val Gln Thr Lys Ala Thr Tyr
 1265 1270 1275
 Val Asn Lys Arg Thr Gly Glu Thr Lys Glu Val Val His Gln Gly
 1280 1285 1290
 Leu Ser Val Lys Thr Gly Glu Lys Ser Lys Ile Thr Leu Phe Arg
 1295 1300 1305
 Pro Leu Met Val Lys Met Ile Pro Val Leu Asp Glu Asn Gly Gln
 1310 1315 1320
 Gln Leu Lys Asn Asp Lys Gly Asn Pro Lys Tyr Lys Lys Leu Ser
 1325 1330 1335
 Glu Ala Ser Leu Gln Glu Lys Ala Leu Val Lys Asp Gly Lys Leu
 1340 1345 1350
 Pro Val Arg Gln Phe Gln Glu Arg Asp Ser Lys Thr Gly Gln Pro
 1355 1360 1365
 Arg Phe Thr Thr Tyr Lys Val Phe Glu Leu Ser Gln Thr Thr Leu
 1370 1375 1380
 Lys Pro Gly Ser Tyr Pro Lys Ala Met Pro Asn Arg His Phe Asn
 1385 1390 1395
 Phe Asn Val Asp Lys Val Lys Thr Lys Glu Val Leu Glu Gly Leu
 1400 1405 1410
 Cys Asp Tyr Ala Glu Lys Ile Gly Val Ser Leu Met Lys Asp Asp
 1415 1420 1425

GBS patentin.ST25

Ala His Val Leu Asp Asn Ala Lys Gly Ala Phe Tyr Ser Glu Glu
1430 1435 1440

Gln Leu Ile Leu Ile Asn Pro Asn Asn Thr Pro Gly Glu Lys Ile
1445 1450 1455

Ala Thr Thr Ile His Glu Leu Ala His Ala Thr Leu His Asn Pro
1460 1465 1470

Lys Leu Glu Lys Gln Tyr Lys Glu Leu Pro Lys Gly Gln Lys Glu
1475 1480 1485

Phe Glu Ala Glu Met Thr Ser Tyr Leu Leu Ser Lys His Phe Gly
1490 1495 1500

Leu Asp Thr Ser Glu Lys Ala Ile His Tyr Met Ala Ser Trp Thr
1505 1510 1515

Asp Asn Leu Lys Ala Leu Glu Asp Lys Gln Leu Ala Asp Ser Leu
1520 1525 1530

Lys Arg Val His Gln Thr Val Ser Lys Met Leu Lys Gln Val Glu
1535 1540 1545

Lys Tyr Thr Asn Pro His Gln Leu Gly Arg Gly Lys Glu His Gly
1550 1555 1560

Leu Asn Phe Pro Lys Ala Pro Thr Lys Gly Ser Ser Arg
1565 1570 1575

<210> 281

<211> 788

<212> PRT

<213> Streptococcus agalactiae

<400> 281

Met Asp Val Ser Ser Ser Pro Asn Ile Thr Phe Met Leu Gln Tyr Thr
1 5 10 15

Glu Ala Asn Pro Gln Tyr Val Asp Tyr Thr Asn Arg Glu Glu Ala Val
20 25 30

Lys Ile Asp Glu Glu Leu Ser Leu Glu Thr Asn Arg Gln Met Ile Glu
35 40 45

Gly Leu Thr Glu Asp Glu Leu Thr Arg Ile Gln Glu Ala Val Pro Glu
50 55 60

GBS patentin.ST25

Thr Gln Leu Asn Phe Arg Glu Tyr Ile Asp Tyr Met Asn Arg Ser Tyr
 65 70 75 80
 Ala Thr Glu Glu Gln Ser Lys Glu Leu Thr Ala Ile Phe Thr Gln Glu
 85 90 95
 Ala Asp Tyr Leu Gln Lys Leu Arg Leu Ile Asp Leu Lys Asn Lys Leu
 100 105 110
 Glu Ser Ala Tyr Gln Asn Gly Ser Leu Leu Trp Gln Gly Val Ile Ser
 115 120 125
 Phe Asp Asn Ala Phe Leu Ala Glu Gln Gly Leu Tyr Asp Val Ala Thr
 130 135 140
 Gly Gln Val Asp Gln Lys Ala Ile Lys Ala Val Met Arg Asp Met Met
 145 150 155 160
 Pro Thr Leu Ile Gln Lys Glu Gly Leu Ser Asp Ser Ala Phe Trp Trp
 165 170 175
 Gly Asn Ile His Leu Asn Thr Asp Asn Ile His Ile His Phe Gly Leu
 180 185 190
 Ser Glu Val Glu Ser Asn Arg Glu Lys Ile Phe Tyr Gln Pro Arg Gly
 195 200 205
 Arg Met Glu Tyr Lys Gly Asn Phe Ser Gln Lys Thr Ile Asn Arg Phe
 210 215 220
 Lys Ser Gly Val Tyr His Gly Leu Leu Lys Glu Glu Thr Arg Ser Asn
 225 230 235 240
 Leu Leu Arg Lys Glu Gln Ile Leu Ala Asn Leu Lys Ala Asp Phe Ile
 245 250 255
 Thr Ser Ile Tyr Gln Lys Asp Lys Ile Thr Ser Ser Ala Glu Lys Asn
 260 265 270
 Phe Leu Glu Gln Ala Tyr Asn His Leu Pro Leu Asn Lys Lys Trp Arg
 275 280 285
 Tyr Gly Ser Asn Ala Arg Asp Phe Ala Val Ser Lys Phe Phe Leu Asp
 290 295 300
 Arg Tyr Leu Asp Ser Tyr Leu Asn Asn Glu Gly Ser Ala Ala Tyr Gln
 305 310 315 320
 Glu Phe Leu Lys Glu Thr Arg Asp Phe Leu Gln Thr Tyr Glu Gly Val
 325 330 335

GBS patentin.ST25

Tyr Ser Ala Glu Lys Asn Lys Ile Tyr Glu Lys Leu Arg Lys Val Asp
340 345 350

Gly Gln Thr Ile Arg Thr Leu Ala Glu Ser Lys Gly Tyr Asp Leu Glu
355 360 365

His His Leu Ala Arg Arg Val Met Asp Leu Arg Glu Arg Leu Ala Asn
370 375 380

Asn Ile Leu Arg Ser Phe Arg Glu Ala Ala Pro Gln Ile Gln Asp Val
385 390 395 400

Gln Leu Glu Lys Asn Leu Glu Ser Phe Ser Val Leu Asn Gln Lys Lys
405 410 415

Ile Leu Glu Gln His Pro Glu Ala Ser Val Val Lys Ser Gln Lys Ala
420 425 430

Trp Gln Lys Leu Gly Tyr Phe Val Lys Ala Gly Glu Gln Pro Leu Glu
435 440 445

Ile Ile Arg Pro Val Tyr Lys Ser Tyr Asp Lys His Gly Lys Gly Ile
450 455 460

Gly Arg Pro Glu Phe Val Ser Asp Thr Val Tyr Asp Ile Ser Gln Leu
465 470 475 480

Thr Glu Asn Ile Gln Leu Lys Ser Leu Thr Leu Lys Asp Leu Ser Leu
485 490 495

Phe Ser Ser Asn Glu Leu Lys Glu Leu Val Asp Ala Ala Lys Leu Lys
500 505 510

Thr Asn Pro Thr Glu Arg Glu Arg Arg Glu Leu Gly Thr Tyr Arg Tyr
515 520 525

Ala Leu Lys Leu Ser Ile Leu Glu Ser Ser Gln Lys Glu Leu Gln Val
530 535 540

Arg Gln Lys Leu Leu Glu Gln Val Gln Pro Leu Ala Ser Asp Gln Pro
545 550 555 560

Phe Leu Asp Phe Lys Lys Gln Leu Ile Ala Gln Glu Leu Gln Ala Ile
565 570 575

Ala Leu Gln Leu Thr Pro Asn Tyr Lys Leu Ser Glu Asp Asp Lys Ala
580 585 590

Leu Lys Asn Arg Leu Lys Arg Gln Phe Glu Asp Ser Val Ala Leu Pro
595 600 605

GBS patentin.ST25

Val Ser Lys Ala Thr Pro Gly Ala Ile Gln Leu Pro Ile Arg Gln Leu
610 615 620

Trp Thr Glu Leu Gly Leu Val His His Ile Gln Asp Glu Asn Ile Leu
625 630 635 640

Thr Leu Leu Lys Gly Thr Ser Thr Thr Lys Gln Ala Tyr Ile Glu Glu
645 650 655

Leu Gln Thr His Ile Ser Ile Phe Gln Leu Lys Tyr Gln Ile Asn Asn
660 665 670

Arg Asn Lys Gln Ile Ser Gln Leu Ser Asp Glu Ala Thr Ile Lys Glu
675 680 685

Met Arg Ile Ala Asn Ala Lys Gly Phe Ser Glu Leu Lys Arg Leu Tyr
690 695 700

Asp Thr Leu Gln Pro Ser Asp Asp Gly Gln Asn Gln Ile Ser Gln Ala
705 710 715 720

Val Ser Lys Gln Leu Gln Glu Arg Lys Val Ile Lys Lys Ala Gln Leu
725 730 735

Gln Gln Thr Gln Arg Ser Gly Lys Ile Asn Thr Asp Phe Met Arg Gln
740 745 750

Leu Thr Ala Ser Leu Asn Arg Ser Gln Gln Ala Ser Lys Lys Ala Leu
755 760 765

Met Glu Arg Ala Arg Ser Asp Glu Arg Glu Glu Gln Glu Glu Arg Arg
770 775 780

Gln Ala Gln Arg
785

<210> 282

<211> 266

<212> PRT

<213> streptococcus agalactiae

<400> 282

Met Lys Lys Asn Lys Phe Leu Leu Val Ser Ile Val Phe Ile Ile Ile
1 5 10 15

Phe Val Val Gln Pro Gln Asn Phe Gln Ser Leu Lys Asn Ile Phe Thr
20 25 30

GBS patentin.ST25

Gln Asn Asp Ile Ala Ser Gln Leu Asn Ile Ser Ser Ser Pro Glu Glu
35 40 45

Lys Asn Asp Gly Leu Gly Thr Ala Tyr Gln Thr Gln Asn Glu Asp Leu
50 55 60

Lys Ser Lys Ser Phe Asp Gly Gln His Gln Val Ile Val Val Asn Glu
65 70 75 80

Lys Ala Gln Phe Thr Ala Glu Glu Leu Ser Met Arg Asn Gly Ser Trp
85 90 95

Glu Lys Tyr Asp Asn Leu Asp Phe Leu Asn Arg Val Gly Val Ala Glu
100 105 110

Ala Met Leu Gly Lys Glu Leu Met Pro Lys Glu Ala Arg Gln Asp Ile
115 120 125

Ser Ser Val Lys Pro Thr Gly Trp Lys Asn Lys Lys Ile Thr Phe Asn
130 135 140

Gly Lys Gln Asp Tyr Leu Tyr Asn Arg Ser His Leu Ile Gly Phe Gln
145 150 155 160

Leu Ser Gly Glu Asn Ala Asn Val Lys Asn Leu Phe Thr Gly Thr Arg
165 170 175

Ala Leu Asn Ala Asn Phe Asn Asp Asp Lys Ser Ser Met Val Tyr Tyr
180 185 190

Glu Asn Glu Val Ala Asn Tyr Ile Lys Lys Thr Asn His His Val Arg
195 200 205

Tyr Arg Val Thr Pro Leu Phe Lys Asn Val Glu Leu Val Ala Arg Gly
210 215 220

Val Arg Ile Glu Ala Gln Ser Ile Glu Asp Glu Thr Ile Ser Phe Asp
225 230 235 240

Val Tyr Ile Phe Asn Gly Gln Pro Gly Tyr Asp Ile Asp Tyr Leu Thr
245 250 255

Gly ser ser Glu Lys Ile Met Ile Thr Lys
260 265

<210> 283

<211> 115

<212> PRT

<213> Streptococcus agalactiae

<400> 283

Val Thr Lys Glu Ile Lys Ile Arg Ser Ile Pro Glu Lys Thr Trp Ala
 1 5 10 15
 Gln Leu His Met Ile Ser Glu Glu Tyr Glu Tyr Pro Ser Phe Asn Glu
 20 25 30
 Phe Met Leu Ala Gln Leu Gln Arg Ile Val Glu Asn Gly Gly Leu Asp
 35 40 45
 Leu Tyr Asp Asn Lys Phe Ala Glu Thr Leu Ala Val Ile Lys Glu Gln
 50 55 60
 Gln Ala Gln Ile Leu Asp Gln Leu Leu Lys Asn Glu Ile Lys Leu Leu
 65 70 75 80
 Ala Tyr His Ala Lys Gln Asp Ile Val Glu Glu Leu Thr Thr Asp Trp
 85 90 95
 Leu Arg Phe Met Asp Asp Val Asp Ala Leu Ala Ala Glu Arg Gly Ala
 100 105 110
 Gly Gly Arg
 115

<210> 284

<211> 280

<212> PRT

<213> Streptococcus agalactiae

<400> 284

Leu Leu Tyr Tyr Phe Ile Tyr Leu Ile Lys Val Ile Gly Asn Gly Leu
 1 5 10 15
 Lys Leu Ser Leu Ile Cys Gly Leu Asn Trp Leu Ile Lys Ile Val Phe
 20 25 30
 Lys Gly Gln Phe Tyr Leu Phe Ser Ala Val Phe Cys Gly Leu Leu Thr
 35 40 45
 Tyr Tyr Met Pro Gln Asp Ile Gln Leu Phe Thr Val Arg Val Leu Glu
 50 55 60
 Leu Ile Ile Met Leu Lys Val Ile Ile Asp Val Thr His Thr Ala Leu
 65 70 75 80

GBS patentin.ST25

Ser Arg Asp Phe Lys Arg Met Lys Thr Pro Leu Phe Leu Gly Val Met
85 90 95

Tyr Val Phe Phe Leu Ala Gly Asn Ser Tyr Ile Lys Ala His Leu Leu
100 105 110

Thr Glu Val Met Val Asn His Leu Ile Ser Phe Trp Leu Ile Ser Leu
115 120 125

Phe Phe Ala Thr Leu Val Ile Val Ile Gln Pro Arg Leu Phe Lys His
130 135 140

Tyr Leu Leu Lys Lys Val Ile Asp Lys Glu Tyr Leu Gly Ile Arg Lys
145 150 155 160

Phe Thr Asp Ser Leu Pro Pro Glu Ile Asn Leu Tyr Lys Asp Ala Asp
165 170 175

Glu Glu Asp Ala Asp Lys Arg Met Arg Leu Ile Asn Gln Asn Val Ile
180 185 190

Lys His Pro Tyr Gln Glu Val Val Glu Leu Ser Phe Leu Asn Arg Glu
195 200 205

Val Ile Thr Ala Ile Gly Tyr Lys Ala Val Pro Phe Glu Lys Glu Thr
210 215 220

Glu Arg Thr Phe Ile Asp Asp Asp Thr Ile Tyr Tyr Pro Ile Phe Thr
225 230 235 240

Val His Pro Phe Arg Asn Leu Glu Gly Lys Ser Asp Phe Tyr His Ile
245 250 255

Leu Met Lys Leu Lys Leu Ser Arg Lys Ala Ala Phe Thr Lys Asn Gly
260 265 270

Glu Arg Leu Leu Ile Arg Asp Phe
275 280

<210> 285

<211> 164

<212> PRT

<213> Streptococcus agalactiae

<400> 285

Met Ile Arg Asn Glu Phe Tyr Asn Gln Leu Ile Asn Ser Glu Pro Ile
1 5 10 15

GBS patentin.ST25

Gly Phe Ile Asp Pro Phe Thr Asp Leu Gly Glu Phe Asp Ser Ile Gln
20 25 30

Met Lys Phe Lys Gln Pro Val Arg Asn Leu Val Asn Lys Tyr Ser Gly
35 40 45

Lys Pro Tyr Asn Leu Ser Trp Gln Asn Lys Ile Glu Gln Met Arg Val
50 55 60

Leu Tyr Ile Lys Tyr Gln Lys Ser Leu Lys Leu Glu Asp Glu Glu Gln
65 70 75 80

Glu Val His Asn Arg Val Lys Asn Lys Lys Ser Lys Lys Tyr Val His
85 90 95

Glu Ile Val Thr Thr Tyr Leu Lys Leu Gly Phe Arg Phe Lys Glu Ile
100 105 110

Glu Ala Arg Val Ser Leu Phe Asn Thr Arg Leu Arg Arg Asn Trp Lys
115 120 125

Arg Ser Asp Tyr Val Thr Thr Asp Asn Pro Glu Phe Tyr Leu Lys Lys
130 135 140

Asp Leu Gln Asn Gly Tyr Cys Ser Pro Asn Ser Phe Leu Pro Arg Ser
145 150 155 160

Met Lys Ile Asn

<210> 286

<211> 423

<212> PRT

<213> Streptococcus agalactiae

<400> 286

Met Asn Glu Ile Lys Cys Pro His Cys Gly Thr Ala Phe Ala Ile Asn
1 5 10 15

Glu Ser Glu Tyr His Gln Leu Leu Glu Gln Ile Arg Gly Asp Ala Phe
20 25 30

Asp Lys Glu Val Ser Glu Arg Leu Glu Lys Glu Arg Leu Ile Leu Gly
35 40 45

Glu Gln Ala Lys Asn Gln Leu Gln Glu Val Val Val Glu Lys Asp Lys
50 55 60

GBS patentin.ST25

Glu Ile Ala Lys Leu Gln Tyr Lys Val Lys Gln Phe Leu Ile Glu Lys
65 70 75 80

Asp Asn Leu Leu Lys Asp Asn Glu Tyr Gln Leu Ala Glu Gln Leu Asn
85 90 95

Gln Lys Asp Met Met Leu Arg Asp Leu Glu Asn Gln Ile Asp Arg Leu
100 105 110

Arg Leu Glu His Glu Asn Ser Leu Gln Glu Ala Leu Thr Lys Val Glu
115 120 125

Arg Glu Arg Asp Ala Ile Gln Asn Gln Leu His Ile Gln Glu Lys Glu
130 135 140

Lys Asp Leu Ala Leu Ala Ser Val Lys Ser Asp Tyr Glu Val Gln Leu
145 150 155 160

Lys Ala Ala Asn Glu Gln Val Glu Phe Tyr Lys Asn Phe Lys Ala Gln
165 170 175

Gln Ser Thr Lys Ala Val Gly Glu Ser Leu Glu His Tyr Ala Glu Thr
180 185 190

Glu Phe Asn Lys Val Arg His Leu Ala Phe Pro Asn Ala Tyr Phe Glu
195 200 205

Lys Asp Asn Thr Leu Ser Ser Arg Gly Ser Lys Gly Asp Phe Ile Tyr
210 215 220

Arg Glu Lys Asp Glu Asn Asp Leu Glu Phe Leu Ser Ile Met Phe Glu
225 230 235 240

Met Lys Asn Glu Ser Asp Asp Thr Ile Lys Lys His Lys Asn Glu Asp
245 250 255

Phe Phe Lys Glu Leu Asp Lys Asp Arg Arg Glu Lys Ser Cys Glu Tyr
260 265 270

Ala Val Leu Val Thr Met Leu Glu Ala Asp Asn Asp Tyr Tyr Asn Thr
275 280 285

Gly Ile Val Asp Val Ser His Lys Tyr Pro Lys Met Tyr Val Ile Arg
290 295 300

Pro Gln Phe Phe Ile Gln Leu Ile Gly Ile Leu Arg Asn Ala Ala Leu
305 310 315 320

Asn Thr Leu Lys Tyr Lys Gln Glu Leu Ala Leu Met Lys Glu Gln Asn
325 330 335

GBS patentin.ST25

Ile Asp Ile Thr His Phe Glu Glu Asp Leu Asp Ile Phe Lys Asn Ala
340 345 350
Phe Ala Lys Asn Tyr Asn Ser Ala Ser Lys Asn Phe Gln Lys Ala Ile
355 360 365
Asp Glu Ile Asp Lys Ser Ile Lys Arg Met Glu Ala Val Lys Ala Ala
370 375 380
Leu Thr Thr Ser Glu Asn Gln Leu Arg Leu Ala Asn Asn Lys Leu Asp
385 390 395 400
Asp Val Ser Val Lys Lys Leu Thr Arg Lys Asn Pro Thr Met Lys Ala
405 410 415
Lys Phe Asp Ala Leu Lys Asp
420

<210> 287

<211> 280

<212> PRT

<213> Streptococcus agalactiae

<400> 287

Met Asn His Phe Glu Leu Phe Lys Leu Lys Lys Ala Gly Leu Thr Asn
1 5 10 15
Leu Asn Ile Asn Asn Ile Ile Asn Tyr Leu Lys Lys Asn Ser Leu Thr
20 25 30
Ser Leu Ser Val Arg Asn Met Ala Val Val Ser Lys Cys Lys Asn Pro
35 40 45
Thr Phe Phe Ile Glu Asn Tyr Lys Gln Leu Asp Leu Lys Lys Leu Arg
50 55 60
Gln Glu Phe Lys Lys Phe Pro Val Leu Ser Ile Leu Asp Ser Asn Tyr
65 70 75 80
Pro Leu Glu Leu Lys Glu Ile Tyr Asn Pro Pro Val Leu Leu Phe Tyr
85 90 95
Gln Gly Asn Ile Glu Leu Leu Ser Lys Pro Lys Leu Ala Val Val Gly
100 105 110
Ala Arg Gln Ala Ser Gln Ile Gly Cys Gln Ser Val Lys Lys Ile Ile
115 120 125

GBS patentin.ST25

Lys Glu Thr Asn Asn Gln Phe Val Ile Val Ser Gly Leu Ala Arg Gly
130 135 140

Ile Asp Thr Ala Ala His Val Ser Ala Leu Lys Asn Gly Gly Ser Ser
145 150 155 160

Ile Ala Val Ile Gly Ser Gly Leu Asp Val Tyr Tyr Pro Thr Glu Asn
165 170 175

Lys Lys Leu Gln Glu Tyr Met Ser Tyr Asn His Leu Val Leu Ser Glu
180 185 190

Tyr Phe Thr Gly Glu Gln Pro Leu Lys Phe His Phe Pro Glu Arg Asn
195 200 205

Arg Ile Ile Ala Gly Leu Cys Gln Gly Ile Val Val Ala Glu Ala Lys
210 215 220

Met Arg Ser Gly Ser Leu Ile Thr Cys Glu Arg Ala Leu Glu Glu Gly
225 230 235 240

Arg Glu Val Phe Ala Ile Pro Gly Asn Ile Ile Asp Gly Lys Ser Asp
245 250 255

Gly Cys His His Leu Ile Gln Glu Gly Ala Lys Cys Ile Ile Ser Gly
260 265 270

Lys Asp Ile Leu Ser Glu Tyr Gln
275 280

<210> 288

<211> 118

<212> PRT

<213> streptococcus agalactiae

<400> 288

Met Thr Glu Arg Thr Phe Glu Asp Ile Glu Leu Asp Leu Lys Leu Phe
1 5 10 15

Gln Ile Lys Leu Asp Asn Ala Glu Asn Ser Lys Arg Leu Leu Gln Lys
20 25 30

Leu Lys Asn Asp Val Met Glu Leu Gln Ile Glu Leu Leu Glu Ser Leu
35 40 45

Lys Leu Gly Asp Ala Tyr Leu Thr Glu Ser Glu Glu Leu Glu Glu Asn
50 55 60

GBS patentin.ST25

Asn Asp Phe Ile Leu Thr Val Asn Ser Glu Thr Leu Ser Leu Ser Tyr
65 70 75 80

Asp Asn Arg Ile Asn Leu Val Ser Lys Glu Ile Met Asp Tyr Glu Asn
85 90 95

Ala Leu Asp Lys Leu Tyr Tyr Glu Lys Gln Ser Leu Met Gln Lys Ser
100 105 110

Asn Glu Arg Lys Gly Gly
115

<210> 289

<211> 410

<212> PRT

<213> Streptococcus agalactiae

<400> 289

Leu Phe Asn Lys Ile Gly Phe Arg Thr Trp Lys Ser Gly Lys Leu Trp
1 5 10 15

Leu Tyr Met Gly Val Leu Gly Ser Thr Ile Ile Leu Gly Ser Ser Pro
20 25 30

Val Ser Ala Met Asp Ser Val Gly Asn Gln Ser Gln Gly Asn Val Leu
35 40 45

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
50 55 60

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
65 70 75 80

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
85 90 95

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
100 105 110

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
115 120 125

Glu Arg Arg Gln Arg Asp Ala Glu Asn Lys Ser Gln Gly Asn Val Leu
130 135 140

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
145 150 155 160

GBS patentin.ST25

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
165 170 175

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
180 185 190

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
195 200 205

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
210 215 220

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
225 230 235 240

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
245 250 255

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
260 265 270

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
275 280 285

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
290 295 300

Glu Arg Arg Gln Arg Asp Ala Glu Asn Lys Ser Gln Val Gly Gln Leu
305 310 315 320

Ile Gly Lys Asn Pro Leu Leu Ser Lys Ser Ile Ile Ser Arg Glu Asn
325 330 335

Asn His Ser Ser Gln Gly Asp Ser Asn Lys Gln Ser Phe Ser Lys Lys
340 345 350

Val Ser Gln Val Thr Asn Val Ala Asn Arg Pro Met Leu Thr Asn Asn
355 360 365

Ser Arg Thr Ile Ser Val Ile Asn Lys Leu Pro Lys Thr Gly Asp Asp
370 375 380

Gln Asn Val Ile Phe Lys Leu Val Gly Phe Gly Leu Ile Leu Leu Thr
385 390 395 400

Ser Arg Cys Gly Leu Arg Arg Asn Glu Asn
405 410

<210> 290

GBS patentin.ST25

<211> 573

<212> PRT

<213> Streptococcus agalactiae

<400> 290

Met Lys Arg Leu Thr Tyr Tyr Phe Lys Gly Tyr Ile Lys Glu Thr Ile
1 5 10 15

Phe Gly Pro Leu Phe Lys Leu Leu Glu Ala Ser Phe Glu Leu Leu Val
20 25 30

Pro Ile Val Ile Ala Lys Met Ile Asp Glu Thr Ile Pro Arg Gly Asp
35 40 45

Arg Ser Ser Leu Leu Leu Gln Ile Gly Leu Ile Phe Phe Leu Ala Ala
50 55 60

Val Gly Val Val Val Ala Ile Thr Ala Gln Tyr Tyr Ser Ser Lys Ala
65 70 75 80

Ala Val Gly Tyr Thr Arg Gln Leu Thr Glu Asp Leu Tyr Gln Lys Val
85 90 95

Met Ser Leu Gly Lys Lys Asp Arg Asp Glu Leu Gly Thr Ala Ser Leu
100 105 110

Ile Thr Arg Leu Thr Ala Asp Thr Phe Gln Ile Gln Thr Gly Leu Asn
115 120 125

Gln Phe Leu Arg Leu Phe Leu Arg Ala Pro Ile Ile Val Phe Gly Ala
130 135 140

Ile Ile Met Ala Phe Ser Ile Ser Pro Ser Leu Thr Ile Trp Phe Leu
145 150 155 160

Val Met Val Val Thr Leu Phe Ile Ile Val Phe Val Met Ser Arg Leu
165 170 175

Leu Asn Pro Ile Tyr Leu Lys Ile Arg Thr Ser Thr Asp Tyr Leu Val
180 185 190

Lys Leu Thr Arg Gln Gln Leu Gln Gly Val Arg Val Ile Arg Ala Phe
195 200 205

Asn Gln Val Asp Arg Glu Ser Glu Ala Phe Asn Asp Ile Asn Tyr His
210 215 220

Tyr Thr Asn Leu Gln Leu Lys Ala Gly Arg Leu Ser Ser Leu Val Thr
225 230 235 240

GBS patentin.ST25

Pro Leu Thr Phe Leu Val Val Asn Ile Thr Leu Val Val Ile Ile Trp
245 250 255

Arg Gly Asn Leu Asn Ile Ala Asn His Leu Leu Ser Gln Gly Met Leu
260 265 270

Val Ala Leu Ile Asn Tyr Leu Leu Gln Ile Leu Val Glu Leu Leu Lys
275 280 285

Met Thr Met Leu Val Thr Ser Leu Asn Gln Ser Tyr Ile Ser Ala Lys
290 295 300

Arg Ile Ile Ala Val Phe Glu Arg Pro Ser Glu Ile Ile Asp Asp Lys
305 310 315 320

Leu Glu Pro Lys Tyr Ser Asn Lys Ala Leu Glu Val Gln Glu Met Ala
325 330 335

Phe Ser Tyr Pro Asn Ser Ser Glu Lys Ala Leu Ser Asp Ile Thr Phe
340 345 350

Ser Met Asn Val Gly Glu Thr Leu Gly Ile Ile Gly Gly Thr Gly Ser
355 360 365

Gly Lys Ser Thr Leu Val Asn Leu Leu Leu His Ile Tyr Lys Val Gln
370 375 380

Glu Gly Asp Ile Asp Ile Tyr His Gln Gly Lys Ser Pro Asp Thr Ile
385 390 395 400

Ser Asn Trp Arg Thr Leu Val Arg Val Val Pro Gln Asn Ala Gln Leu
405 410 415

Phe Lys Gly Thr Ile Arg Ser Asn Leu Ser Leu Gly Leu Gly Lys Val
420 425 430

Ser Glu Glu Lys Leu Trp Thr Ala Leu Glu Ile Ala Gln Ala Ser Asp
435 440 445

Phe Val Lys Glu Lys Asp Gly Gln Leu Asp Ala Pro Val Glu Ser Phe
450 455 460

Gly Arg Asn Phe Ser Gly Gly Gln Arg Gln Arg Leu Thr Ile Ala Arg
465 470 475 480

Ala Leu Val Gln Asp Lys Ile Pro Phe Leu Ile Leu Asp Asp Ala Thr
485 490 495

Ser Ala Leu Asp Tyr Leu Thr Glu Ala Arg Leu Phe Lys Ala Ile Thr
500 505 510

GBS patentin.ST25

Lys His Phe Asn Gln Thr Asn Leu Ile Ile Val Ser Gln Arg Ile Asn
515 520 525

Ser Ile Gln Asn Ala Asp Arg Ile Leu Leu Leu Asp Lys Gly Lys Gln
530 535 540

Val Gly Phe Asp Asn His Gln Ser Leu Leu Ala His Asn Lys Val Tyr
545 550 555 560

Lys Ser Ile Tyr His Ser Gln Asn Phe Lys Glu Glu Glu
565 570

<210> 291

<211> 424

<212> PRT

<213> streptococcus agalactiae

<400> 291

Met Lys Phe Asn Glu Gln Ser Asn Ser Gln Ala Ala Leu Leu Gly Leu
1 5 10 15

Gln His Leu Leu Ala Met Tyr Ala Gly Ser Ile Leu Val Pro Ile Met
20 25 30

Ile Ala Ser Ala Leu Gly Tyr Asn Ala Glu Gln Leu Thr Tyr Leu Ile
35 40 45

Ala Thr Asp Ile Phe Met Cys Gly Ile Ala Thr Leu Leu Gln Leu Gln
50 55 60

Leu Ser Lys His Phe Gly Val Gly Leu Pro Val Val Leu Gly Cys Ala
65 70 75 80

Phe Gln Ser Val Ala Pro Leu Ser Ile Ile Gly Ala Gln Gln Gly Ser
85 90 95

Gly Tyr Met Phe Gly Ala Leu Ile Ala Ser Gly Ile Tyr Val Val Leu
100 105 110

Val Ala Gly Ile Phe Ser Lys Val Ala Asn Phe Phe Pro Pro Ile Val
115 120 125

Thr Gly Ser Val Ile Thr Thr Ile Gly Leu Thr Leu Ile Pro Val Ala
130 135 140

Met Gly Asn Met Gly Asp Asn Ala Lys Glu Pro Ser Leu Gln Ser Leu
145 150 155 160

GBS patentin.ST25

Thr Leu Ser Leu Val Thr Ile Gly Val Val Leu Leu Ile Asn Ile Phe
165 170 175

Ala Lys Gly Phe Leu Lys Ser Ile Ser Ile Leu Ile Gly Leu Ile Ser
180 185 190

Gly Thr Ile Leu Ala Ala Phe Met Gly Leu Val Asp Ala Ser Val Val
195 200 205

Ala Glu Ala Pro Leu Val His Ile Pro Lys Pro Phe Tyr Phe Gly Ala
210 215 220

Pro Arg Phe Glu Phe Thr Ser Ile Leu Met Met Cys Ile Ile Ala Thr
225 230 235 240

Val Ser Met Val Glu Ser Thr Gly Val Tyr Leu Ala Leu Ser Asp Ile
245 250 255

Thr Asn Asp Lys Leu Asp Ser Lys Arg Leu Arg Asn Gly Tyr Arg Ser
260 265 270

Glu Gly Leu Ala Val Leu Leu Gly Gly Leu Phe Asn Thr Phe Pro Tyr
275 280 285

Thr Gly Phe Ser Gln Asn Val Gly Leu Val Gln Ile Ser Gly Ile Arg
290 295 300

Thr Arg Lys Pro Ile Tyr Phe Thr Ala Leu Phe Leu Val Ile Leu Gly
305 310 315 320

Leu Leu Pro Lys Phe Gly Ala Met Ala Gln Met Ile Pro Ser Pro Val
325 330 335

Leu Gly Gly Ala Met Leu Val Leu Phe Gly Met Val Ala Leu Gln Gly
340 345 350

Met Lys Met Leu Asn Gln Val Asp Phe Glu His Asn Glu His Asn Phe
355 360 365

Ile Ile Ala Ala Val Ser Ile Ala Ala Gly Val Gly Phe Asn Gly Thr
370 375 380

Asn Leu Phe Ile Ser Leu Pro Asn Thr Leu Gln Met Phe Leu Thr Asn
385 390 395 400

Gly Ile Val Ile Ser Thr Leu Thr Ala Val Val Leu Asn Ile Ile Leu
405 410 415

Asn Gly Leu Pro Lys Lys Leu Ile
420

GBS patentin.ST25

<210> 292

<211> 1078

<212> PRT

<213> Streptococcus agalactiae

<400> 292

Met Ala Asn Thr Tyr Asp Leu Ile Ser Gln Arg Ile Glu Ala Gln Arg
1 5 10 15

Gln Lys Leu Ile Ala Ile Asp Ile Val Ala Val Ala Ser Ser Leu Gly
20 25 30

Leu Asn Leu Lys Gln Gly Ser Gly Gly His Leu Tyr Trp Asp Glu His
35 40 45

Asp Ser Phe His Ile Tyr Pro Gln Thr Asn Thr Phe Arg Trp Trp Ser
50 55 60

Arg Ser Met Gly Thr Asn Thr Ile Asp Leu Val Gln Val Ile Gln Glu
65 70 75 80

Glu Leu Thr Gly Lys Lys Pro Ser Phe Arg Glu Thr Val Asn Phe Leu
85 90 95

Glu Thr Gly Gln Phe Glu Ser Val Thr Val Thr Pro Val Val Arg Glu
100 105 110

Pro Phe Lys His Tyr Leu Ala Pro Tyr Glu His His Asn Phe Asp Leu
115 120 125

Gly Arg Gln Tyr Leu Lys Glu Glu Arg Gly Leu Ser Asp Glu Thr Ile
130 135 140

Asp Phe Ala Leu Ala Ser Gly Ser Met Ser Ser Ala Thr Leu Lys Lys
145 150 155 160

Gly Asp Tyr Phe Glu Pro Val Ile Ile Phe Lys Ser Phe Ala Glu Asp
165 170 175

Gly Arg Met Ile Gly Gly Ser Leu Gln Gly Ile Val Glu Asn Lys Val
180 185 190

Gln His Pro Glu Arg Gly Arg Leu Lys Gln Ile Met Lys His Ser Asp
195 200 205

Gly Leu Ala Gly Phe His Leu Asp Val Gly Thr Pro Lys Arg Leu Val
210 215 220

GBS patentin.ST25

Phe Ser Glu Ala Pro Ile Asp Leu Leu Ser Tyr Tyr Glu Leu His Lys
225 230 235 240

Glu Ser Leu Gln Asn Val Arg Leu Val Ala Met Asp Gly Val Lys Lys
245 250 255

Gly Val Ile Ser Arg Tyr Thr Ala Asp Leu Leu Thr Asp Gly Gln Tyr
260 265 270

Ser Gln Thr Met Pro Arg Glu Ser Ile Arg Gly Ala Ile Asp Ala Ile
275 280 285

Asn Gln Thr Thr Arg Ile Leu Lys Asn Asn Pro Asn Met Ile Thr Ile
290 295 300

Ala Val Asp Asn Asp Glu Ala Gly Arg Asn Phe Ile Lys Glu Leu Gln
305 310 315 320

Glu Asp Gly Ile Pro Ile Asn Val Asp Leu Pro Pro Arg Lys Glu His
325 330 335

Gln Ser Lys Met Asp Trp Asn Asn Tyr Leu Lys Gln Lys Lys Gly Leu
340 345 350

Leu Lys Met Pro Gln Thr Glu Gly Thr Gln Lys Ala Pro Glu Gln Val
355 360 365

Leu Glu His Glu Lys Met Asp Arg Ser Gln Ile Ser Ser Gly Ser Leu
370 375 380

Glu Asp Asp Pro Gln Gly Ser Ala Lys Pro Val Ser Lys Arg Asp Thr
385 390 395 400

Phe Glu Gln Ala Val Thr Ser His Pro Thr Phe Ser Tyr Pro Leu Leu
405 410 415

Gln Phe Ser Thr Glu Glu Ala Phe Val Ser Asn Val Arg Asp Gly Tyr
420 425 430

His Ile Ala Ser Glu Glu Asp Ile Arg Asn Leu Asn Tyr Tyr Ala Pro
435 440 445

Ser Leu Gln Gln Thr Ala Asn Trp Tyr Arg Asp Asn Leu Ala Asp Arg
450 455 460

Gln Val Thr Tyr Met Leu Lys Gly Asp Lys Glu Ile Lys Ala Leu Gln
465 470 475 480

Val Ser Phe Ala Lys Asp Lys Phe Ala His Leu Thr Gly Ile Arg Pro
485 490 495

GBS patentin.ST25

Ile Gly Lys Gly Leu Ser Ala Glu Lys Leu Leu Asp Asp Phe Ala Lys
500 505 510

Gly Arg Gly Ser Tyr Pro Asn Leu Thr Leu Ser Asn Gly Phe Asn Asp
515 520 525

Lys Ile Gln Val Leu Pro Met Ile Gln Glu Leu Ser Gln Ser Lys Ser
530 535 540

Phe Val Phe Thr Asp Leu Glu Glu Val Gln Lys Met Arg Asn Leu Lys
545 550 555 560

Ala Ser His Ala Ile Gln Ser Asn Asn Arg Ser Leu Val Val Ala Leu
565 570 575

Lys Thr Ile Asp Asp Val Thr Phe Pro Ser Ser Leu Leu Arg Gly Lys
580 585 590

Lys Asn Leu Asn Asp Asp Leu Ile Gln Lys Ala Lys Glu Asn Glu Val
595 600 605

Leu Gly Val Leu Ser Glu Lys Asp Gly Asn Ile Thr Val Leu Ser Val
610 615 620

Asn Asp Lys Tyr Ile Gln Asp Gly Gly Gln Ala Leu Lys Asp Met Ile
625 630 635 640

Lys Asn Gly Glu Leu Glu Pro Leu Gln Met Glu Thr Ile Gln Arg His
645 650 655

Val Pro His Glu Asn Ala Tyr Pro Lys Asp Ser Asp Gly Asp Gly Leu
660 665 670

Thr Asp Asp Glu Glu Ile Ala Leu Gly Thr Asn Pro Phe Ser Ser Asp
675 680 685

Ser Asp Gly Asp Gly Thr Pro Asp Asn Val Glu Lys Ala Asn Gly Thr
690 695 700

Asp Pro Thr Asn Ala Ser Asp Asn Glu Val Thr Arg Gln Gln Glu Ala
705 710 715 720

Asn Lys Arg Asp Phe Thr Leu Ser Glu Met Ile Lys Ala Lys Asn Thr
725 730 735

Ala Ala Leu Asn Gln His Leu Gln Asp Gly Ile Lys Gln Tyr Phe Asp
740 745 750

Ser Asp Thr Tyr Lys Gln Tyr Leu Glu Gly Met Ala His Phe Asn Asn
755 760 765

GBS patentin.ST25

Tyr Ser Pro Arg Asn Ile Gln Leu Ile Met Ser Gln Phe Pro Glu Ala
770 775 780

Ser Met Val Ala Ser Phe Gln Glu Trp Arg Lys Arg Asn Gly Ser Val
785 790 795 800

Lys Lys Gly Glu Lys Ala Ile Tyr Ile Gln Ala Pro Val Ser Val Met
805 810 815

Lys Lys Asp Glu Asn Gly Lys Pro Ile Leu Asn Pro Glu Thr Gly Glu
820 825 830

Lys Glu Thr Ile Thr Tyr Phe Lys Pro Val Pro Val Phe Asp Ile Lys
835 840 845

Gln Val Ser Pro Gln Glu Gly Lys Glu Leu Asn Leu Pro Lys Ala Met
850 855 860

Gly Thr Ile Pro Glu Gln Leu Asp Lys Glu Tyr Tyr Gln Asn Val Tyr
865 870 875 880

Arg Ser Leu Arg Asp Ile Ser Gln Asn Asn Asn Lys Val Pro Ile Arg
885 890 895

Phe Arg Glu Leu Gly Gln Glu Asp Gly Phe Tyr Ser Pro Gln Thr Asn
900 905 910

Glu Ile Val Ile Lys Lys Gly Met Ser Tyr Glu Arg Thr Leu Ser Thr
915 920 925

Leu Ile His Glu Met Ala His Ser Glu Leu His Asn Lys Gln Ser Leu
930 935 940

Thr Glu Arg Phe Asp Gly Lys Leu Thr Arg Ser Thr Lys Glu Leu Gln
945 950 955 960

Ala Glu Ser Ile Ala Tyr Val Val Ser Ser His Leu Gly Phe Asp Thr
965 970 975

Ser Gln Glu Ser Phe Pro Tyr Leu Ala Ser Trp Ser Lys Glu Lys Asp
980 985 990

Gly Leu Ala Asn Leu Thr Ala Gln Leu Glu Ile Val Gln Glu Glu Ala
995 1000 1005

Lys Asn Leu Met Glu Arg Ile Asp Gln Gln Leu Ser Gln Tyr Gln
1010 1015 1020

Thr Val Thr Leu Asn Lys Glu Thr Gln Gln Leu Thr Lys Gln Glu
1025 1030 1035

GBS patentin.ST25

Met Lys Lys Gln Thr His Pro Phe Tyr Gln Ser Leu Ala Ala Ala
1040 1045 1050

Lys Thr Ser Arg Ala Gln Val Thr Thr Gln Glu Lys Glu Ala Ser
1055 1060 1065

Val Lys Lys Asp Asn Arg Pro Thr Met Pro
1070 1075

<210> 293

<211> 932

<212> PRT

<213> streptococcus agalactiae

<400> 293

Met Asn Ser Gln Glu Thr Lys Gly His Gly Phe Phe Arg Lys Ser Lys
1 5 10 15

Ala Tyr Gly Leu Val Cys Gly Ile Ala Leu Ala Gly Ala Phe Thr Leu
20 25 30

Ala Thr Ser Gln Val Ser Ala Asp Gln Val Thr Thr Gln Ala Thr Thr
35 40 45

Gln Thr Val Thr Gln Asn Gln Ala Glu Thr Val Thr Ser Thr Gln Leu
50 55 60

Asp Lys Ala Val Asp Thr Ala Lys Lys Ala Ala Val Ala Val Thr Thr
65 70 75 80

Thr Thr Ala Val Asn His Ala Thr Thr Thr Asp Ala Gln Ala Asp Leu
85 90 95

Ala Asn Gln Thr Gln Ala Val Lys Asp Val Thr Ala Lys Ala Gln Ala
100 105 110

Asn Thr Gln Ala Ile Lys Asp Ala Thr Ala Glu Asn Ala Lys Ile Asp
115 120 125

Ala Glu Asn Lys Ala Glu Ala Glu Arg Val Ala Lys Ala Asn Lys Ala
130 135 140

Gly Gln Ala Glu Val Asp Ala Arg Asn Lys Ala Gly Gln Ala Ala Val
145 150 155 160

Asp Ala Arg Asn Lys Ala Lys Gln Gln Ala Gln Asp Asp Gln Lys Ala
165 170 175

GBS patentin.ST25

Lys Ile Asp Ala Glu Asn Lys Ala Glu Ser Gln Arg Val Ser Gln Leu
180 185 190

Asn Ala Gln Asn Lys Ala Lys Ile Asp Ala Glu Asn Lys Asp Ala Gln
195 200 205

Ala Lys Ala Asp Ala Thr Asn Ala Gln Leu Gln Lys Asp Tyr Gln Thr
210 215 220

Lys Leu Ala Asn Ile Lys Ser Val Glu Ala Tyr Asn Ala Gly Val Arg
225 230 235 240

Gln Arg Asn Lys Asp Ala Gln Ala Lys Ala Asp Ala Thr Asn Ala Gln
245 250 255

 Leu Gln Lys Asp Tyr Gln Ala Lys Leu Ala Leu Tyr Asn Gln Ala Leu
260 265 270


Lys Ala Lys Ala Glu Ala Asp Lys Gln Ser Ile Asn Asn Val Ala Phe
275 280 285

Asp Ile Lys Ala Gln Ala Lys Gly Val Asp Asn Ala Glu Tyr Gly Asn
290 295 300

Ser Ile Met Thr Ala Lys Thr Lys Pro Asp Gly Ser Phe Glu Phe Asn
305 310 315 320

His Asp Met Ile Asp Gly Val Lys Thr Ile Gly Tyr Gly Lys Leu Thr
325 330 335

Gly Lys Val Asn His His Tyr Val Ala Asn Lys Asp Gly Ser Val Thr
340 345 350

 Ala Phe Val Asp Ser Val Thr Leu Tyr Lys Tyr Glu Tyr Arg Asn Val
355 360 365

Ala Gln Asn Ala Ala Val Asn Gln Asn Ile Val Phe Arg Val Leu Thr
370 375 380

Lys Asp Gly Arg Pro Ile Phe Glu Lys Ala His Asn Gly Asn Lys Thr
385 390 395 400

Phe Ala Glu Thr Leu Asn Lys Thr Leu Gln Leu Asn Leu Lys Tyr Glu
405 410 415

Leu Lys Pro His Ala Ser Ser Gly Asn Val Glu Val Phe Lys Ile His
420 425 430

Asp Asp Trp Val His Asp Thr His Gly Ser Ala Leu Val Ser Tyr Val
435 440 445

GBS patentin.ST25

Asn 450 Asn Asp Ala Val Pro 455 Asn Val Val Ile Pro 460 Glu Gln Pro Thr
 Pro 465 Pro Lys Pro Glu 470 Lys Val Thr Pro Glu Ala 475 Glu Lys Pro Val Pro 480
 Glu Lys Pro Val 485 Glu Pro Lys Leu Val Thr 490 Pro Val Leu Lys Thr Tyr 495
 Thr Pro Val 500 Lys Phe Ile Pro Arg Glu 505 Tyr Lys Pro Val Pro 510 Ser Thr
 Pro Glu Thr 515 Phe Thr Pro Glu 520 Lys Phe Thr Pro Ala Gln 525 Pro Lys Val
 Lys 530 Pro His Val Ser Val Pro 535 Glu Lys Ile Asn Tyr 540 Lys Val Ala Val
 His 545 Pro Val Gln Ile Pro 550 Lys Ala Thr Pro Thr 555 Lys Lys Val Leu Asp 560
 Glu Asn Gly Gln Ser 565 Ile Asn Gly Lys Ser 570 Val Leu Pro Asn Ala Thr 575
 Leu Asp Tyr Val 580 Ala Lys Gln Asn Phe 585 Ser Gln Tyr Lys Gly 590 Ile Lys
 Ala Ser Ala 595 Glu Ala Ile Ala Lys 600 Gly Phe Ala Phe Val 605 Asp Gln Pro
 Asn 610 Glu Ala Leu Ala Glu 615 Leu Thr Val Lys Ser Ile 620 Lys Ala Ser Asn
 Gly 625 Asp Asp Val Ser 630 Ser Leu Leu Glu Met Arg 635 His Val Leu Ser Lys 640
 Asp Thr Leu Asp 645 Gln Lys Leu Gln Ser Leu 650 Ile Lys Glu Ala Gly Ile 655
 Ser Pro Val 660 Gly Glu Phe Tyr Met Trp 665 Thr Ala Lys Asp Pro 670 Gln Ala
 Phe Tyr 675 Lys Ala Tyr Val Gln Lys 680 Gly Leu Asp Ile Thr Tyr Asn Leu 685
 Ser 690 Phe Lys Val Lys Lys Glu 695 Phe Thr Lys Gly Gln 700 Ile Lys Asn Gly
 Val 705 Ala Gln Ile Asp Phe 710 Gly Asn Gly Tyr Thr 715 Gly Asn Ile Val Val 720

GBS patentin.ST25

Asn Asp Leu Thr Thr Pro Glu Val His Lys Asp Val Leu Asp Lys Glu
725 730 735

Asp Gly Lys Ser Ile Asn Asn Gly Thr Val Lys Leu Gly Asp Glu Val
740 745 750

Thr Tyr Lys Leu Glu Gly Trp Val Val Pro Ala Asn Arg Gly Tyr Asp
755 760 765

Leu Phe Glu Tyr Lys Phe Val Asp His Leu Gln His Thr His Asp Leu
770 775 780

Tyr Leu Lys Asp Lys Val Val Ala Lys Val Ala Ile Thr Leu Lys Asp
785 790 795 800

Gly Thr Val Ile Pro Lys Gly Thr Asn Leu Val Gln Tyr Thr Glu Thr
805 810 815

Val Tyr Asn Lys Glu Thr Gly Arg Tyr Glu Leu Ala Phe Lys Ala Asp
820 825 830

Phe Leu Ala Gln Val Ser Arg Ser Ser Ala Phe Gly Ala Asp Asp Phe
835 840 845

Ile Val Val Lys Arg Ile Lys Ala Gly Asp Val Tyr Asn Thr Ala Asp
850 855 860

Phe Phe Val Asn Gly Asn Lys Val Lys Thr Glu Thr Val Val Thr His
865 870 875 880

Thr Pro Glu Lys Pro Lys Pro Val Met Pro Gln Lys Val Thr Pro Lys
885 890 895

Ala Pro Ala Leu Pro Ser Thr Gly Glu Gln Gly Val Ser Val Leu Thr
900 905 910

Val Leu Gly Ala Ala Leu Leu Ser Leu Leu Gly Leu Val Gly Phe Lys
915 920 925

Lys Arg Gln Gln
930

<210> 294

<211> 743

<212> PRT

<213> streptococcus agalactiae

GBS patentin.ST25

<400> 294

Met Asn Gln Ile Lys Ile Ile Thr Gly Leu Thr Val Ala Thr Leu Ser
 1 5 10 15
 Ala Val Val Gly Asn Val Tyr Ala Glu Asp Ile Thr Pro Thr Ala Pro
 20 25 30
 Val Asn Glu Pro Gln Val Ser Ser Glu Thr Ala Lys Thr Pro Gln Val
 35 40 45
 Thr Glu Ser Gln Val Asn Ser Ala Lys Val Thr Ala Asp Gln Ala Thr
 50 55 60
 Ser Asp Val Asn Ala Gln Lys Asn Val Val Asn Asn Ala Gln Asn Gln
 65 70 75 80
 Lys Asn Gln Ala Gln Gln Lys Leu Val Asn Ala Thr Thr Thr Leu Asn
 85 90 95
 Glu Thr Gln Lys Leu Val Gln Glu Ser Thr Asn Gln Asn Gln Val Gln
 100 105 110
 Gln Thr Val Asp Ser Ala Lys Gln Arg Leu Ser Gln Thr Glu Ala Asn
 115 120 125
 Gln Lys Ile Thr Gln Thr Glu Gln Val Lys Ala Gln Asn Gln Val Asn
 130 135 140
 Ala Gln Gln Thr Val Val Val Asn Asn Glu His Asp Val Ala Thr Lys
 145 150 155 160
 Thr Ala Asp Val Lys Gln Ala Gln Ala Ser Val Asp Thr Ala Lys Asp
 165 170 175
 Ala Leu Thr Asn Thr Ile Val Asn Ser Asp Leu Asn Lys Ala Gln Ser
 180 185 190
 Asn Val Thr Thr Lys Thr Ala Asp Val Lys Thr Ala Thr Asp Ala Leu
 195 200 205
 Thr Lys Ala Gln Ala Thr Asp Lys Thr Leu Thr Asn Gln Lys Ala Lys
 210 215 220
 Ala Gln Gln Ile Val Asp Ser Ala Lys Gln Asn Leu Ser Ala Lys Asp
 225 230 235 240
 Thr Gln Leu Ser Gln Ala Asn Ala Glu Val Asn His His Lys Phe Lys
 245 250 255
 Thr Ala Leu Gly Gln Ser His Tyr Tyr Asn Gln Arg Asp Asn Ala Trp
 260 265 270

GBS patentin.ST25

Ala Gly Val Tyr Gly Gly His Thr Phe Ala Ser Thr Gly Cys Val Pro
275 280 285

Ser Ala Leu Ala Met Val Tyr Ser Asp Leu Ser Asn Arg Thr Ile Thr
290 295 300

Pro Arg Glu Ile Ala Asp Tyr Leu Tyr Asn Asn Thr Asp Glu Phe Asn
305 310 315 320

Lys Arg Phe Gly Gly Thr Ser Gly Lys Gly Ile Ile Ser Ala Thr Lys
325 330 335

Ala Phe Gly Tyr Val Val Thr His Leu Ala Ser Lys Asn Ala Ile Thr
340 345 350

 Glu Ala Leu Lys Ala Gly His His Val Val Ala Ala Val Gln Asn Asn
355 360 365

Lys Phe Ser Pro Trp Gly Pro Gln Tyr Ser His Glu Ile Val Leu Arg
370 375 380

Gly Ser Ser Asn Gly Asn Thr Tyr Val Tyr Asp Pro Tyr Asn Arg Asp
385 390 395 400

Asn Asn Gly Phe Tyr Ser Val Asp Arg Ile Trp Asn Glu Gln Ser Arg
405 410 415

Asp Ser Ile Asp Thr Ala Gly Val Gly Val Pro Phe Phe Ala Ile Met
420 425 430

Thr Lys Asn Met Ala Asn Ala Leu Thr Lys Gln Ser Gln Ala Leu Ala
435 440 445

 Ser Gln Gln Val Ala Gln Lys Gln Leu Asn Asp Ala Gln Ala Lys Ala
450 455 460

Thr Gly Leu Asn Ala Val Thr Met Gln Thr Pro Ile Ala Gln Ala Asn
465 470 475 480

Leu Ile Lys Ala Gln Ser Asn Leu Lys Asp Ala Gln Lys Arg Leu Ala
485 490 495

Glu Ala Gln Ala Ser Val Lys Leu Ala Asn Gln Asp Asn Val Lys Lys
500 505 510

Gln Ala Asp Leu Thr Lys Ala Glu Ser Lys Leu Lys Asp Ala Gln Lys
515 520 525

Gln Leu Ala Ala Ala Gln Ala Lys Leu Thr Thr Ser Lys Thr Lys Leu
530 535 540

GBS patentin.ST25

Asn Gln Leu Lys Gln Val Leu Ala Glu Ala Ser Gln Gln Val Ala Gln
545 550 555 560

Ala Asn Gln Asp Tyr Lys Gln Ala Lys Asp Asn Leu Thr Gln Lys Thr
565 570 575

Ala Tyr Leu Thr Asn Leu Arg Asn Ala Gln Ala Asn Leu Ile Lys Ala
580 585 590

Gln Ser Asp Val Ala Gln Ala Lys Asp Asn Leu Ala Asn Lys Ile Ala
595 600 605

Lys Leu Gln Arg Glu Val Ala Tyr Leu Gln Glu Leu Lys Thr Lys Ala
610 615 620

Val Asp Ala Gln Ser Gln Tyr Gln Lys Val Leu Ser Ala Tyr Lys Ser
625 630 635 640

Val Leu Ser Ala Lys Ala Ser Leu Lys Leu Ala Glu Glu Lys Ala Arg
645 650 655

Leu Asp Lys Lys Gly His Glu Ala Val Ala Val Val Asp Glu Thr Gly
660 665 670

Lys Ile Thr Ser Tyr Ile Thr Ser Lys His Lys Ile Glu Met Lys Ser
675 680 685

Leu Val Ala Thr Lys Thr Thr Asp Val Lys Gln Val Ser Val Ala Lys
690 695 700

Ala Ser Val Leu Pro Ser Thr Gly Asp Val Lys Gln Val Ser Val Ala
705 710 715 720

Leu Leu Gly Met Leu Leu Thr Phe Ser Gly Phe Leu Gly Ile Arg Lys
725 730 735

Gln Ser Lys Lys Val Ile Asn
740

<210> 295

<211> 253

<212> PRT

<213> Streptococcus agalactiae

<400> 295

Met Ile Ser Arg Lys Val Ala Leu Val Thr Gly Ala Ser Ala Gly Phe
1 5 10 15

GBS patentin.ST25

Gly Ala Ala Ile Val Thr Lys Leu Val Ser Asp Gly Tyr Ser Val Ile
20 25 30

Gly Cys Ala Arg Arg Met Asp Lys Leu Lys Cys Phe Gly Glu Lys Phe
35 40 45

Ser Glu Gly Tyr Phe Tyr Pro Leu Gln Met Asp Ile Thr Ser Arg Glu
50 55 60

Ser Val Asp Lys Ala Leu Glu Ser Leu Pro Lys Asn Leu Gln Ser Ile
65 70 75 80

Asp Leu Leu Val Asn Asn Ala Gly Leu Ala Leu Gly Leu Asp Lys Ser
85 90 95

Tyr Glu Ala Asp Phe Glu Asp Trp Met Thr Met Ile Asn Thr Asn Val
100 105 110

Val Gly Leu Ile Tyr Leu Thr Arg Cys Ile Leu Pro Lys Met Val Glu
115 120 125

Val Asn Arg Gly Leu Ile Ile Asn Leu Gly Ser Thr Ala Gly Thr Ile
130 135 140

Pro Tyr Pro Gly Ala Asn Val Tyr Gly Ala Ser Lys Ala Phe Val Lys
145 150 155 160

Gln Phe Ser Leu Asn Leu Arg Ala Asp Leu Ala Gly Thr Lys Ile Arg
165 170 175

Val Thr Asn Leu Glu Pro Gly Leu Cys Glu Gly Thr Glu Phe Ser Thr
180 185 190

Val Arg Phe Lys Gly Asp His Lys Arg Val Glu Lys Leu Tyr Glu Gly
195 200 205

Ala His Ala Ile Gln Ala Glu Asp Ile Ala Asn Thr Val Ser Trp Val
210 215 220

Ala Ser Gln Pro Glu His Ile Asn Ile Asn Arg Ile Glu Ile Met Pro
225 230 235 240

Val Ser Gln Thr Tyr Gly Pro Gln Pro Val Tyr Arg Asp
245 250

<210> 296

<211> 371

<212> PRT

<213> Streptococcus agalactiae GBS patentin.ST25

<400> 296

Met Ile Tyr Leu Asp Asn Ala Ala Thr Thr Ala Leu Thr Pro Ser Val
1 5 10 15

Ile Glu Lys Met Thr Asn Val Met Thr Ser Asn Tyr Gly Asn Pro Ser
20 25 30

Ser Ile His Thr Phe Gly Arg Gln Ala Asn Gln Leu Leu Arg Glu Cys
35 40 45

Arg Gln Ile Ile Ala Glu Tyr Leu Asn Val Asn Ser Arg Glu Ile Ile
50 55 60

Phe Thr Ser Gly Gly Thr Glu Ser Asn Asn Thr Ala Ile Lys Gly Tyr
65 70 75 80

Ala Leu Ala Asn Gln Leu Lys Gly Lys His Ile Ile Thr Ser Glu Ile
85 90 95

Glu His His Ser Val Leu His Thr Met Thr Tyr Leu Ser Glu Arg Phe
100 105 110

Gly Phe Asp Ile Thr Tyr Leu Lys Pro Asn His Gly Gln Ile Thr Ala
115 120 125

Lys Asp Val Gln Glu Ala Leu Arg Asp Asp Thr Ile Met Val Ser Leu
130 135 140

Met Phe Ala Asn Asn Glu Thr Gly Asp Phe Leu Pro Ile Gln Glu Ile
145 150 155 160

Gly Gln Leu Leu Arg Asn His Gln Ala Val Phe His Val Asp Ala Val
165 170 175

Gln Val Phe Ser Lys Met Glu Leu Asp Pro His Ser Leu Gly Ile Asp
180 185 190

Phe Leu Ala Ala Ser Ala His Lys Phe His Gly Pro Lys Gly Val Gly
195 200 205

Ile Leu Tyr Cys Ala Pro His His Phe Asp Ser Leu Leu His Gly Gly
210 215 220

Asp Gln Glu Glu Lys Arg Arg Ala Ser Thr Glu Asn Ile Ile Gly Ile
225 230 235 240

Ala Gly Met Ser Gln Ala Leu Thr Asp Ala Thr Thr Asn Thr Leu Lys
245 250 255

GBS patentin.ST25

Asn Trp Thr His Ile Ser Gln Leu Arg Thr Thr Phe Leu Asp Ala Ile
260 265 270

Ser Asp Leu Asp Phe Tyr Leu Asn Asn Gly Gln Asp Cys Leu Pro His
275 280 285

Val Leu Asn Ile Gly Phe Pro Arg Gln Asn Asn Gly Leu Leu Leu Thr
290 295 300

Gln Leu Asp Leu Ala Gly Phe Ala Val Ser Thr Gly Ser Ala Cys Thr
305 310 315 320

Ala Gly Thr Val Glu Pro Ser His Val Leu Thr Ser Leu Tyr Gly Ala
325 330 335

Asn Ser Pro Arg Leu Asn Glu Ser Ile Arg Ile Ser Phe Ser Glu Leu
340 345 350

Asn Thr Gln Glu Glu Ile Leu Glu Leu Ala Lys Thr Leu Arg Lys Ile
355 360 365

Ile Gly Asp
370

<210> 297

<211> 447

<212> PRT

<213> Streptococcus agalactiae

<400> 297

Met Ser Arg Lys Thr Phe Lys His Ile Leu Ser Ile Gly Val Cys Thr
1 5 10 15

Leu Val Leu Ser Met Ser Leu Tyr Tyr Thr Glu Lys Ala His Ala Ile
20 25 30

Ala Gly Pro Ser Asp Arg Gln Tyr Val Glu Asn Pro Asn Pro His Ile
35 40 45

Ile Val Asn Val Thr Gly Thr Asp Gln Asn Gly Asn Ser Ile Leu Pro
50 55 60

His Tyr Ile Glu Val Asn Val Lys Met Gly Gln Thr Leu Ser Lys Glu
65 70 75 80

Glu Ile Leu Asp Tyr Ile Ala Arg Asn Leu Asn Ser Ser Val Gly Gly
85 90 95

GBS patentin.ST25

Glu Ser Lys Asn Val Gln Tyr Ser Asn Ile Glu Phe Lys Glu Ser Ala
 100 105 110
 Tyr Leu Lys Arg Gln Leu Asp Asp Gly Lys Thr Glu Glu Ile Ala Ile
 115 120 125
 Asp Asn Asp Gly Val Thr Val Pro Lys Asp Gly Pro Asn Lys Phe Trp
 130 135 140
 Ile Asp Val Pro Val Thr Cys Thr Val Thr Pro Ile Val Thr Glu Thr
 145 150 155 160
 His Glu Val Arg Trp Gly Thr Pro Val Ala Ile Ser His Arg Ile Tyr
 165 170 175
 Phe Val Glu Glu Ser Ser Gly Lys Val Leu Asp Glu Tyr Thr Asn Leu
 180 185 190
 His Thr Ala Asp Ser Glu Leu Asn Gly Tyr Arg Val Gly Asp Tyr Ile
 195 200 205
 Thr Asp Tyr Ala Leu Ser Lys Ser Ala Tyr Glu Ala Phe Leu Asn Ser
 210 215 220
 Arg Leu Asp Lys Glu Gly Tyr Lys Leu Gln His Arg Ile Ser Thr Asn
 225 230 235 240
 Val Arg Gln Asn Leu Gln Ile Asp Lys Leu Ile Phe Asn Tyr Asp Phe
 245 250 255
 Asn Glu Glu Asn Ile Tyr Tyr Gln Ile Gly Asn Ile Arg Pro Leu Leu
 260 265 270
 Ser Arg Ser Ser Ala Glu Val Glu Ser Asp Ile Ile Thr Glu Arg Tyr
 275 280 285
 Tyr Val Ser Lys Asn Ala Lys Ser Leu Ala Arg Thr Glu Ser Thr Ile
 290 295 300
 Ser Ile Lys Met Val Asp Ala Lys Thr Glu Gln Pro Leu Phe Asn His
 305 310 315 320
 Thr Leu Thr Gly Tyr Gln Leu Ala Thr Val Ser His Val Tyr Asn Arg
 325 330 335
 Leu Phe Glu Glu Asn Leu Ile Pro Thr Thr Lys Ser Gly Glu Arg Tyr
 340 345 350
 Phe Ile Gln Asn Met Lys Lys Thr Ala Glu Gln Glu Tyr Thr Val Tyr
 355 360 365

GBS patentin.ST25

Leu Ser Glu Thr Pro Tyr Ser Lys Glu Asn Ala Pro Val Ile Ser Tyr
370 375 380

Asp Ala Arg Pro Val Asp Trp Asp Tyr His Ser Gly Ala Ser Gly Ser
385 390 395 400

Leu Glu Asn Gln Pro Asn Ile Tyr Thr Glu Glu Asp Ser Thr Glu Phe
405 410 415

Leu Gly Asn Lys Pro Gln Ala Ala Cys Tyr Pro Asn Lys Gln Phe Ala
420 425 430

Cys Glu Asn Thr Asp Ser Lys Tyr Asn Tyr Ser Tyr Leu Glu Lys
435 440 445

<210> 298

<211> 759

<212> PRT

<213> Streptococcus agalactiae

<400> 298

Met Asn Pro Leu Ile Ile Gly Met Asn Asp Lys Gln Ala Glu Ala Val
1 5 10 15

Gln Thr Thr Asp Gly Pro Leu Leu Ile Met Ala Gly Ala Gly Ser Gly
20 25 30

Lys Thr Arg Val Leu Thr His Arg Ile Ala Tyr Leu Ile Asp Glu Lys
35 40 45

Tyr Val Asn Pro Trp Asn Ile Leu Ala Ile Thr Phe Thr Asn Lys Ala
50 55 60

Ala Arg Glu Met Arg Glu Arg Ala Ile Ala Leu Asn Pro Ala Thr Gln
65 70 75 80

Asp Thr Leu Ile Ala Thr Phe His Ser Met Cys Val Arg Ile Leu Arg
85 90 95

Arg Glu Ala Asp Tyr Ile Gly Tyr Asn Arg Asn Phe Thr Ile Val Asp
100 105 110

Pro Gly Glu Gln Arg Thr Leu Met Lys Arg Ile Ile Lys Gln Leu Asn
115 120 125

Leu Asp Thr Lys Lys Trp Asn Glu Arg Ser Ile Leu Gly Thr Ile Ser
130 135 140

GBS patentin.ST25

Asn Ala Lys Asn Asp Leu Leu Asp Glu Ile Ala Tyr Glu Lys Gln Ala
 145 150 155 160
 Gly Asp Met Tyr Thr Gln Val Ile Ala Lys Cys Tyr Lys Ala Tyr Gln
 165 170 175
 Glu Glu Leu Arg Arg Ser Glu Ala Met Asp Phe Asp Asp Leu Ile Met
 180 185 190
 Met Thr Leu Arg Leu Phe Asp Gln Asn Lys Asp Val Leu Ala Tyr Tyr
 195 200 205
 Gln Gln Arg Tyr Gln Tyr Ile His Val Asp Glu Tyr Gln Asp Thr Asn
 210 215 220
 His Ala Gln Tyr Gln Leu Val Lys Leu Leu Ala Ser Arg Phe Lys Asn
 225 230 235 240
 Ile Cys Val Val Gly Asp Ala Asp Gln Ser Ile Tyr Gly Trp Arg Gly
 245 250 255
 Ala Asp Met Gln Asn Ile Leu Asp Phe Glu Lys Asp Tyr Pro Gln Ala
 260 265 270
 Lys Val Val Leu Leu Glu Glu Asn Tyr Arg Ser Thr Lys Lys Ile Leu
 275 280 285
 Gln Ala Ala Asn Asn Val Ile Asn His Asn Lys Asn Arg Arg Pro Lys
 290 295 300
 Lys Leu Trp Thr Gln Asn Asp Glu Gly Glu Gln Ile Val Tyr His Arg
 305 310 315 320
 Ala Asn Asn Glu Gln Glu Glu Ala Val Phe Val Ala Ser Thr Ile Asp
 325 330 335
 Asn Ile Val Arg Glu Gln Gly Lys Asn Phe Lys Asp Phe Ala Val Leu
 340 345 350
 Tyr Arg Thr Asn Ala Gln Ser Arg Thr Ile Glu Glu Ala Leu Leu Lys
 355 360 365
 Ser Asn Ile Pro Tyr Thr Met Val Gly Gly Thr Lys Phe Tyr Ser Arg
 370 375 380
 Lys Glu Ile Arg Asp Val Ile Ala Tyr Leu Asn Ile Leu Ala Asn Thr
 385 390 395 400
 Ser Asp Asn Ile Ser Phe Glu Arg Ile Val Asn Glu Pro Lys Arg Gly
 405 410 415

GBS patentin.ST25

Val Gly Pro Gly Thr Leu Glu Lys Ile Arg Ser Phe Ala Tyr Glu Gln
420 425 430

Asn Met Ser Leu Leu Asp Ala Ser Ser Asn Val Met Met Ser Pro Leu
435 440 445

Lys Gly Lys Ala Ala Gln Ala Val Trp Asp Leu Ala Asn Leu Ile Leu
450 455 460

Thr Leu Arg Ser Lys Leu Asp Ser Leu Thr Val Thr Glu Ile Thr Glu
465 470 475 480

Asn Leu Leu Asp Lys Thr Gly Tyr Leu Glu Ala Leu Gln Val Gln Asn
485 490 495

Thr Leu Glu Ser Gln Ala Arg Ile Glu Asn Ile Glu Glu Phe Leu Ser
500 505 510

Val Thr Lys Asn Phe Asp Asp Asn Pro Glu Ile Thr Val Glu Gly Glu
515 520 525

Thr Gly Leu Asp Arg Leu Ser Arg Phe Leu Asn Asp Leu Ala Leu Ile
530 535 540

Ala Asp Thr Asp Asp Ser Ala Thr Glu Thr Ala Glu Val Thr Leu Met
545 550 555 560

Thr Leu His Ala Ala Lys Gly Leu Glu Phe Pro Val Val Phe Leu Ile
565 570 575

Gly Met Glu Glu Gly Val Phe Pro Leu Ser Arg Ala Ile Glu Asp Ala
580 585 590

Asp Glu Leu Glu Glu Glu Arg Arg Leu Ala Tyr Val Gly Ile Thr Arg
595 600 605

Ala Glu Gln Ile Leu Phe Leu Thr Asn Ala Asn Thr Arg Thr Leu Phe
610 615 620

Gly Lys Thr Ser Tyr Asn Arg Pro Thr Arg Phe Ile Arg Glu Ile Asp
625 630 635 640

Asp Glu Leu Ile Gln His Gln Gly Leu Ala Arg Pro Val Asn Ser Ser
645 650 655

Phe Gly Val Lys Tyr Ser Lys Glu Gln Pro Thr Gln Phe Gly Gln Gly
660 665 670

Met Ser Leu Gln Gln Ala Leu Gln Ala Arg Lys Ser Asn Ser Gln Pro
675 680 685

GBS patentin.ST25

Gln Val Thr Ala Gln Leu Gln Ala Leu Asn Ala Asn Asn Ser His Glu
690 695 700

Thr Ser Trp Glu Ile Gly Asp Val Ala Thr His Lys Lys Trp Gly Asp
705 710 715 720

Gly Thr Val Leu Glu Val Ser Gly Ser Gly Lys Thr Gln Glu Leu Lys
725 730 735

Ile Asn Phe Pro Gly Ile Gly Leu Lys Lys Leu Leu Ala Ser Val Ala
740 745 750

Pro Ile Ser Lys Lys Glu Asn
755

<210> 299

<211> 130

<212> PRT

<213> Streptococcus agalactiae

<400> 299

Met Lys Leu Tyr Val Gln Leu Met Val Ile Leu Thr Phe Ser Phe Ala
1 5 10 15

Gly Glu Val Leu Ser Thr Ile Phe Asn Leu Pro Val Pro Gly Ser Ile
20 25 30

Ile Gly Leu Ile Leu Leu Phe Leu Ala Leu Lys Tyr Lys Ile Ile Arg
35 40 45

Leu Arg His Ile Asp Ala Val Gly Asn Phe Leu Leu Ala Asn Met Thr
50 55 60

Ile Leu Phe Leu Pro Pro Ala Val Gly Leu Met Glu His Phe Gln Asp
65 70 75 80

Ile Lys Pro Tyr Leu Phe Gly Ile Ala Ile Ile Ile Leu Gly Ala Leu
85 90 95

Phe Leu Asn Ile Leu Thr Ile Gly Leu Val Ser Gln Trp Ile Lys Lys
100 105 110

Arg Tyr Glu Gly Asp Tyr Pro Glu Ile Gly Gly Lys Asn Gly Asn Phe
115 120 125

Asn Glu
130

GBS patentin.ST25

<210> 300

<211> 157

<212> PRT

<213> Streptococcus agalactiae

<400> 300

Met Ile Phe Val Thr Val Gly Thr His Glu Gln Gln Phe Asn Arg Leu
1 5 10 15

Ile Lys Glu Val Asp Arg Leu Lys Gly Thr Gly Ala Ile Asp Gln Glu
20 25 30

Val Phe Ile Gln Thr Gly Tyr Ser Asp Phe Glu Pro Gln Asn Cys Gln
35 40 45

Trp Ser Lys Phe Leu Ser Tyr Asp Asp Met Asn Ser Tyr Met Lys Glu
50 55 60

Ala Glu Ile Val Ile Thr His Gly Gly Pro Ala Thr Phe Met Ser Val
65 70 75 80

Ile Ser Leu Gly Lys Leu Pro Val Val Val Pro Arg Arg Lys Gln Phe
85 90 95

Gly Glu His Ile Asn Asp His Gln Ile Gln Phe Phe Lys Lys Ile Ala
100 105 110

His Leu Tyr Pro Leu Ala Trp Ile Glu Asp Val Asp Gly Leu Ala Glu
115 120 125

Val Leu Lys Arg Asn Ile Ala Thr Glu Lys Tyr Gln Gly Asn Asn Asp
130 135 140

Met Phe Cys His Lys Leu Glu Lys Ile Ile Gly Glu Ile
145 150 155

<210> 301

<211> 253

<212> PRT

<213> Streptococcus agalactiae

<400> 301

Met Val Met Lys Ile Ile Glu Leu Lys Glu Ala Thr Val Gln Val Ser
1 5 10 15

GBS patentin.ST25

Asn Gly Leu Ala Glu Met Lys Thr Ile Leu Asp His Val Asn Leu Ser
20 25 30

Ile Tyr Glu His Asp Phe Ile Thr Ile Leu Gly Gly Asn Gly Ala Gly
35 40 45

Lys Ser Thr Leu Phe Asn Val Ile Ala Gly Thr Leu Met Leu Ser Gly
50 55 60

Gly Asn Ile Tyr Ile Met Gly Gln Asp Val Thr Asn Leu Pro Ala Glu
65 70 75 80

Lys Arg Ala Lys Tyr Leu Ser Arg Val Phe Gln Asp Pro Lys Met Gly
85 90 95

Thr Ala Pro Arg Met Thr Val Ala Glu Asn Leu Leu Val Ala Lys Phe
100 105 110

Arg Gly Glu Lys Arg Pro Leu Val Pro Arg Lys Ile Thr Asn Tyr Thr
115 120 125

Glu Glu Phe Gln Lys Leu Ile Ala Arg Thr Gly Asn Gly Leu Asp Arg
130 135 140

His Leu Glu Thr Pro Thr Gly Leu Leu Ser Gly Gly Gln Arg Gln Ala
145 150 155 160

Leu Ser Leu Leu Met Ala Thr Leu Lys Lys Pro Asn Leu Leu Leu Leu
165 170 175

Asp Glu His Thr Ala Ala Leu Asp Pro Arg Thr Ser Val Ser Leu Met
180 185 190

Gly Leu Thr Asp Glu Phe Ile Lys Gln Asp Ser Leu Thr Ala Leu Met
195 200 205

Ile Thr His His Met Glu Asp Ala Leu Lys Tyr Gly Asn Arg Ile Leu
210 215 220

Val Met Lys Asp Gly Lys Ile Val Arg Asp Leu Asn Gln Ala Gln Lys
225 230 235 240

Asn Lys Met Ala Ile Ala Asp Tyr Tyr Gln Leu Phe Asp
245 250

<210> 302

<211> 1072

<212> PRT

GBS patentin.ST25
<213> streptococcus agalactiae

<400> 302

Met Glu Ile Lys Lys Lys His Arg Ile Met Leu Tyr Ser Ala Leu Ile
1 5 10 15

Leu Gly Thr Ile Leu Val Asn Asn Ser Tyr Gln Ala Lys Ala Glu Glu
20 25 30

Leu Thr Lys Thr Thr Ser Thr Ser Gln Ile Arg Asp Thr Gln Thr Asn
35 40 45

Asn Ile Glu Val Leu Gln Thr Glu Ser Thr Thr Val Lys Glu Thr Ser
50 55 60

Thr Thr Thr Thr Gln Gln Asp Leu Ser Asn Pro Thr Ala Ser Thr Ala
65 70 75 80

Thr Ala Thr Ala Thr His Ser Thr Met Lys Gln Val Val Asp Asn Gln
85 90 95

Thr Gln Asn Lys Glu Leu Val Lys Asn Gly Asp Phe Asn Gln Thr Asn
100 105 110

Pro Val Ser Gly Ser Trp Ser His Thr Ser Ala Arg Glu Trp Ser Ala
115 120 125

Trp Ile Asp Lys Glu Asn Thr Ala Asp Lys Ser Pro Ile Ile Gln Arg
130 135 140

Thr Glu Gln Gly Gln Val Ser Leu Ser Ser Asp Lys Gly Phe Arg Gly
145 150 155 160

Ala Val Thr Gln Lys Val Asn Ile Asp Pro Thr Lys Lys Tyr Glu Val
165 170 175

Lys Phe Asp Ile Glu Thr Ser Asn Lys Ala Gly Gln Ala Phe Leu Arg
180 185 190

Ile Met Glu Lys Lys Asp Asn Asn Thr Arg Leu Trp Leu Ser Glu Met
195 200 205

Thr Ser Gly Thr Thr Asn Lys His Thr Leu Thr Lys Ile Tyr Asn Pro
210 215 220

Lys Leu Asn Val Ser Glu Val Thr Leu Glu Leu Tyr Tyr Glu Lys Gly
225 230 235 240

Thr Gly Ser Ala Thr Phe Asp Asn Ile Ser Met Lys Ala Lys Gly Pro
245 250 255

GBS patentin.ST25

Lys Asp Ser Glu His Pro Gln Pro Val Thr Thr Gln Ile Glu Glu Ser
 260 265 270
 Val Asn Thr Ala Leu Asn Lys Asn Tyr Val Phe Asn Lys Ala Asp Tyr
 275 280 285
 Gln Tyr Thr Leu Thr Asn Pro Ser Leu Gly Lys Ile Val Gly Gly Ile
 290 295 300
 Leu Tyr Pro Asn Ala Thr Gly Ser Thr Thr Val Lys Ile Ser Asp Lys
 305 310 315 320
 Ser Gly Lys Ile Ile Lys Glu Val Pro Leu Ser Val Thr Ala Ser Thr
 325 330 335
 Glu Asp Lys Phe Thr Lys Leu Leu Asp Lys Trp Asn Asp Val Thr Ile
 340 345 350
 Gly Asn His Val Tyr Asp Thr Asn Asp Ser Asn Met Gln Lys Ile Asn
 355 360 365
 Gln Lys Leu Asp Glu Thr Asn Ala Lys Asn Ile Lys Thr Ile Lys Leu
 370 375 380
 Asp Ser Asn His Thr Phe Leu Trp Lys Asp Leu Asp Asn Leu Asn Asn
 385 390 395 400
 Ser Ala Gln Leu Thr Ala Thr Tyr Arg Arg Leu Glu Asp Leu Ala Lys
 405 410 415
 Gln Ile Thr Asn Pro His Ser Thr Ile Tyr Lys Asn Glu Lys Ala Ile
 420 425 430
 Arg Thr Val Lys Glu Ser Leu Ala Trp Leu His Gln Asn Phe Tyr Asn
 435 440 445
 Val Asn Lys Asp Ile Glu Gly Ser Ala Asn Trp Trp Asp Phe Glu Ile
 450 455 460
 Gly Val Pro Arg Ser Ile Thr Ala Thr Leu Ala Leu Met Asn Asn Tyr
 465 470 475 480
 Phe Thr Asp Ala Glu Ile Lys Thr Tyr Thr Asp Pro Ile Glu His Phe
 485 490 495
 Val Pro Asp Ala Gly Tyr Phe Arg Lys Thr Leu Asp Asn Pro Phe Lys
 500 505 510
 Ala Leu Gly Gly Asn Leu Val Asp Met Gly Arg Val Lys Ile Ile Glu
 515 520 525

GBS patentin.ST25

Gly Leu Leu Arg Lys Asp Asn Thr Ile Ile Glu Lys Thr Ser His Ser
530 535 540

Leu Lys Asn Leu Phe Thr Thr Ala Thr Lys Ala Glu Gly Phe Tyr Ala
545 550 555 560

Asp Gly ser Tyr Ile Asp His Thr Asn Val Ala Tyr Thr Gly Ala Tyr
565 570 575

Gly Asn Val Leu Ile Asp Gly Leu Thr Gln Leu Leu Pro Ile Ile Gln
580 585 590

Glu Thr Asp Tyr Lys Ile Ser Asn Gln Glu Leu Asp Met Val Tyr Lys
595 600 605

Trp Ile Asn Gln Ser Phe Leu Pro Leu Ile Val Lys Gly Glu Leu Met
610 615 620

Asp Met Ser Arg Gly Arg ser Ile Ser Arg Glu Ala Ala Ser Ser His
625 630 635 640

Ala Ala Ala Val Glu Val Leu Arg Gly Phe Leu Arg Leu Ala Asn Met
645 650 655

Ser Asn Glu Glu Arg Asn Leu Asp Leu Lys Ser Thr Ile Lys Thr Ile
660 665 670

Ile Thr Ser Asn Lys Phe Tyr Asn Val Phe Asn Asn Leu Lys Ser Tyr
675 680 685

Ser Asp Ile Ala Asn Met Asn Lys Met Leu Asn Asp Ser Thr Val Ala
690 695 700

Thr Lys Pro Leu Lys Ser Asn Leu Ser Thr Phe Asn Ser Met Asp Arg
705 710 715 720

Leu Ala Tyr Tyr Asn Ala Glu Lys Asp Phe Gly Phe Ala Leu Ser Leu
725 730 735

His Ser Lys Arg Thr Leu Asn Tyr Glu Gly Met Asn Asp Glu Asn Thr
740 745 750

Arg Asp Trp Tyr Thr Gly Asp Gly Met Phe Tyr Leu Tyr Asn Ser Asp
755 760 765

Gln Ser His Tyr Ser Asn His Phe Trp Pro Thr Val Asn Pro Tyr Lys
770 775 780

Met Ala Gly Thr Thr Glu Lys Asp Ala Lys Arg Glu Asp Thr Thr Lys
785 790 795 800

GBS patentin.ST25

Glu Phe Met Ser Lys His Ser Lys Asp Ala Lys Glu Lys Thr Gly Gln
805 810 815

Val Thr Gly Thr Ser Asp Phe Val Gly Ser Val Lys Leu Asn Asp His
820 825 830

Phe Ala Leu Ala Ala Met Asp Phe Thr Asn Trp Asp Arg Thr Leu Thr
835 840 845

Ala Gln Lys Gly Trp Val Ile Leu Asn Asp Lys Ile Val Phe Leu Gly
850 855 860

Ser Asn Ile Lys Asn Thr Asn Gly Ile Gly Asn Val Ser Thr Thr Ile
865 870 875 880

Asp Gln Arg Lys Asp Asp Ser Lys Thr Pro Tyr Thr Thr Tyr Val Asn
885 890 895

Gly Lys Thr Ile Asp Leu Lys Gln Ala Ser Ser Gln Gln Phe Thr Asp
900 905 910

Thr Lys Ser Val Phe Leu Glu Ser Lys Glu Pro Gly Arg Asn Ile Gly
915 920 925

Tyr Ile Phe Phe Lys Asn Ser Thr Ile Asp Ile Glu Arg Lys Glu Gln
930 935 940

Thr Gly Thr Trp Asn Ser Ile Asn Arg Thr Ser Lys Asn Thr Ser Ile
945 950 955 960

Val Ser Asn Pro Phe Ile Thr Ile Ser Gln Lys His Asp Asn Lys Gly
965 970 975

Asp Ser Tyr Gly Tyr Met Met Val Pro Asn Ile Asp Arg Thr Ser Phe
980 985 990

Asp Lys Leu Ala Asn Ser Lys Glu Val Glu Leu Leu Glu Asn Ser Ser
995 1000 1005

Lys Gln Gln Val Ile Tyr Asp Lys Asn Ser Gln Thr Trp Ala Val
1010 1015 1020

Ile Lys His Asp Asn Gln Glu Ser Leu Ile Asn Asn Gln Phe Lys
1025 1030 1035

Met Asn Lys Ala Gly Leu Tyr Leu Val Gln Lys Val Gly Asn Asp
1040 1045 1050

Tyr Gln Asn Val Tyr Tyr Gln Pro Gln Thr Met Thr Lys Thr Asp
1055 1060 1065

Gln Leu Ala Ile
1070

<210> 303

<211> 77

<212> PRT

<213> Streptococcus agalactiae

<400> 303

Met His Ser Phe Ser Asn Pro Gly Tyr Pro Tyr Asp Asn Ala Val Thr
1 5 10 15

Glu Ala Phe Phe Lys Tyr Leu Lys His Arg Gln Ile Asn Arg Lys His
20 25 30

Tyr Gln Asn Ile Lys Gln Val Gln Leu Asp Cys Phe Glu Tyr Ile Glu
35 40 45

Asn Phe Tyr Asn Asn Tyr Asn Pro His Thr Ala Asn Leu Gly Leu Thr
50 55 60

Pro Asn Gln Lys Glu Glu Asn Tyr Phe Asn Ala Ile Lys
65 70 75

<210> 304

<211> 822

<212> PRT

<213> Streptococcus agalactiae

<400> 304

Val Lys Lys Thr Tyr Gly Tyr Ile Gly Ser Val Ala Ala Ile Leu Leu
1 5 10 15

Ala Thr His Ile Gly Ser Tyr Gln Leu Gly Lys His His Met Gly Leu
20 25 30

Ala Thr Lys Asp Asn Gln Ile Ala Tyr Ile Asp Asp Ser Lys Gly Lys
35 40 45

Ala Lys Ala Pro Lys Thr Asn Lys Thr Met Asp Gln Ile Ser Ala Glu
50 55 60

Glu Gly Ile Ser Ala Glu Gln Ile Val Val Lys Ile Thr Asp Gln Gly
65 70 75 80

GBS patentin.ST25

Tyr Val Thr Ser His Gly Asp His Tyr His Phe Tyr Asn Gly Lys Val
 85 90 95
 Pro Tyr Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Thr Asp Pro Asn
 100 105 110
 Tyr Arg Phe Lys Gln Ser Asp Val Ile Asn Glu Ile Leu Asp Gly Tyr
 115 120 125
 Val Ile Lys Val Asn Gly Asn Tyr Tyr Val Tyr Leu Lys Pro Gly Ser
 130 135 140
 Lys Arg Lys Asn Ile Arg Thr Lys Gln Gln Ile Ala Glu Gln Val Ala
 145 150 155 160
 Lys Gly Thr Lys Glu Ala Lys Glu Lys Gly Leu Ala Gln Val Ala His
 165 170 175
 Leu Ser Lys Glu Glu Val Ala Ala Val Asn Glu Ala Lys Arg Gln Gly
 180 185 190
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Ser Pro Thr Asp Ile Ile
 195 200 205
 Asp Asp Leu Gly Asp Ala Tyr Leu Val Pro His Gly Asn His Tyr His
 210 215 220
 Tyr Ile Pro Lys Lys Asp Leu Ser Pro Ser Glu Leu Ala Ala Ala Gln
 225 230 235 240
 Ala Tyr Trp Ser Gln Lys Gln Gly Arg Gly Ala Arg Pro Ser Asp Tyr
 245 250 255
 Arg Pro Thr Pro Ala Pro Gly Arg Arg Lys Ala Pro Ile Pro Asp Val
 260 265 270
 Thr Pro Asn Pro Gly Gln Gly His Gln Pro Asp Asn Gly Gly Tyr His
 275 280 285
 Pro Ala Pro Pro Arg Pro Asn Asp Ala Ser Gln Asn Lys His Gln Arg
 290 295 300
 Asp Glu Phe Lys Gly Lys Thr Phe Lys Glu Leu Leu Asp Gln Leu His
 305 310 315 320
 Arg Leu Asp Leu Lys Tyr Arg His Val Glu Glu Asp Gly Leu Ile Phe
 325 330 335
 Glu Pro Thr Gln Val Ile Lys Ser Asn Ala Phe Gly Tyr Val Val Pro
 340 345 350

GBS patentin.ST25

His Gly Asp His Tyr His Ile Ile Pro Arg Ser Gln Leu Ser Pro Leu
355 360 365

Glu Met Glu Leu Ala Asp Arg Tyr Leu Ala Gly Gln Thr Glu Asp Asn
370 375 380

Asp Ser Gly Ser Glu His Ser Lys Pro Ser Asp Lys Glu Val Thr His
385 390 395 400

Thr Phe Leu Gly His Arg Ile Lys Ala Tyr Gly Lys Gly Leu Asp Gly
405 410 415

Lys Pro Tyr Asp Thr Ser Asp Ala Tyr Val Phe Ser Lys Glu Ser Ile
420 425 430

His Ser Val Asp Lys Ser Gly Val Thr Ala Lys His Gly Asp His Phe
435 440 445

His Tyr Ile Gly Phe Gly Glu Leu Glu Gln Tyr Glu Leu Asp Glu Val
450 455 460

Ala Asn Trp Val Lys Ala Lys Gly Gln Ala Asp Glu Leu Ala Ala Ala
465 470 475 480

Leu Asp Gln Glu Gln Gly Lys Glu Lys Pro Leu Phe Asp Thr Lys Lys
485 490 495

Val Ser Arg Lys Val Thr Lys Asp Gly Lys Val Gly Tyr Met Met Pro
500 505 510

Lys Asp Gly Lys Asp Tyr Phe Tyr Ala Arg Asp Gln Leu Asp Leu Thr
515 520 525

Gln Ile Ala Phe Ala Glu Gln Glu Leu Met Leu Lys Asp Lys Lys His
530 535 540

Tyr Arg Tyr Asp Ile Val Asp Thr Gly Ile Glu Pro Arg Leu Ala Val
545 550 555 560

Asp Val Ser Ser Leu Pro Met His Ala Gly Asn Ala Thr Tyr Asp Thr
565 570 575

Gly Ser Ser Phe Val Ile Pro His Ile Asp His Ile His Val Val Pro
580 585 590

Tyr Ser Trp Leu Thr Arg Asp Gln Ile Ala Thr Val Lys Tyr Val Met
595 600 605

Gln His Pro Glu Val Arg Pro Asp Val Trp Ser Lys Pro Gly His Glu
610 615 620

GBS patentin.ST25

Glu Ser Gly Ser Val Ile Pro Asn Val Thr Pro Leu Asp Lys Arg Ala
625 630 635 640

Gly Met Pro Asn Trp Gln Ile Ile His Ser Ala Glu Glu Val Gln Lys
645 650 655

Ala Leu Ala Glu Gly Arg Phe Ala Thr Pro Asp Gly Tyr Ile Phe Asp
660 665 670

Pro Arg Asp Val Leu Ala Lys Glu Thr Phe Val Trp Lys Asp Gly Ser
675 680 685

Phe Ser Ile Pro Arg Ala Asp Gly Ser Ser Leu Arg Thr Ile Asn Lys
690 695 700

Ser Asp Leu Ser Gln Ala Glu Trp Gln Gln Ala Gln Glu Leu Leu Ala
705 710 715 720

Lys Lys Asn Thr Gly Asp Ala Thr Asp Thr Asp Lys Pro Lys Glu Lys
725 730 735

Gln Gln Ala Asp Lys Ser Asn Glu Asn Gln Gln Pro Ser Glu Ala Ser
740 745 750

Lys Glu Glu Lys Glu Ser Asp Asp Phe Ile Asp Ser Leu Pro Asp Tyr
755 760 765

Gly Leu Asp Arg Ala Thr Leu Glu Asp His Ile Asn Gln Leu Ala Gln
770 775 780

Lys Ala Asn Ile Asp Pro Lys Tyr Leu Ile Phe Gln Pro Glu Gly Val
785 790 795 800

Gln Phe Tyr Asn Lys Asn Gly Glu Leu Val Thr Tyr Asp Ile Lys Thr
805 810 815

Leu Gln Gln Ile Asn Pro
820

<210> 305

<211> 306

<212> PRT

<213> Streptococcus agalactiae

<400> 305

Met Lys Lys Gly Phe Phe Leu Met Ala Met Val Val Ser Leu Val Met
1 5 10 15

GBS patentin.ST25

Ile Ala Gly Cys Asp Lys Ser Ala Asn Pro Lys Gln Pro Thr Gln Gly
20 25 30

Met Ser Val Val Thr Ser Phe Tyr Pro Met Tyr Ala Met Thr Lys Glu
35 40 45

Val Ser Gly Asp Leu Asn Asp Val Arg Met Ile Gln Ser Gly Ala Gly
50 55 60

Ile His Ser Phe Glu Pro Ser Val Asn Asp Val Ala Ala Ile Tyr Asp
65 70 75 80

Ala Asp Leu Phe Val Tyr His Ser His Thr Leu Glu Ala Trp Ala Arg
85 90 95

Asp Leu Asp Pro Asn Leu Lys Lys Ser Lys Val Asp Val Phe Glu Ala
100 105 110

Ser Lys Pro Leu Thr Leu Asp Arg Val Lys Gly Leu Glu Asp Met Glu
115 120 125

Val Thr Gln Gly Ile Asp Pro Ala Thr Leu Tyr Asp Pro His Thr Trp
130 135 140

Thr Asp Pro Val Leu Ala Gly Glu Glu Ala Val Asn Ile Ala Lys Glu
145 150 155 160

Leu Gly Arg Leu Asp Pro Lys His Lys Asp Ser Tyr Thr Lys Lys Ala
165 170 175

Lys Ala Phe Lys Lys Glu Ala Glu Gln Leu Thr Glu Glu Tyr Thr Gln
180 185 190

Lys Phe Lys Lys Val Arg Ser Lys Thr Phe Val Thr Gln His Thr Ala
195 200 205

Phe Ser Tyr Leu Ala Lys Arg Phe Gly Leu Lys Gln Leu Gly Ile Ser
210 215 220

Gly Ile Ser Pro Glu Gln Glu Pro Ser Pro Arg Gln Leu Lys Glu Ile
225 230 235 240

Gln Asp Phe Val Lys Glu Tyr Asn Val Lys Thr Ile Phe Ala Glu Asp
245 250 255

Asn Val Asn Pro Lys Ile Ala His Ala Ile Ala Lys Ser Thr Gly Ala
260 265 270

Lys Val Lys Thr Leu Ser Pro Leu Glu Ala Ala Pro Ser Gly Asn Lys
275 280 285

GBS patentin.ST25

Thr Tyr Leu Glu Asn Leu Arg Ala Asn Leu Glu Val Leu Tyr Gln Gln
290 295 300

Leu Lys
305

<210> 306

<211> 1150

<212> PRT

<213> Streptococcus agalactiae

<400> 306

Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
1 5 10 15

Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
20 25 30

Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Thr Val Glu Thr Pro
35 40 45

Gln Pro Thr Ala Val Ser Glu Glu Ala Pro Ser Ser Lys Glu Thr Lys
50 55 60

Thr Pro Gln Thr Pro Ser Asp Ala Gly Glu Thr Val Ala Asp Asp Ala
65 70 75 80

Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
85 90 95

Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
100 105 110

Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
115 120 125

Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
130 135 140

Lys Ala Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
145 150 155 160

Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
165 170 175

Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
180 185 190

GBS patentin.ST25

His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
195 200 205

Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
210 215 220

Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
225 230 235 240

Asn Tyr Ala Gln Ala Ile Arg Asp Ala Ile Asn Leu Gly Ala Lys Val
245 250 255

Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
260 265 270

Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
275 280 285

Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
290 295 300

Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
305 310 315 320

Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
325 330 335

Leu Thr Glu Thr Ala Thr Val Lys Thr Ala Asp Gln Gln Asp Lys Glu
340 345 350

Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
355 360 365

Tyr Ala Tyr Ala Asn Arg Gly Thr Lys Glu Asp Asp Phe Lys Asp Val
370 375 380

Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp
385 390 395 400

Lys Ile Ala Lys Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
405 410 415

Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
420 425 430

Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
435 440 445

Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
450 455 460

GBS patentin.ST25

Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
465 470 475 480

Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
485 490 495

Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
500 505 510

Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
515 520 525

Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu
530 535 540

Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
545 550 555 560

Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
565 570 575

Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
580 585 590

Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
595 600 605

Thr Val Thr Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr
610 615 620

Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
625 630 635 640

Ala Pro Lys Ala Leu Tyr Glu Thr Ser Trp Gln Lys Ile Thr Ile Pro
645 650 655

Ala Asn Ser Ser Lys Gln Val Thr Val Pro Ile Asp Ala Ser Arg Phe
660 665 670

Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
675 680 685

Phe Val Arg Phe Lys Gln Asp Pro Lys Lys Glu Glu Leu Met Ser Ile
690 695 700

Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
705 710 715 720

Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala
725 730 735

GBS patentin.ST25

Asn Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
740 745 750

Ala Leu Lys Asn Asn Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
755 760 765

Thr Ile Ile Lys Ala Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
770 775 780

Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
785 790 795 800

Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
805 810 815

Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
820 825 830

Gln Phe Gln Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
835 840 845

Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
850 855 860

Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
865 870 875 880

Thr Arg Phe Glu Lys Thr Arg Trp Asp Gly Lys Asp Lys Asp Gly Lys
885 890 895

Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
900 905 910

Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
915 920 925

Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
930 935 940

Arg Arg Leu Thr Leu Ala Ser Lys Pro Lys Thr Ser Gln Pro Val Tyr
945 950 955 960

Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
965 970 975

Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
980 985 990

Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
995 1000 1005

GBS patentin.ST25

Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro
1010 1015 1020

Val Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp
1025 1030 1035

Gly Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu
1040 1045 1050

Gln Asp Gly Ser Gly Gln Thr Pro Asp Lys Lys Thr Glu Thr Lys
1055 1060 1065

Pro Glu Lys Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln
1070 1075 1080

Lys Gly Gln Pro Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg
1085 1090 1095

Ala Leu Ala Thr Lys Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr
1100 1105 1110

Asn Asp Lys Asp Thr Asn Arg Leu His Leu Leu Lys Leu Val Met
1115 1120 1125

Thr Thr Phe Phe Leu Gly Leu Val Ala His Ile Phe Lys Thr Lys
1130 1135 1140

Arg Gln Lys Glu Thr Lys Lys
1145 1150

<210> 307

<211> 403

<212> PRT

<213> Streptococcus agalactiae

<400> 307

Phe Ser Val Thr Tyr Ser Gln Ser Glu Arg Thr Val Val Phe Ser Phe
1 5 10 15

Gly Glu Ile Thr Phe Ser Arg Ser Arg Trp Thr Asn Gly Phe Glu Thr
20 25 30

Arg Ile Pro Val Asp Glu Trp Leu Gly Leu Glu Lys Tyr Lys Arg Tyr
35 40 45

Ser Ile Glu Phe Leu Tyr His Val Ala Lys Leu Ala Thr Met Met Pro
50 55 60

GBS patentin.ST25

Tyr Arg Gln Val Cys Lys Val Ile Asp Ser Thr Leu Gln Thr Ile Ile
65 70 75 80

Thr Lys Asp Cys Val Leu Lys Ala Val Lys Phe Val Glu Lys Leu Leu
85 90 95

Lys Glu Lys Glu Arg Tyr Arg Phe Tyr Leu Glu Glu Pro Pro Glu Arg
100 105 110

Lys Lys Val Lys Lys Leu Tyr Val Glu Gly Asp Gly Val Met Ile Lys
115 120 125

Ser Thr Asp Ser Arg Glu Glu Arg Arg Tyr Leu Asp Leu Thr His Phe
130 135 140

Val Ile His Thr Gly Ser Lys Lys Val Ser Thr Lys Arg Tyr Glu Leu
145 150 155 160

Gln Asp Lys His Glu Ile Leu Gln Leu Asn Tyr Asp Lys Ala Lys Tyr
165 170 175

Asn Leu Leu Asp Tyr Ile Tyr Asn Asn Tyr Glu Val Asp Asp Asp Thr
180 185 190

Ile Leu Ile Thr Asn Ser Asp Met Gly Lys Gly Tyr Thr Ser Arg Val
195 200 205

Phe Lys Glu Leu Gly Lys Ala Leu Lys Val Lys Lys His Glu His Phe
210 215 220

Trp Asp Ile Tyr His Val Lys Glu Lys Leu Ser Ser Tyr Leu Arg Lys
225 230 235 240

Tyr Pro Ile Glu Leu Thr Asp Phe Ala Leu Asp Ala Val Lys Lys Tyr
245 250 255

Asn Ser Asp Lys Leu Glu Leu Val Phe Asp Thr Val Glu Ser Leu Ile
260 265 270

Cys Asp Glu Leu Glu Asp Gln Glu Phe Gln Lys Phe Lys Lys Lys Val
275 280 285

Leu Asn Asn Phe Lys Tyr Ile Lys Pro Ala His Leu Arg Asn Leu Ser
290 295 300

Asn Arg Gly Ile Gly Ile Met Glu Ser Gln His Arg Lys Ile Thr Tyr
305 310 315 320

Arg Met Lys Arg Arg Gly Met Tyr Trp Ser Lys Trp Gly Ile Ser Thr
325 330 335

GBS patentin.ST25

Met Ala Asn Met Ile Ile Leu Glu Arg Ala Asn Gly Leu Arg Glu Leu
340 345 350

Phe Phe Gly Ser Trp Arg Lys Val Tyr Ser Glu Tyr Lys Glu Gly Ser
355 360 365

Phe Ser Ala Gly Arg Leu Phe Lys Lys Thr Asp Glu Leu Asp Lys Phe
370 375 380

Ser Lys Pro Leu Leu Lys Asn Gly Arg Lys Trp Ser Ile Thr Gly Ile
385 390 395 400

Lys Thr Lys

<210> 308

<211> 278

<212> PRT

<213> Streptococcus agalactiae

<400> 308

Lys Ala Ser Ser Gly Asp Tyr Gly Thr Lys Arg Glu Ile Ile Thr Ala
1 5 10 15

Asn Lys Asp Lys Tyr Ser Ile Ser Lys Met Cys Arg Trp Leu Asn Met
20 25 30

Pro Arg Ser Ser Tyr Tyr Tyr Gln Ala Val Glu Ser Val Ser Lys Thr
35 40 45

Glu Phe Glu Glu Thr Ile Lys Arg Ile Phe Leu Asp Ser Glu Ser Arg
50 55 60

Tyr Gly Ser Arg Lys Ile Lys Ile Cys Leu Asn Asn Glu Gly Ile Thr
65 70 75 80

Leu Ser Arg Arg Arg Ile Arg Arg Ile Met Lys Arg Leu Asn Leu Val
85 90 95

Ser Val Tyr Gln Lys Ala Thr Phe Lys Pro His Ser Arg Gly Lys Asn
100 105 110

Glu Ala Pro Ile Pro Asn His Leu Asp Arg Gln Phe Lys Gln Glu Arg
115 120 125

Pro Leu Gln Ala Leu Val Thr Asp Leu Thr Tyr Val Arg Val Gly Asn
130 135 140

GBS patentin.ST25

Arg Trp Ala Tyr Val Cys Leu Ile Ile Asp Leu Tyr Asn Arg Glu Ile
145 150 155 160

Ile Gly Leu Ser Leu Gly Trp His Lys Thr Ala Glu Leu Val Lys Gln
165 170 175

Ala Ile Gln Ser Ile Pro Tyr Ala Leu Thr Lys Val Lys Met Phe His
180 185 190

Ser Asp Arg Gly Lys Glu Phe Asp Asn Gln Leu Ile Asp Glu Ile Leu
195 200 205

Glu Ala Phe Gly Ile Thr Arg Ser Leu Ser Gln Ala Gly Cys Pro Tyr
210 215 220

Asp Asn Ala Val Ala Glu Ser Thr Tyr Arg Ala Phe Lys Ile Glu Phe
225 230 235 240

Val Tyr Gln Glu Thr Phe Gln Ser Leu Glu Glu Leu Ala Leu Lys Thr
245 250 255

Glu Lys Ala Thr Leu Phe Cys Thr Thr Phe Ile Lys Cys Cys Leu Phe
260 265 270

Arg Phe Leu Pro Met Leu
275

<210> 309

<211> 104

<212> PRT

<213> Streptococcus agalactiae

<400> 309

Met Lys Thr Arg Asn Arg Lys Gly Gly Tyr Leu Ala Asn Thr Ala Asn
1 5 10 15

Glu Tyr Ile Asp Ser Lys Gln Ala Ile His Cys Leu Ser Val Glu Leu
20 25 30

Glu Pro Gln Ile Arg Phe Glu Glu Gly Gln Pro Thr Gly Glu Ile Ile
35 40 45

Ala Tyr Lys Ala Trp Phe Ser Gln Lys Gly Leu Pro Pro Phe Met Val
50 55 60

Lys Phe Glu Asn Glu Val Thr Leu Pro Ala Tyr Met Val Met Val Gln
65 70 75 80

GBS patentin.ST25

Phe Glu Asn Leu Gln Ala Cys Glu Val Gly Phe Asn Val Tyr Phe Lys
85 90 95

Ala Asp Asn Leu Lys Glu Val Lys
100

<210> 310

<211> 2066

<212> PRT

<213> Streptococcus agalactiae

<400> 310

Leu Ser Thr Phe Asp Ser Val Thr Gly Arg Thr Asn His Leu Glu Ala
1 5 10 15

Tyr Glu Gly Leu Asn Leu Ser Glu Lys Phe Ala Ile Leu Ser His Phe
20 25 30

Asp Lys Leu Arg Asn Glu Leu Gln Thr Pro Ser Ile Gln Leu Gly Glu
35 40 45

Phe Asp Arg Glu Met Glu Ala Phe Ser Ile Thr Leu Gly Asn Glu Leu
50 55 60

Leu Gly Tyr Leu Glu Ala Asn Gly Ser Pro Tyr Glu Leu Lys Arg Glu
65 70 75 80

Leu Asn Gln Ala Glu Met Met Ala Val Leu Glu Leu Ser Arg Gln Leu
85 90 95

Val Ala Lys Phe Ser Thr Lys Leu Glu Glu Leu Gly Ile Asp Leu Gly
100 105 110

Ser Phe Gln Pro Asp Gln Val Asn Ile Leu Leu Asp Ala Val Gly Arg
115 120 125

Phe Arg Leu Lys Asn Ala Asp Ile Ala Leu Leu Gly Gly Tyr Pro Lys
130 135 140

Ala Ser Val Ser Gln Leu Ala Leu Ala Thr Glu Leu Leu Gln Met Gly
145 150 155 160

Leu Ser His Asp Lys Val Glu Phe Phe Leu Thr Ser Gln Leu Gln Leu
165 170 175

Glu Asp Met Arg Gln Val Ala Phe Ala Phe Leu His Glu Ser Leu Thr
180 185 190

GBS patentin.ST25

Arg Glu Glu Ala Glu Gln Phe Glu Thr Asp Arg Phe Arg His Thr Ser
195 200 205

Leu Asn Phe Arg Glu Trp Arg Glu Leu Leu Glu Lys Gln Glu Pro Glu
210 215 220

Met Val Glu Met Ser Asp Val Ser Pro Leu Val Arg Glu Val Leu His
225 230 235 240

His Tyr Pro Leu Gly Ser Arg Val Thr Tyr Lys Gly Gln Glu Phe Glu
245 250 255

Ile Leu Ser Ile Glu Ala Ala Asp Met Asp Asn Leu Ile Arg Ile Glu
260 265 270

Leu Gln Asn Asp Phe Ser Tyr Leu Ile Glu Gln Asn Pro Val Leu Tyr
275 280 285

Phe Gln Asn Leu Ala Glu Ile Arg Gln Val Leu His Leu Ser Arg Ser
290 295 300

Glu Ile Val Glu Arg Glu Glu Gln Pro Glu Glu Glu Trp Thr Leu Phe
305 310 315 320

Ser Phe Met Asp Glu Gly Thr Glu Asp Asn Glu Lys Glu Pro Glu Ile
325 330 335

Val Phe Glu Ser Thr Asp Lys Val Val Thr Leu Asp Ser Gln Pro Ala
340 345 350

Gln Val Ser Glu Thr Ile Ser Glu Ser Val Pro Glu Thr Lys Glu Val
355 360 365

Ile Glu Ala Glu Gln Ala Ile Ala Val Asp Phe Ser Phe Pro Glu Asp
370 375 380

Leu Thr Asn Phe Tyr Pro Lys Thr Ala Arg Asp Lys Val Val Ala Asn
385 390 395 400

Leu Val Ala Ile Arg Leu Val Lys Glu Leu Glu Ser Ala Asn Gln Ser
405 410 415

Ala Thr Pro Asn Glu Gln Glu Ile Leu Ala Lys Tyr Val Gly Trp Gly
420 425 430

Gly Leu Ala Asn Glu Phe Phe Asp Glu Tyr Asn Pro Lys Phe Ser Lys
435 440 445

Glu Arg Glu Glu Leu Lys Thr Leu Val Ser Asp Lys Glu Tyr Ser Asp
450 455 460

GBS patentin.ST25

Met Lys Gln Ser Ser Leu Thr Ala Tyr Tyr Thr Asp Pro Leu Leu Ile
465 470 475 480

Arg Gln Met Trp Ser Lys Leu Glu Gln Asp Gly Phe Ser Gly Gly Lys
485 490 495

Ile Leu Asp Pro Ser Met Gly Thr Gly Asn Phe Phe Ala Ala Met Pro
500 505 510

Ala His Leu Arg Glu Lys Ser Glu Leu Cys Gly Val Glu Leu Asp Thr
515 520 525

Ile Thr Gly Ala Ile Ala Lys Gln Leu His Ser Asn Val His Ile Glu
530 535 540

Val Lys Gly Phe Glu Thr Val Ala Phe Asn Asp Asn Ser Phe Asp Leu
545 550 555 560

Val Ile Ser Asn Val Pro Phe Ala Asn Ile Arg Ile Ala Asp Asn Gln
565 570 575

Tyr Asp Lys Pro Tyr Met Ile His Asp Tyr Phe Val Lys Lys Ser Leu
580 585 590

Asp Leu Val His Asp Gly Gly Gln Val Ala Ile Ile Ser Ser Thr Gly
595 600 605

Thr Met Asp Lys Arg Thr Glu Asn Ile Leu Gln Asp Ile Arg Glu Thr
610 615 620

Thr Asp Phe Leu Gly Gly Val Arg Leu Pro Asp Thr Ala Phe Lys Ala
625 630 635 640

Ile Ala Gly Thr Ser Val Thr Thr Asp Met Leu Phe Phe Gln Lys His
645 650 655

Leu Asn Lys Gly Tyr Gln Ala Asp Asp Ile Ala Phe Ser Gly Ser Val
660 665 670

Arg Tyr Asp Lys Asp Glu Arg Ile Trp Leu Asn Pro Tyr Phe Asp Gly
675 680 685

Glu Tyr Asn Ala Gln Val Leu Gly Arg Tyr Glu Ile Lys Asn Phe Asn
690 695 700

Gly Gly Thr Leu Ser Val Lys Glu Thr Thr Asp Asn Leu Ile Ala Ser
705 710 715 720

Val Arg Glu Ala Leu Gln His Val Lys Ala Pro Arg Val Ile Asp Lys
725 730 735

GBS patentin.ST25

Thr Glu Val Met Ile Asn Ser Asp Val Ile Ala Arg Gln Val Ile Asp
740 745 750

Thr Thr Ile Pro Pro Glu Ile Arg Glu Asn Leu Glu Gln Tyr Ser Tyr
755 760 765

Gly Tyr Lys Gly Ser Thr Ile Tyr Tyr Arg Asp Asn Lys Gly Ile Arg
770 775 780

Val Gly Thr Lys Thr Glu Glu Ile Ser Tyr Tyr Val Asp Asp Glu Gly
785 790 795 800

Asn Phe Gln Ala Trp Glu Ser Lys His Ser Gln Lys Gln Ile Asp Arg
805 810 815

Phe Asn Asn Leu Glu Val Thr Asp Ser Thr Ala Leu Asp Val Tyr Val
820 825 830

Thr Glu Glu Pro Ala Lys Arg Gly Gln Phe Lys Gly Tyr Phe Lys Lys
835 840 845

Ala Val Phe Tyr Glu Ala Pro Leu Ser Glu Lys Glu Val Ala Arg Ile
850 855 860

Lys Gly Met Val Asp Ile Arg Asn Ala Tyr Gln Glu Val Ile Ala Ile
865 870 875 880

Gln Arg Asn Tyr Asp Tyr Asp Lys Asn Glu Phe Asn Arg Leu Leu Gly
885 890 895

Asn Leu Asn Arg Thr Tyr Asp Ser Phe Val Lys Arg Tyr Gly Phe Leu
900 905 910

Asn Ser Pro Val Asn Arg Asn Leu Phe Asp Ser Asp Asp Lys Tyr Ser
915 920 925

Leu Leu Ala Ser Leu Glu Asp Glu Ser Leu Asp Pro Ser Gly Lys Thr
930 935 940

Val Ile Tyr Thr Lys Ser Leu Ala Phe Glu Lys Ala Leu Val Arg Pro
945 950 955 960

Glu Lys Met Val Lys Glu Val Ser Thr Ala Leu Asp Ala Leu Asn Ser
965 970 975

Ser Leu Ala Asp Gly Arg Gly Val Asp Phe Asp Tyr Met Ala Ser Ile
980 985 990

Tyr Gln Thr Ala Ser Lys Ala Ala Leu Ile Glu Glu Leu Gly Asp Gln
995 1000 1005

GBS patentin.ST25

Ile Ile Pro Asp Pro Glu Ser Tyr Leu Lys Gly Gln Leu Thr Tyr
1010 1015 1020

Val Ser Arg Gln Glu Phe Leu Ser Gly Asp Ile Val Thr Lys Leu
1025 1030 1035

Glu Val Met Asp Leu Leu Leu Lys Gln Asp Asn His Asp Phe Asn
1040 1045 1050

Trp Ala His Tyr Gly Asn Leu Leu Glu Ser Val Arg Pro Ala Arg
1055 1060 1065

Val Met Leu Ala Asp Ile Asp Tyr Arg Ile Gly Ser Arg Trp Ile
1070 1075 1080

Pro Leu Ala Val Tyr Gly Lys Phe Val Gln Glu Ala Phe Met Gly
1085 1090 1095

Lys Asn Tyr Asp Leu Thr Ala Thr Glu Val Glu Glu Val Leu Ser
1100 1105 1110

Val Ser Pro Ile Asp Gly Thr Met Glu Phe Arg Thr Arg Phe Ala
1115 1120 1125

Tyr Thr Tyr Ser Thr Ala Thr Asp Arg Ser Leu Gly Val Ala Gly
1130 1135 1140

Ser Arg Tyr Asp Ser Gly Arg Lys Ile Phe Glu Asn Leu Leu Asn
1145 1150 1155

Ser Asn Gln Pro Thr Ile Thr Lys Gln Ile Gln Glu Gly Asp Lys
1160 1165 1170

Lys Lys Asn Val Thr Asp Val Glu Lys Thr Thr Val Leu Arg Ala
1175 1180 1185

Lys Glu Ala Gln Ile Gln Asp Leu Phe Gln Asp Phe Val Ala Ser
1190 1195 1200

Tyr Pro Glu Ala Gln Gln Met Ile Glu Asp Thr Tyr Asn Ser Leu
1205 1210 1215

Tyr Asn Arg Thr Val Ser Lys Val Tyr Asp Gly Ser Arg Leu Glu
1220 1225 1230

Ile Asp Gly Leu Ala Gln Asn Ile Ser Leu Arg Pro His Gln Lys
1235 1240 1245

Asn Ala Ile Gln Arg Ile Val Glu Glu Lys Arg Ala Leu Leu Ala
1250 1255 1260

GBS patentin.ST25

His Glu Val Gly Ser Gly Lys Thr Leu Thr Ile Leu Gly Ala Gly
1265 1270 1275

Phe Lys Leu Lys Glu Leu Gly Met Val His Lys Pro Leu Tyr Val
1280 1285 1290

Val Pro Ser Ser Leu Thr Ala Gln Phe Gly Gln Glu Ile Met Lys
1295 1300 1305

Phe Phe Pro Thr Lys Lys Val Tyr Val Thr Thr Lys Lys Asp Phe
1310 1315 1320

Ala Lys Ala Arg Arg Lys Gln Phe Val Ser Arg Ile Ile Thr Gly
1325 1330 1335

Asp Tyr Asp Ala Ile Val Ile Gly Asp Ser Gln Phe Glu Lys Ile
1340 1345 1350

Pro Met Ser Gln Glu Lys Gln Val Thr Tyr Ile Gln Asp Lys Leu
1355 1360 1365

Glu Gln Leu Arg Glu Ile Lys Gln Gly Ser Asp Ser Asp Tyr Thr
1370 1375 1380

Val Lys Glu Ala Glu Arg Ser Ile Lys Gly Leu Glu Asn Gln Leu
1385 1390 1395

Glu Glu Leu Gln Lys Leu Asp Arg Asp Thr Phe Ile Glu Phe Glu
1400 1405 1410

Asn Leu Gly Ile Asp Phe Leu Phe Val Asp Glu Ala His His Phe
1415 1420 1425

Lys Asn Ile Arg Pro Ile Thr Gly Leu Gly Asn Val Ala Gly Ile
1430 1435 1440

Thr Asn Thr Thr Ser Lys Lys Asn Val Asp Met Glu Met Lys Val
1445 1450 1455

Arg Gln Ile Gln Ala Glu Tyr Gly Asp Arg Asn Val Val Phe Ala
1460 1465 1470

Thr Gly Thr Pro Val Ser Asn Ser Ile Ser Glu Leu Tyr Thr Met
1475 1480 1485

Met Asn Tyr Ile Gln Pro Asp Val Leu Glu Arg Tyr Gln Val Ser
1490 1495 1500

Asn Phe Asp Ser Trp Val Gly Ala Phe Gly Asn Ile Glu Asn Ser
1505 1510 1515

GBS patentin.ST25

Met Glu Leu Ala Pro Thr Gly Asp Lys Tyr Gln Pro Lys Lys Arg
1520 1525 1530

Phe Lys Lys Phe Val Asn Leu Pro Glu Leu Met Arg Ile Tyr Lys
1535 1540 1545

Glu Thr Ala Asp Ile Gln Thr Ser Asp Met Leu Asp Leu Pro Val
1550 1555 1560

Pro Glu Ala Thr Val Ile Ala Val Glu Ser Glu Leu Thr Glu Ala
1565 1570 1575

Gln Lys Asn Tyr Leu Glu Glu Leu Val Asp Arg Ser Asp Ala Ile
1580 1585 1590

Lys Ser Gly Ser Val Asp Pro Ser Val Asp Asn Met Leu Lys Val
1595 1600 1605

Ile Gly Glu Ala Arg Lys Leu Ala Ile Asp Met Arg Leu Ile Asp
1610 1615 1620

Pro Ala Tyr Thr Leu Ser Asp Asn Gln Lys Ile Met Gln Val Val
1625 1630 1635

Asp Asn Val Glu Arg Ile Tyr Arg Glu Gly Lys Gly Asp Lys Ala
1640 1645 1650

Thr Gln Met Ile Phe Ser Asp Ile Gly Thr Pro Lys Ser Lys Glu
1655 1660 1665

Glu Gly Phe Asp Val Tyr Asn Glu Leu Lys Ala Leu Leu Val Asp
1670 1675 1680

Arg Gly Ile Pro Lys Glu Glu Ile Ala Phe Val His Asp Ala Asn
1685 1690 1695

Thr Asp Glu Lys Lys Asn Ser Leu Ser Arg Lys Val Asn Ser Gly
1700 1705 1710

Glu Val Arg Ile Leu Met Ala Ser Thr Glu Lys Gly Gly Thr Gly
1715 1720 1725

Leu Asn Val Gln Ala Arg Met Lys Ala Val His His Leu Asp Val
1730 1735 1740

Pro Trp Arg Pro Ser Asp Ile Gln Gln Arg Asn Gly Arg Leu Ile
1745 1750 1755

Arg Gln Gly Asn Gln His Gln Asn Val Glu Ile Tyr His Tyr Ile
1760 1765 1770

GBS patentin.ST25

Thr	Lys 1775	Gly	Ser	Phe	Asp	Asn 1780	Tyr	Leu	Trp	Ala	Thr 1785	Gln	Glu	Asn
Lys	Leu 1790	Arg	Tyr	Ile	Lys	Gln 1795	Ile	Met	Thr	Ser	Lys 1800	Asp	Pro	Val
Arg	Ser 1805	Ala	Glu	Asp	Ile	Asp 1810	Glu	Gln	Thr	Met	Thr 1815	Ala	Ser	Asp
Phe	Lys 1820	Ala	Leu	Ala	Thr	Gly 1825	Asn	Pro	Tyr	Leu	Lys 1830	Leu	Lys	Met
Glu	Leu 1835	Glu	Asn	Glu	Leu	Thr 1840	Val	Leu	Glu	Asn	Gln 1845	Lys	Arg	Ala
Phe	Asn 1850	Arg	Ser	Lys	Asp	Glu 1855	Tyr	Arg	His	Thr	Ile 1860	Ser	Tyr	Cys
Glu	Lys 1865	Asn	Leu	Pro	Val	Met 1870	Glu	Lys	Arg	Leu	Arg 1875	Gln	Tyr	Asp
Arg	Asp 1880	Ile	Glu	Lys	Ser	Gln 1885	Ala	Thr	Lys	Asn	Gln 1890	Glu	Phe	Ile
Met	Arg 1895	Phe	Asp	Asn	Gln	Thr 1900	Ile	Asp	Asn	Arg	Ser 1905	Glu	Ala	Gly
Asp	Tyr 1910	Leu	Arg	Lys	Leu	Ile 1915	Thr	Tyr	Asn	Arg	Ser 1920	Glu	Thr	Lys
Glu	Val 1925	Arg	Thr	Leu	Ala	Thr 1930	Phe	Arg	Gly	Phe	Glu 1935	Leu	Lys	Met
Ala	Thr 1940	Arg	Ser	Pro	Gly	Glu 1945	Pro	Leu	Ser	Asp	Met 1950	Val	Ser	Leu
Thr	Ile 1955	Ser	Gly	Asp	Asn	Gln 1960	Tyr	Ser	Val	Ser	Leu 1965	Asp	Leu	Lys
Ser	Asp 1970	Val	Gly	Thr	Ile	Gln 1975	Arg	Ile	Asn	Asn	Ala 1980	Ile	Asp	His
Ile	Leu 1985	Glu	Asp	Lys	Glu	Lys 1990	Thr	Glu	Glu	Met	Thr 1995	Asn	Asn	Leu
Lys	Asp 2000	Lys	Leu	Ala	Val	Ala 2005	Arg	Val	Glu	Val	Glu 2010	Lys	Val	Phe
Ala	Lys 2015	Glu	Glu	Glu	Tyr	Gln 2020	Leu	Val	Lys	Ala	Lys 2025	Tyr	Asp	Val

GBS patentin.ST25

Leu Ala Pro Leu Val Glu Arg Glu Ala Asp Leu Glu Glu Ile Asp
2030 2035 2040

Val Ala Leu Ser Gln Phe Ser Ser Ser Asp Pro Cys Leu Lys Lys
2045 2050 2055

Asp Gln Gln Leu Val Leu Asp Ile
2060 2065

<210> 311

<211> 1634

<212> PRT

<213> Streptococcus agalactiae

<400> 311

Met Thr Thr Lys Cys Asn His His Phe Leu Ile Asn Gln Glu Lys Gly
1 5 10 15

Glu Lys Tyr Val Phe Arg Lys Ser Lys Gln Tyr Arg Thr Leu Cys Ser
20 25 30

Val Ala Leu Gly Thr Val Val Met Ala Phe Val Ala Leu Ala Gly Pro
35 40 45

Met Val Gln Ala Asp Glu Val Gly Arg Thr Val Ala Thr Ser Val Gln
50 55 60

Thr Glu Thr Asn Pro Ala Thr Asn Leu Lys Glu Asn Gln Pro Ser Pro
65 70 75 80

Ile Ala Glu Gln Lys Asp Ser Leu Ala Ala Thr Gly Gln Ser Thr Gly
85 90 95

Thr Val Thr Val Thr Val Pro His Asp Lys Val Thr Gln Ala Val Asp
100 105 110

Lys Ala Lys Thr Glu Gly Ile Lys Ala Val Gln Asp Lys Pro Met Asp
115 120 125

Leu Gly Asn Thr Val Ser Ala Ala Glu Thr Ser Gln Gln Leu Lys Lys
130 135 140

Ala Glu Glu Asp Ala Thr Asn Gln Thr Thr Thr Ile Ser Lys Thr Val
145 150 155 160

Glu Ile Tyr Lys Ser Asp Lys Ala Thr Tyr Glu Ala Glu Lys Lys Trp
165 170 175

GBS patentin.ST25

Val Glu Lys Arg Asn Glu Glu Leu Thr Ala Ala Tyr Asp Lys Ala Glu
180 185 190

Gln Thr Gly Thr Gly Leu Asn His Ser Val Asp Thr Thr Val Ser Glu
195 200 205

Leu Lys Ser Gln Asp Gln Asn Ala His Val Thr Val Asn Thr Gln Thr
210 215 220

Val Lys Ser Gly Asp Gly Thr Ser Val Ser Gly Tyr Gln Glu Tyr Val
225 230 235 240

Lys Ser Val Ala Ala Ile Asp Lys Lys Asn Lys Ala Asn Leu Ala Asp
245 250 255

Tyr Arg Thr Lys Lys Gln Ala Ala Asp Ala Val Val Ala Lys Asn Gln
260 265 270

Leu Ile Gln Lys Glu Asn Glu Ala Gly Leu Ala Lys Ala Lys Ala Glu
275 280 285

Asn Glu Ala Ile Asp Arg Arg Asn Lys Glu Gly Gln Lys Ala Val Asp
290 295 300

Glu Ala Asn Lys Ala Gly Gln Ala Ala Val Glu Gln Ala Asn Gln Glu
305 310 315 320

Lys Gln Lys Gln Ala Ala Asn Arg Ala Phe Glu Ile Ala Thr Ile Thr
325 330 335

Lys Arg Asn Lys Glu Arg Glu Glu Val Ala Lys Lys Glu Asn Ala Ala
340 345 350

Ile Asp Ala Tyr Asn Ala Lys Glu Trp Ile Arg Tyr Lys Arg Asp Leu
355 360 365

Ala Asn Ile Ser Lys Gly Glu Glu Gly Tyr Ile Ser Glu Ala Leu Ala
370 375 380

Gln Ala Leu Asp Leu Asn His Gly Glu Pro Gln Val Lys His Gly Ala
385 390 395 400

Gly Thr Arg Asn Pro Asp Arg Ile Ile Ser Lys Gly Asp Ala Met Leu
405 410 415

Gly Gly Tyr Ser Asn Ile Leu Asp Ser Thr Gly Phe Phe Val Tyr Asn
420 425 430

His Phe Lys Thr Gly Glu Thr Leu Asn Phe Thr Tyr Gln Asn Leu Lys
435 440 445

GBS patentin.ST25

His Ala Arg Phe Asp Gly Lys Lys Ile Thr Ala Ile Thr Tyr Asp Ile
450 455 460

Thr Asn Leu Val Ser Pro Thr Gly Thr Asn Ala Val Gln Leu Val Val
465 470 475 480

Pro Asn Asp Pro Thr Glu Gly Phe Ile Ala Tyr Arg Asn Asp Gly Ala
485 490 495

Gly Asn Trp Arg Thr Asp Lys Met Glu Phe Arg Val Lys Ala Arg Tyr
500 505 510

Phe Leu Glu Asp Gly Ser Gln Val Thr Phe Thr Lys Glu Lys Pro Gly
515 520 525

Val Phe Thr His Ser Ser Leu Asn His Asn Asp Ile Gly Leu Glu Tyr
530 535 540

Val Lys Asp Ser Ser Gly Lys Phe Val Pro Ile His Gly Ser Ser Val
545 550 555 560

Gln Val Thr Asn Glu Gly Leu Ala Arg Ser Leu Gly Ser Asn Arg Ala
565 570 575

Ser Asp Leu Lys Leu Pro Glu Glu Trp Asp Thr Thr Ser Ser Arg Tyr
580 585 590

Ala Tyr Lys Gly Ala Ile Val Ser Thr Val Thr Ser Gly Asn Ile Tyr
595 600 605

Thr Val Thr Phe Gly Gln Gly Asp Met Pro Thr Gln Val Gly Gly Lys
610 615 620

Thr Tyr Trp Phe Ala Leu Asn Thr Leu Pro Val Ala Lys Thr Val Thr
625 630 635 640

Pro Tyr Asn Pro Lys Thr His Val Arg Pro Gln Leu Asp Pro Val Pro
645 650 655

Glu Pro Ile Lys Val Thr Pro Glu Thr Tyr Thr Pro Lys Ile Phe Thr
660 665 670

Pro Glu Lys Pro Val Thr Phe Thr Pro Lys Ser Val Glu Lys Val Pro
675 680 685

Gln Pro Ser Leu Thr Leu Thr Lys Val Thr Leu Pro Thr Asn Leu Lys
690 695 700

Leu Glu Pro Leu Pro Lys Ala Pro Gln Lys Pro Thr Val His Tyr His
705 710 715 720

GBS Patentin.ST25

Asp Tyr Leu Leu Thr Thr Thr Pro Ala Ile Ala Lys Glu Val Met Asn
725 730 735

Val Asp Lys Val Asn Leu His Gly Lys Gln Val Ala Lys Asp Ser Thr
740 745 750

Val Ile Tyr Pro Leu Thr Val Asp Val Leu Ser Pro Asn Arg Ser Lys
755 760 765

Ile Thr Ser Leu Ile Phe Glu Asp Tyr Leu Pro Ala Gly Tyr Ala Phe
770 775 780

Asp Met Thr Lys Thr Gln Ala Glu Asn Ser Asp Tyr Asp Leu Thr Phe
785 790 795 800

Asp Lys Asn Lys Asn Phe Val Thr Leu Lys Ala Lys Asp Ser Leu Leu
805 810 815

Gln Thr Leu Asn Lys Glu Leu Asn Lys Ser Tyr Gln Leu Ser Ala Pro
820 825 830

Lys Leu Tyr Gly Ser Val Gln Asn Asp Gly Ala Thr Tyr Ser Asn Ser
835 840 845

Tyr Lys Leu Leu Ile Asn Lys Asp Thr Pro Asn Thr Tyr Thr Val Ile
850 855 860

Ser Asn Val Val Arg Ile Arg Thr Pro Gly Asp Gly Glu Thr Thr Ser
865 870 875 880

Arg Ile Arg Pro Lys Lys Asp Asn Glu Asn Ala Asp Gly Val Leu Ile
885 890 895

Asn Asp Thr Val Val Ala Leu Ser Thr Thr Asn His Tyr Arg Leu Thr
900 905 910

Trp Asp Leu Asp Gln Tyr Lys Gly Asp Thr Ser Ser Lys Asp Thr Ile
915 920 925

Ala Arg Gly Phe Leu Phe Val Asp Asp Tyr Pro Glu Glu Ala Leu Asp
930 935 940

Leu Val Asp Lys Gly Thr Val Ile Thr Thr Leu Asp Gly Lys Ala Val
945 950 955 960

Ser Gly Ile Ser Val Tyr Ser Tyr Thr Ser Leu Asp Lys Ala Pro Lys
965 970 975

Glu Leu Gln Asp Lys Leu Ala Arg Ala Asn Ile Ser Pro Lys Gly Ala
980 985 990

GBS patentin.ST25

Phe Gln Val Phe Glu Pro Asp Asn His Gln Ala Phe Tyr Asp Thr Tyr
995 1000 1005

Val Lys Thr Gly Gln Ser Leu Ala Leu Leu Thr Lys Met Lys Val
1010 1015 1020

Lys Asp Ser Leu Tyr Gly Gln Thr Val Arg Tyr Lys Asn Lys Ala
1025 1030 1035

Tyr Gln Val Asp Phe Gly Asn Gly Tyr Glu Thr Lys Glu Val Val
1040 1045 1050

Asn Thr Val Val His Pro Glu Pro Lys Lys Gln Asn Leu Asn Lys
1055 1060 1065

Asp Lys Val Asp Ile Asn Gly Lys Ala Met Leu Val Gly Ser Gln
1070 1075 1080

Asn Phe Tyr Thr Leu Ser Trp Asp Leu Asp Gln Tyr Arg Gly Leu
1085 1090 1095

Gln Ala Asp Lys Ser Gln Ile Ala Gln Gly Phe Tyr Phe Val Asp
1100 1105 1110

Asp Tyr Pro Glu Asp Val Leu Leu Pro Asp Thr Lys Ala Ile Gln
1115 1120 1125

Ile Met Thr Lys Asp Gly Lys Ala Val Lys Gly Met Glu Ile Lys
1130 1135 1140

Thr Tyr His Gln Leu Ser Asp Ala Pro Lys Glu Leu Gln Ala Ala
1145 1150 1155

Leu Ala Lys Arg Asn Ile Thr Pro Lys Gly Ala Phe Gln Val Phe
1160 1165 1170

Met Pro Lys Asp Pro Gln Ala Phe Tyr Lys Ala Tyr Val Thr Thr
1175 1180 1185

Gly Gln Asn Leu Thr Ile Val Asn Pro Met Thr Val Arg Glu Ala
1190 1195 1200

Val Tyr Asn Ser Gly Lys Ser Tyr Asp Asn Val Ala Tyr Gln Val
1205 1210 1215

Asp Phe Gly Gln Ala Tyr Glu Thr Asn Ile Val Thr Asn His Val
1220 1225 1230

Pro Thr Val Asn Pro His Lys Ser Asn Thr Asn Lys Glu Gly Val
1235 1240 1245

GBS patentin.ST25

Ser Ile Glu Gly Lys Thr Val Leu Pro Asn Thr Val Asn Tyr Tyr
1250 1255 1260

Lys Ile Val Leu Asp Tyr Ser Gln Tyr Lys Asn Met Ile Val Thr
1265 1270 1275

Asp Asp Val Leu Val Lys Gly Phe Tyr Met Val Asp Asp Tyr Pro
1280 1285 1290

Glu Glu Ala Leu Thr Pro His Pro Asp Gly Thr Gln Val Met Asp
1295 1300 1305

Gln Asn Gly Lys Phe Val Arg Gly Leu Ser Val Arg Thr Tyr Ala
1310 1315 1320

Ser Leu Ala Asp Ala Pro Lys Ala Val Gln Glu Ala Met Lys Ser
1325 1330 1335

Arg Asn Phe Ile Pro Lys Gly Ala Ile Gln Val Phe Gln Ala Asp
1340 1345 1350

Asp Pro Lys Thr Phe Phe Glu Thr Tyr Val Lys Thr Gly Gln Lys
1355 1360 1365

Leu Val Val Thr Thr Pro Met Thr Val Lys Asn Glu Arg Ile Gln
1370 1375 1380

Thr Gly Gly Gln Tyr Glu Asn Thr Ala Tyr Gln Ile Asp Phe Gly
1385 1390 1395

Ile Ala Tyr Val Thr Glu Thr Val Val Asn Asn Val Pro Lys Leu
1400 1405 1410

Glu Pro Gln Lys Asp Val Val Ile Asp Leu Ser Gln Lys Asp Lys
1415 1420 1425

Ser Leu Asn Gly Lys Ala Ile Ala Leu Asp Gln Val Phe Asn Tyr
1430 1435 1440

Arg Leu Val Gly Ser Leu Ile Pro Arg Asn Arg Ala Thr Ala Leu
1445 1450 1455

Val Glu Tyr Ser Phe Lys Asp Asp Tyr Asp Glu Lys His Asp Glu
1460 1465 1470

Tyr Lys Gly Val Tyr Lys Ala Tyr Thr Leu Arg Asp Val Thr Leu
1475 1480 1485

Lys Asp Gly Thr Val Leu Lys Gln Gly Thr Glu Val Thr Lys Tyr
1490 1495 1500

GBS patentin.ST25

Thr Leu Gln Ser Val Asp Lys Ala Lys Gly Thr Ile Ala Ile Arg
1505 1510 1515

Phe Asp Thr Ala Phe Leu Glu Asn Ile Ala Asp Glu Ser Glu Phe
1520 1525 1530

Gln Ala Glu Leu Tyr Leu Gln Met Lys Arg Ile Ala Ser Gly Asp
1535 1540 1545

Val Glu Asn Thr Val Ile His Ser Val Asn Gly Tyr Asn Ile Arg
1550 1555 1560

Ser Asn Thr Val Lys Thr Thr Thr Pro Gln Pro Glu Ser Pro Thr
1565 1570 1575

Pro Asp Asn Pro Pro Ser Pro Gln Pro Pro Val Pro Thr Thr Glu
1580 1585 1590

Ser Pro Val Gln Ala Ser Val Leu Pro Ser Thr Gly Glu Ser Gln
1595 1600 1605

Ser Leu Leu Ala Leu Ile Gly Gly Gly Leu Leu Leu Gly Leu Ala
1610 1615 1620

Tyr Gly Leu Ser Lys Arg Lys Lys Glu Lys Asn
1625 1630

<210> 312

<211> 702

<212> PRT

<213> streptococcus agalactiae

<400> 312

Met Ala Asn Asn Asn Phe Tyr Asn Arg Asp Pro Phe Gly Asn Met Asp
1 5 10 15

Asp Ile Phe Asn Ser Leu Met Gly Asn Met Gly Gly Tyr Asn Ser Glu
20 25 30

Asn Lys Arg Tyr Leu Ile Asn Gly Arg Glu Val Thr Pro Glu Glu Phe
35 40 45

Ser Gln Tyr Arg Gln Thr Gly Lys Leu Pro Gly Gln Glu Leu Asn Asn
50 55 60

Gln Asn Thr Pro Thr Asn Gln Val Ser Ala Asp Ser Val Leu Thr Lys
65 70 75 80

GBS patentin.ST25

Leu Gly Thr Asn₈₅ Leu Thr Asp Gln Ala Arg₉₀ Gln His Leu Leu Asp₉₅ Pro

Val Ile Gly Arg₁₀₀ Asn Lys Glu Ile Gln₁₀₅ Glu Thr Ala Glu Ile₁₁₀ Leu Ala

Arg Arg Thr₁₁₅ Lys Asn Asn Pro Val₁₂₀ Leu Val Gly Asp Ala₁₂₅ Gly Val Gly

Lys Thr Ala Val Ile Glu Gly₁₃₅ Leu Ala Gln Ala Ile₁₄₀ Ile Asn Gly Asp

Val₁₄₅ Pro Ala Ala Ile Lys₁₅₀ Asn Lys Glu Ile Ile₁₅₅ Ser Ile Asp Ile Ser₁₆₀

Ser Leu Glu Ala Gly₁₆₅ Thr Gln Tyr Arg Gly₁₇₀ Ser Phe Glu Glu Asn₁₇₅ Ile

Gln Asn Ile Ile₁₈₀ Lys Glu Val Lys₁₈₅ Thr Gly Asn Ile Ile₁₉₀ Leu Phe

Phe Asp Glu Ile His Gln Ile Leu₂₀₀ Gly Ala Gly Ser Thr₂₀₅ Gly Gly Asp

Ser Gly₂₁₀ Ser Lys Gly Leu Ala₂₁₅ Asp Ile Leu Lys Pro₂₂₀ Ala Leu Ser Arg

Gly₂₂₅ Glu Leu Thr Val Ile₂₃₀ Gly Ala Thr Thr Gln₂₃₅ Asp Glu Tyr Arg Asn₂₄₀

Thr Ile Leu Lys Asn₂₄₅ Ala Ala Leu Ala Arg₂₅₀ Arg Phe Asn Glu Val₂₅₅ Lys

Val Asn Ala Pro₂₆₀ Ser Ala Gln Asp Thr₂₆₅ Phe Asn Ile Leu Met₂₇₀ Gly Ile

Arg Asn Leu₂₇₅ Tyr Glu Gln His His₂₈₀ Asn Val Val Leu Pro₂₈₅ Asp Ser Val

Leu Lys₂₉₀ Ala Ala Val Asp Leu₂₉₅ Ser Ile Gln Tyr Ile₃₀₀ Pro Gln Arg Ser

Leu₃₀₅ Pro Asp Lys Ala Ile₃₁₀ Asp Leu Ile Asp Met₃₁₅ Thr Ala Ala His Leu₃₂₀

Ala Ala Gln His Pro₃₂₅ Val Thr Asp Leu Lys₃₃₀ Ser Leu Glu Lys Glu₃₃₅ Ile

Ala Ala Gln Arg₃₄₀ Asp Lys Gln Glu Lys₃₄₅ Ala Val Asn Thr Glu₃₅₀ Asp Phe

GBS patentin.ST25

Glu Glu Ala Leu Lys Val Lys Thr Arg Ile Glu Glu Leu Gln Asn Gln
355 360 365

Ile Asp Asn His Thr Glu Gly Gln Lys Val Thr Ala Thr Ile Asn Asp
370 375 380

Ile Ala Met Ser Ile Glu Arg Leu Thr Gly Val Pro Val Ser Asn Met
385 390 395 400

Gly Ala Ser Asp Ile Glu Arg Leu Lys Glu Leu Gly Asn Arg Leu Lys
405 410 415

Gly Lys Val Ile Gly Gln Asn Asp Ala Val Glu Ala Val Ala Arg Ala
420 425 430

Ile Arg Arg Asn Arg Ala Gly Phe Asp Asp Gly Asn Arg Pro Ile Gly
435 440 445

Ser Phe Leu Phe Val Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Ala
450 455 460

Lys Gln Leu Ala Phe Asp Met Phe Gly Ser Lys Asp Ala Ile Val Arg
465 470 475 480

Leu Asp Met Ser Glu Tyr Asn Asp Arg Thr Ala Val Ser Lys Leu Ile
485 490 495

Gly Ala Thr Ala Gly Tyr Val Gly Tyr Asp Asp Asn Ser Asn Thr Leu
500 505 510

Thr Glu Arg Ile Arg Arg Asn Pro Tyr Ser Ile Val Leu Leu Asp Glu
515 520 525

Ile Glu Lys Ala Asp Pro Gln Val Ile Thr Leu Leu Leu Gln Val Leu
530 535 540

Asp Asp Gly Arg Leu Thr Asp Gly Gln Gly Asn Thr Ile Asn Phe Lys
545 550 555 560

Asn Thr Val Ile Ile Ala Thr Ser Asn Ala Gly Phe Gly Asn Glu Ala
565 570 575

Phe Thr Gly Asp Ser Asp Lys Asp Leu Lys Ile Met Glu Arg Ile Ser
580 585 590

Pro Tyr Phe Arg Pro Glu Phe Leu Asn Arg Phe Asn Gly Val Ile Glu
595 600 605

Phe Ser His Leu Ser Lys Asp Asp Leu Asn Glu Ile Val Asp Leu Met
610 615 620

GBS patentin.ST25

Leu Asp Glu Val Asn Gln Thr Ile Gly Lys Lys Gly Ile Asp Leu Val
625 630 635 640

Val Asp Glu Asn Val Lys Ser His Leu Ile Asp Leu Gly Tyr Asp Glu
645 650 655

Ala Met Gly Val Arg Pro Leu Arg Arg Val Ile Glu Gln Glu Ile Arg
660 665 670

Asp Arg Ile Thr Asp Tyr Tyr Leu Asp His Thr Asp Val Lys His Leu
675 680 685

Lys Ala Asn Leu Gln Asp Gly Gln Ile Val Ile Ser Glu Arg
690 695 700

<210> 313

<211> 314

<212> PRT

<213> Streptococcus agalactiae

<400> 313

Met Gly Arg Phe Lys Glu Leu Leu Glu Ser Lys Lys Ala Leu Ile Leu
1 5 10 15

His Gly Ala Leu Gly Thr Glu Leu Glu Ser Arg Gly Cys Asp Val Ser
20 25 30

Gly Lys Leu Trp Ser Asp Lys Tyr Leu Ile Glu Asp Pro Ala Ala Ile
35 40 45

Gln Thr Ile His Glu Asp Tyr Ile Arg Ala Gly Ala Asp Ile Val Thr
50 55 60

Thr Ser Thr Tyr Gln Ala Thr Leu Gln Gly Leu Ala Gln Val Gly Val
65 70 75 80

Ser Glu Ser Gln Ala Glu Asp Leu Ile Arg Leu Thr Val Gln Leu Ala
85 90 95

Lys Ala Val Arg Glu Gln Val Trp Lys Ser Leu Thr Lys Glu Glu Lys
100 105 110

Ser Glu Arg Ile Tyr Pro Leu Ile Ser Gly Asp Val Gly Pro Tyr Ala
115 120 125

Ala Phe Leu Ala Asp Gly Ser Glu Tyr Thr Gly Leu Tyr Asp Ile Tyr
130 135 140

GBS patentin.ST25

Lys Glu Gly Leu Lys Asn Phe His Arg His Arg Ile Glu Leu Leu Leu
145 150 155 160

Asp Glu Gly Val Asp Leu Leu Ala Leu Glu Thr Ile Pro Asn Ala Gln
165 170 175

Glu Ala Glu Ala Leu Ile Glu Leu Leu Val Glu Asp Phe Pro Gln Val
180 185 190

Glu Ala Tyr Met Ser Phe Thr Ser Gln Asp Gly Lys Thr Ile Ser Asp
195 200 205

Gly Ser Ala Val Ala Gly Leu Ala Lys Ala Ile Asp Val Ser Pro Gln
210 215 220

Val Val Ala Leu Gly Ile Asn Cys Ser Ser Pro Ser Leu Val Ala Asp
225 230 235 240

Phe Leu Gln Ala Ile Ala Glu Gln Thr Asp Lys Pro Leu Val Thr Tyr
245 250 255

Pro Asn Ser Gly Glu Ile Tyr Asp Gly Ala Ser Gln Ser Trp Gln Ser
260 265 270

Ser Arg Asp His Ser His Thr Leu Leu Glu Asn Thr Ser Asp Trp Gln
275 280 285

Lys Leu Gly Ala Gln Val Val Gly Gly Cys Cys Arg Thr Arg Pro Ala
290 295 300

Asp Ile Ala Asp Leu Ser Glu His Leu Thr
305 310

<210> 314

<211> 390

<212> PRT

<213> Streptococcus agalactiae

<400> 314

Met Lys Ile Gly Ile Asp Lys Ile Gly Phe Ala Thr Ser Gln Tyr Val
1 5 10 15

Leu Glu Met Thr Asp Leu Ala Ile Ala Arg Gln Val Asp Pro Glu Lys
20 25 30

Phe Ser Lys Gly Leu Leu Leu Asp Ser Leu Ser Ile Thr Pro Val Thr
35 40 45

GBS patentin.ST25

Glu Asp Ile Val Thr Leu Ala Ala Ser Ala Ala Asn Asp Ile Leu Ser
50 55 60

Asp Glu Asp Lys Glu Thr Ile Asp Met Val Ile Val Ala Thr Glu Ser
65 70 75 80

Ser Ile Asp Gln Ser Lys Ala Ala Ser Val Tyr Val His Gln Leu Leu
85 90 95

Glu Ile Gln Pro Phe Ala Arg Ser Phe Glu Met Lys Glu Ala Cys Tyr
100 105 110

Ser Ala Thr Ala Ala Leu Asp Tyr Ala Lys Leu His Val Glu Lys His
115 120 125

Pro Asp Ser Lys Val Leu Val Ile Ala Ser Asp Ile Ala Lys Tyr Gly
130 135 140

Ile Lys Ser Thr Gly Glu Ser Thr Gln Gly Ala Gly Ser Ile Ala Met
145 150 155 160

Leu Ile Ser Gln Asn Pro Ser Ile Leu Glu Leu Lys Glu Asp Arg Leu
165 170 175

Ala Gln Thr Arg Asp Ile Met Asp Phe Trp Arg Pro Asn Tyr Ser Asp
180 185 190

Val Pro Tyr Val Asn Gly Met Phe Ser Thr Lys Gln Tyr Leu Asp Met
195 200 205

Leu Lys Thr Thr Trp Lys Glu Tyr Gln Lys Arg Phe Asn Thr Ser Leu
210 215 220

Ser Asp Tyr Ala Ala Phe Cys Phe His Ile Pro Phe Pro Lys Leu Ala
225 230 235 240

Leu Lys Gly Phe Asn Lys Ile Leu Asp Asn Asn Leu Asp Glu Gln Lys
245 250 255

Lys Ala Glu Leu Gln Glu Asn Phe Glu His Ser Ile Thr Tyr Ser Lys
260 265 270

Lys Ile Gly Asn Cys Tyr Thr Gly Ser Leu Tyr Leu Gly Leu Leu Ser
275 280 285

Leu Leu Glu Asn Ser Gln Asn Leu Lys Ala Gly Asp Gln Ile Ala Phe
290 295 300

Phe Ser Tyr Gly Ser Gly Ala Val Ala Glu Ile Phe Thr Gly Gln Leu
305 310 315 320

GBS patentin.ST25

Val Asp Gly Tyr Gln Asn Lys Leu Gln Ser Asp Arg Met Asp Gln Leu
325 330 335

Asn Lys Arg Gln Lys Ile Thr Val Thr Glu Tyr Glu Lys Leu Phe Phe
340 345 350

Glu Lys Thr Ile Leu Asp Glu Asn Gly Asn Ala Asn Phe Asn Thr Tyr
355 360 365

Arg Thr Gly Thr Phe Ser Leu Asp Ser Ile Cys Glu His Gln Arg Ile
370 375 380

Tyr Lys Lys Ile Asn Asn
385 390

<210> 315

<211> 304

<212> PRT

<213> Streptococcus agalactiae

<400> 315

Met Lys Ser Ala Tyr Ile Phe Phe Asn Pro Lys Ser Gly Lys Asp Glu
1 5 10 15

Gln Ala Leu Ala Gln Glu Val Lys Ser Tyr Leu Ile Glu His Asp Phe
20 25 30

Gln Asp Asp Tyr Val Arg Ile Ile Thr Pro Ser Ser Val Glu Glu Ala
35 40 45

Val Ala Leu Ala Lys Lys Ala Ser Glu Asp His Ile Asp Leu Val Ile
50 55 60

Pro Leu Gly Gly Asp Gly Thr Ile Asn Lys Ile Cys Gly Gly Val Tyr
65 70 75 80

Ala Gly Gly Ala Tyr Pro Thr Ile Gly Leu Val Pro Ala Gly Thr Val
85 90 95

Asn Asn Phe Ser Lys Ala Leu Asn Ile Pro Gln Glu Arg Asn Leu Ala
100 105 110

Leu Glu Asn Leu Leu Asn Gly His Val Lys Ser Val Asp Ile Cys Lys
115 120 125

Val Asn Asp Asp Tyr Met Ile Ser Ser Leu Thr Leu Gly Leu Leu Ala
130 135 140

GBS patentin.ST25

Asp Ile Ala Ala Asn Val Thr Ser Glu Met Lys Arg Lys Leu Gly Pro
145 150 155 160

Phe Ala Phe Val Gly Asp Ala Tyr Arg Ile Leu Lys Arg Asn Arg Ser
165 170 175

Tyr Ser Ile Thr Leu Ala Tyr Asp Asn Asn Val Arg Ser Leu Arg Thr
180 185 190

Arg Leu Leu Leu Ile Thr Met Thr Asn Ser Ile Ala Gly Met Pro Ala
195 200 205

Phe Ser Pro Glu Ala Thr Ile Asp Asp Gly Leu Phe Arg Val Tyr Thr
210 215 220

Met Glu His Ile His Phe Phe Lys Leu Leu Leu His Leu Arg Gln Phe
225 230 235 240

Arg Lys Gly Asp Phe Ser Gln Ala Lys Glu Ile Lys His Phe His Thr
245 250 255

Asn Asn Leu Thr Ile Ser Thr Phe Lys Arg Lys Lys Ser Ala Ile Pro
260 265 270

Lys Val Arg Ile Asp Gly Asp Pro Gly Asp Gln Leu Pro Val Lys Val
275 280 285

Glu Val Ile Pro Lys Ala Leu Lys Phe Ile Ile Pro Asn Ser Leu Pro
290 295 300

<210> 316

<211> 284

<212> PRT

<213> Streptococcus agalactiae

<400> 316

Met Thr Thr Phe Thr Ala Lys Phe Ile Asp Gln Glu Trp Glu Val Pro
1 5 10 15

Val Glu Ser Gly Arg Tyr His Met Ile Val Gly Glu Phe Cys Pro Tyr
20 25 30

Ala Gln Arg Pro Gln Ile Ala Arg Gln Leu Leu Gly Leu Asp Lys His
35 40 45

Ile Ser Ile Ser Phe Val Asp Asp Val Pro Ser Asp Ile Gly Leu Ile
50 55 60

GBS patentin.ST25

Phe Ser Gln Pro Glu Gln Val Thr Gly Ala Lys Ser Leu Arg Asp Ile
65 70 75 80

Tyr His Leu Thr Asp Pro Thr Tyr Lys Gly Pro Tyr Thr Ile Pro Ile
85 90 95

Leu Ile Asp Lys Thr Asp Asn Arg Ile Val Cys Lys Glu Ser Ala Asp
100 105 110

Met Leu Arg Leu Phe Thr Thr Asp Phe Ser Asp Leu His Gln Glu Asp
115 120 125

Ala Pro Val Leu Phe Ser Gln Glu Thr Ala Ser Leu Ile Asp Asn Asp
130 135 140

Ile Lys Asp Ile Asn Asn Asn Phe Gln Ser Leu Met Tyr Lys Leu Ala
145 150 155 160

Phe Leu Asp Lys Gln Ala Asp Tyr Asp Thr Tyr Ser Lys Glu Phe Phe
165 170 175

Thr Phe Leu Asp Gln Lys Glu His Leu Leu Gly Gln Arg Pro Phe Leu
180 185 190

Leu Gly Asp Asn Leu Ser Glu Val Asp Ile His Phe Phe Thr Pro Leu
195 200 205

Val Arg Trp Asp Ile Ala Gly Arg Asp Leu Leu Leu Leu Asn Gln Lys
210 215 220

Ala Leu Glu Asp Tyr Pro Asn Ile Phe Ser Trp Ala Lys Thr Leu Tyr
225 230 235 240

Asn Asp Phe Asn Leu Lys Thr Leu Thr Asn Pro Gln Ser Ile Lys Asn
245 250 255

Asn Tyr Tyr Leu Gly Lys Phe Gly Arg Ala Val Arg His His Thr Ile
260 265 270

Val Pro Thr Gly Pro Asn Met Val Lys Trp Glu Lys
275 280

<210> 317

<211> 690

<212> PRT

<213> Streptococcus agalactiae

<400> 317

Met Lys Lys Lys Ile Ile Leu Lys Ser Ser Val Leu Gly Leu Val Ala
 1 5 10 15

Gly Thr Ser Ile Met Phe Ser Ser Ala Phe Ala Asp Gln Val Gly Val
 20 25 30

Gln Val Ile Gly Val Asn Asp Phe His Gly Ala Leu Asp Asn Thr Gly
 35 40 45

Thr Ala Asn Met Pro Asp Gly Lys Val Thr Asn Ala Gly Thr Ala Ala
 50 55 60

Gln Leu Asp Ala Tyr Ile Asp Asp Ala Gln Lys Asp Phe Lys Gln Thr
 65 70 75 80

Asn Pro Asn Gly Glu Ser Ile Arg Val Gln Ala Gly Asp Met Val Gly
 85 90 95

Ala Ser Pro Ala Asn Ser Gly Leu Leu Gln Asp Glu Pro Thr Val Lys
 100 105 110

Thr Phe Asn Ala Met Asn Val Glu Tyr Gly Thr Leu Gly Asn His Glu
 115 120 125

Phe Asp Glu Gly Leu Ala Glu Tyr Asn Arg Ile Val Thr Gly Lys Ala
 130 135 140

Pro Ala Pro Asp Ser Asn Ile Asn Asn Ile Thr Lys Ser Tyr Pro His
 145 150 155 160

Glu Ala Ala Lys Gln Glu Ile Val Val Ala Asn Val Ile Asp Lys Val
 165 170 175

Asn Lys Gln Ile Pro Tyr Asn Trp Lys Pro Tyr Ala Ile Lys Asn Ile
 180 185 190

Pro Val Asn Asn Lys Ser Val Asn Val Gly Phe Ile Gly Ile Val Thr
 195 200 205

Lys Asp Ile Pro Asn Leu Val Leu Arg Lys Asn Tyr Glu Gln Tyr Glu
 210 215 220

Phe Leu Asp Glu Ala Glu Thr Ile Val Lys Tyr Ala Lys Glu Leu Gln
 225 230 235 240

Ala Lys Asn Val Lys Ala Ile Val Val Leu Ala His Val Pro Ala Thr
 245 250 255

Ser Lys Asp Asp Ile Ala Glu Gly Glu Ala Ala Glu Met Met Lys Lys
 260 265 270

GBS patentin.ST25

Val Asn Gln Leu Phe Pro Glu Asn Ser Val Asp Ile Val Phe Ala Gly
275 280 285

His Asn His Gln Tyr Thr Asn Gly Leu Val Gly Lys Thr Arg Ile Val
290 295 300

Gln Ala Leu Ser Gln Gly Lys Ala Tyr Ala Asp Val Arg Gly Val Leu
305 310 315 320

Asp Thr Asp Thr Gln Asp Phe Ile Glu Thr Pro Ser Ala Lys Val Val
325 330 335

Ala Val Ala Pro Gly Lys Lys Thr Gly Ser Ala Asp Ile Gln Ala Ile
340 345 350

Val Asp Gln Ala Asn Thr Ile Val Lys Gln Val Thr Glu Ala Lys Ile
355 360 365

Gly Thr Ala Glu Val Ser Gly Met Ile Thr Arg Ser Val Asp Gln Asp
370 375 380

Asn Val Ser Pro Val Gly Ser Leu Ile Thr Glu Ala Gln Leu Ala Ile
385 390 395 400

Ala Arg Lys Ser Trp Pro Asp Ile Asp Phe Ala Met Thr Asn Asn Gly
405 410 415

Gly Ile Arg Ala Asp Leu Leu Ile Lys Pro Asp Gly Thr Ile Thr Trp
420 425 430

Gly Ala Ala Gln Ala Val Gln Pro Phe Gly Asn Ile Leu Gln Val Val
435 440 445

Glu Ile Thr Gly Arg Asp Leu Tyr Lys Ala Leu Asn Glu Gln Tyr Asp
450 455 460

Gln Lys Gln Asn Phe Phe Leu Gln Ile Ala Gly Leu Arg Tyr Thr Tyr
465 470 475 480

Thr Asp Asn Lys Glu Gly Gly Glu Glu Thr Pro Phe Lys Val Val Lys
485 490 495

Ala Tyr Lys Ser Asn Gly Glu Glu Ile Asn Pro Asp Ala Lys Tyr Lys
500 505 510

Leu Val Ile Asn Asp Phe Leu Phe Gly Gly Gly Asp Gly Phe Ala Ser
515 520 525

Phe Arg Asn Ala Lys Leu Leu Gly Ala Ile Asn Pro Asp Thr Glu Val
530 535 540

GBS patentin.ST25

Phe Met Ala Tyr Ile Thr Asp Leu Glu Lys Ala Gly Lys Lys Val Ser
545 550 555 560

Val Pro Asn Asn Lys Pro Lys Ile Tyr Val Thr Met Lys Met Val Asn
565 570 575

Glu Thr Ile Thr Gln Asn Asp Gly Thr His Ser Ile Ile Lys Lys Leu
580 585 590

Tyr Leu Asp Arg Gln Gly Asn Ile Val Ala Gln Glu Ile Val Ser Asp
595 600 605

Thr Leu Asn Gln Thr Lys Ser Lys Ser Thr Lys Ile Asn Pro Val Thr
610 615 620

Thr Ile His Lys Lys Gln Leu His Gln Phe Thr Ala Ile Asn Pro Met
625 630 635 640

Arg Asn Tyr Gly Lys Pro Ser Asn Ser Thr Thr Val Lys Ser Lys Gln
645 650 655

Leu Pro Lys Thr Asn Ser Glu Tyr Gly Gln Ser Phe Leu Met Ser Val
660 665 670

Phe Gly Val Gly Leu Ile Gly Ile Ala Leu Asn Thr Lys Lys Lys His
675 680 685

Met Lys
690

<210> 318

<211> 579

<212> PRT

<213> Streptococcus agalactiae

<400> 318

Met Ala Tyr Ile Trp Ser Tyr Leu Lys Arg Tyr Pro Asn Trp Leu Trp
1 5 10 15

Leu Asp Leu Leu Gly Ala Met Leu Phe Val Thr Val Ile Leu Gly Met
20 25 30

Pro Thr Ala Leu Ala Gly Met Ile Asp Asn Gly Val Thr Lys Gly Asp
35 40 45

Arg Thr Gly Val Tyr Leu Trp Thr Phe Ile Met Phe Ile Phe Val Val
50 55 60

GBS patentin.ST25

Leu Gly Ile Ile Gly Arg Ile Thr Met Ala Tyr Ala Ser Ser Arg Leu
 65 70 75 80
 Thr Thr Thr Met Ile Arg Asp Met Arg Asn Asp Met Tyr Ala Lys Leu
 85 90 95
 Gln Glu Tyr Ser His His Glu Tyr Glu Gln Ile Gly Val Ser Ser Leu
 100 105 110
 Val Thr Arg Met Thr Ser Asp Thr Phe Val Leu Met Gln Phe Ala Glu
 115 120 125
 Met Ser Leu Arg Leu Gly Leu Val Thr Pro Met Val Met Ile Phe Ser
 130 135 140
 Val Val Met Ile Leu Ile Thr Ser Pro Ser Leu Ala Trp Leu Val Ala
 145 150 155 160
 Val Ala Met Pro Leu Leu Val Gly Val Val Leu Tyr Val Ala Ile Lys
 165 170 175
 Thr Lys Pro Leu Ser Glu Arg Gln Gln Thr Met Leu Asp Lys Ile Asn
 180 185 190
 Gln Tyr Val Arg Glu Asn Leu Thr Gly Leu Arg Val Val Arg Ala Phe
 195 200 205
 Ala Arg Glu Asn Phe Gln Ser Gln Lys Phe Gln Val Ala Asn Gln Arg
 210 215 220
 Tyr Thr Asp Thr Ser Thr Gly Leu Phe Lys Leu Thr Gly Leu Thr Glu
 225 230 235 240
 Pro Leu Phe Val Gln Ile Ile Ile Ala Met Ile Val Ala Ile Val Trp
 245 250 255
 Phe Ala Leu Asp Pro Leu Gln Arg Gly Ala Ile Lys Ile Gly Asp Leu
 260 265 270
 Val Ala Phe Ile Glu Tyr Ser Phe His Ala Leu Phe Ser Phe Leu Leu
 275 280 285
 Phe Ala Asn Leu Phe Thr Met Tyr Pro Arg Met Val Val Ser Ser His
 290 295 300
 Arg Ile Arg Glu Val Met Asp Met Pro Ile Ser Ile Asn Pro Asn Ala
 305 310 315 320
 Glu Gly Val Thr Asp Thr Lys Leu Lys Gly His Leu Glu Phe Asp Asn
 325 330 335

GBS patentin.ST25

Val Thr Phe Ala Tyr Pro Gly Glu Thr Glu ser Pro Val Leu His Asp
340 345 350

Ile Ser Phe Lys Ala Lys Pro Gly Glu Thr Ile Ala Phe Ile Gly Ser
355 360 365

Thr Gly Ser Gly Lys Ser Ser Leu Val Asn Leu Ile Pro Arg Phe Tyr
370 375 380

Asp Val Thr Leu Gly Lys Ile Leu Val Asp Gly Val Asp Val Arg Asp
385 390 395 400

Tyr Asn Leu Lys Ser Leu Arg Gln Lys Ile Gly Phe Ile Pro Gln Lys
405 410 415

D Ala Leu Leu Phe Thr Gly Thr Ile Gly Glu Asn Leu Lys Tyr Gly Lys
420 425 430

Ala Asp Ala Thr Ile Asp Asp Leu Arg Gln Ala Val Asp Ile Ser Gln
435 440 445

Ala Lys Glu Phe Ile Glu Ser His Gln Glu Ala Phe Glu Thr His Leu
450 455 460

Ala Glu Gly Gly Ser Asn Leu Ser Gly Gly Gln Lys Gln Arg Leu Ser
465 470 475 480

Ile Ala Arg Ala Val Val Lys Asp Pro Asp Leu Tyr Ile Phe Asp Asp
485 490 495

Ser Phe Ser Ala Leu Asp Tyr Lys Thr Asp Ala Thr Leu Arg Ala Arg
500 505 510

D Leu Lys Glu Val Thr Gly Asp Ser Thr Val Leu Ile Val Ala Gln Arg
515 520 525

Val Gly Thr Ile Met Asp Ala Asp Gln Ile Ile Val Leu Asp Glu Gly
530 535 540

Glu Ile Val Gly Arg Gly Thr His Ala Gln Leu Ile Glu Asn Asn Ala
545 550 555 560

Ile Tyr Arg Glu Ile Ala Glu Ser Gln Leu Lys Asn Gln Asn Leu Ser
565 570 575

Glu Gly Glu

<210> 319

GBS patentin.ST25

<211> 543

<212> PRT

<213> Streptococcus agalactiae

<400> 319

Met Lys Lys Gly Gln Val Asn Asp Thr Lys Gln Ser Tyr Ser Leu Arg
1 5 10 15
Lys Tyr Lys Phe Gly Leu Ala Ser Val Ile Leu Gly Pro Phe Ile Met
20 25 30
Val Thr Ser Pro Val Phe Ala Asp Gln Thr Thr Ser Val Gln Val Asn
35 40 45
Asn Gln Thr Gly Thr Ser Val Asp Ala Asn Asn Ser Ser Asn Glu Thr
50 55 60
Ser Ala Ser Ser Val Ile Thr Ser Asn Asn Asp Ser Val Gln Ala Ser
65 70 75 80
Asp Lys Val Val Asn Ser Gln Asn Thr Ala Thr Lys Asp Ile Thr Thr
85 90 95
Pro Leu Val Glu Thr Lys Pro Met Val Glu Lys Thr Leu Pro Glu Gln
100 105 110
Gly Asn Tyr Val Tyr Ser Lys Glu Thr Glu Val Lys Asn Thr Pro Ser
115 120 125
Lys Ser Ala Pro Val Ala Phe Tyr Ala Lys Lys Gly Asp Lys Val Phe
130 135 140
Tyr Asp Gln Val Phe Asn Lys Asp Asn Val Lys Trp Ile Ser Tyr Lys
145 150 155 160
Ser Phe Cys Gly Val Arg Arg Tyr Ala Ala Ile Glu Ser Leu Asp Pro
165 170 175
Ser Gly Gly Ser Glu Thr Lys Ala Pro Thr Pro Val Thr Asn Ser Gly
180 185 190
Ser Asn Asn Gln Glu Lys Ile Ala Thr Gln Gly Asn Tyr Thr Phe Ser
195 200 205
His Lys Val Glu Val Lys Asn Glu Ala Lys Val Ala Ser Pro Thr Gln
210 215 220
Phe Thr Leu Asp Lys Gly Asp Arg Ile Phe Tyr Asp Gln Ile Leu Thr
225 230 235 240

GBS patentin.ST25

Ile Glu Gly Asn Gln Trp Leu Ser Tyr Lys Ser Phe Asn Gly Val Arg
245 250 255

Arg Phe Val Leu Leu Gly Lys Ala Ser Ser Val Glu Lys Thr Glu Asp
260 265 270

Lys Glu Lys Val Ser Pro Gln Pro Gln Ala Arg Ile Thr Lys Thr Gly
275 280 285

Arg Leu Thr Ile Ser Asn Glu Thr Thr Thr Gly Phe Asp Ile Leu Ile
290 295 300

Thr Asn Ile Lys Asp Asp Asn Gly Ile Ala Ala Val Lys Val Pro Val
305 310 315 320

Trp Thr Glu Gln Gly Gly Gln Asp Asp Ile Lys Trp Tyr Thr Ala Val
325 330 335

Thr Thr Gly Asp Gly Asn Tyr Lys Val Ala Val Ser Phe Ala Asp His
340 345 350

Lys Asn Glu Lys Gly Leu Tyr Asn Ile His Leu Tyr Tyr Gln Glu Ala
355 360 365

Ser Gly Thr Leu Val Gly Val Thr Gly Thr Lys Val Thr Val Ala Gly
370 375 380

Thr Asn Ser Ser Gln Glu Pro Ile Glu Asn Gly Leu Ala Lys Thr Gly
385 390 395 400

Val Tyr Asn Ile Ile Gly Ser Thr Glu Val Lys Asn Glu Ala Lys Ile
405 410 415

Ser Ser Gln Thr Gln Phe Thr Leu Glu Lys Gly Asp Lys Ile Asn Tyr
420 425 430

Asp Gln Val Leu Thr Ala Asp Gly Tyr Gln Trp Ile Ser Tyr Lys Ser
435 440 445

Tyr Ser Gly Val Arg Arg Tyr Ile Pro Val Lys Lys Leu Thr Thr Ser
450 455 460

Ser Glu Lys Ala Lys Asp Glu Ala Thr Lys Pro Thr Ser Tyr Pro Asn
465 470 475 480

Leu Pro Lys Thr Gly Thr Tyr Thr Phe Thr Lys Thr Val Asp Val Lys
485 490 495

Ser Gln Pro Lys Val Ser Ser Pro Val Glu Phe Asn Phe Gln Lys Gly
500 505 510

GBS patentin.ST25

Glu Lys Ile His Tyr Asp Gln Val Leu Val Val Asp Gly His Gln Trp
515 520 525

Ile Ser Tyr Lys Ser Tyr Ser Gly Ile Arg Arg Tyr Ile Glu Ile
530 535 540

<210> 320

<211> 415

<212> PRT

<213> Streptococcus agalactiae

<400> 320

Met Glu Asn Trp Lys Phe Ala Leu Ser Ser Ile Leu Gly His Lys Met
1 5 10 15

Arg Ala Phe Leu Thr Met Leu Gly Ile Ile Ile Gly Val Ala Ser Val
20 25 30

Val Leu Ile Met Ala Leu Gly Lys Gly Met Lys Asp Ser Val Thr Asn
35 40 45

Glu Ile Thr Lys Ser Gln Lys Asn Leu Gln Ile Tyr Tyr Lys Thr Lys
50 55 60

Glu Asp Gln Lys Asn Glu Asp Asn Phe Gly Ala Gln Gly Ala Phe Met
65 70 75 80

Gln Gly Ser Asp Thr Asn Arg Lys Glu Pro Ile Ile Gln Glu Ser Trp
85 90 95

Leu Lys Lys Ile Ala Lys Glu Val Asp Gly Val Ser Gly Tyr Tyr Val
100 105 110

Thr Asn Gln Thr Asn Ala Pro Val Ala Tyr Leu Glu Lys Lys Ala Lys
115 120 125

Thr Val Asn Ile Thr Gly Val Asn Arg Thr Tyr Leu Gly Ile Lys Lys
130 135 140

Phe Lys Ile Lys Ser Gly Arg Gln Phe Gln Glu Glu Asp Tyr Asn Gln
145 150 155 160

Phe Ser Arg Val Ile Leu Leu Glu Glu Lys Leu Ala Gln Arg Leu Phe
165 170 175

Gln Thr Asn Glu Ala Ala Leu Asn Lys Val Val Thr Val Lys Asn Lys
180 185 190

GBS patentin.ST25

Ser Tyr Leu Val Val Gly Val Tyr Ser Asp Pro Glu Ala Gly Ser Gly
195 200 205

Leu Tyr Gly Ser Asn Ser Asp Gly Asn Ala Ile Leu Thr Asn Thr Gln
210 215 220

Leu Ala Ser Glu Phe Gly Ala Lys Glu Ala Glu Asn Ile Tyr Phe His
225 230 235 240

Leu Asn Asp Val Ser Gln Ser Asn Arg Ile Gly Lys Glu Ile Gly Lys
245 250 255

Arg Leu Thr Asp Ile Ser His Ala Lys Asp Gly Tyr Tyr Asp Asn Phe
260 265 270

Asp Met Thr Ser Ile Val Lys Ser Ile Asn Thr Gln Val Gly Ile Met
275 280 285

Thr Gly Val Ile Gly Ala Ile Ala Ala Ile Ser Leu Leu Val Gly Gly
290 295 300

Ile Gly Val Met Asn Ile Met Leu Val Ser Val Thr Glu Arg Thr Arg
305 310 315 320

Glu Ile Gly Leu Arg Lys Ala Leu Gly Ala Thr Arg Arg Lys Ile Leu
325 330 335

Ala Gln Phe Leu Ile Glu Ser Met Val Leu Thr Ile Leu Gly Gly Leu
340 345 350

Ile Gly Leu Leu Leu Ala Tyr Gly Gly Thr Met Leu Ile Ala Asn Ala
355 360 365

Gln Asp Lys Ile Thr Pro Ser Val Ser Leu Asn Val Ala Ile Gly Ser
370 375 380

Leu Ile Phe Ser Ala Phe Ile Gly Ile Ile Phe Gly Leu Leu Pro Ala
385 390 395 400

Asn Lys Ala Ser Lys Leu Asn Pro Ile Asp Ala Leu Arg Tyr Glu
405 410 415

<210> 321

<211> 404

<212> PRT

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 321

Met Gln Tyr Ser Glu Ile Met Ile Arg Tyr Gly Glu Leu Ser Thr Lys
 1 5 10 15
 Lys Lys Asn Arg Met Arg Phe Ile Asn Lys Leu Lys Asn Asn Met Glu
 20 25 30
 His Val Leu Ser Ile Tyr Pro Asp Val Ser Val Lys Thr Asp Arg Asp
 35 40 45
 Arg Gly His Val Tyr Leu Asn Gly Thr Asp Tyr His Glu Val Ala Glu
 50 55 60
 Ser Leu Lys Glu Ile Phe Gly Ile Gln Ala Phe Ser Pro Ser Phe Lys
 65 70 75 80
 Val Glu Lys Asn Val Asp Thr Leu Val Lys Ala Val Gln Glu Ile Met
 85 90 95
 Thr Ser Val Tyr Lys Asp Gly Met Thr Phe Lys Ile Thr Ala Lys Arg
 100 105 110
 Ser Asp His Ser Phe Glu Leu Asp Ser Arg Ala Leu Asn His Thr Leu
 115 120 125
 Gly Asp Ala Val Phe Ser Val Leu Pro Asn Ile Lys Ala Gln Met Lys
 130 135 140
 Gln Pro Asp Ile Asn Leu Lys Val Glu Ile Arg Asp Glu Ala Ala Tyr
 145 150 155 160
 Ile Ser Tyr Glu Asn Ile Arg Gly Ala Gly Gly Leu Pro Val Gly Thr
 165 170 175
 Ser Gly Lys Gly Met Leu Met Leu Ser Gly Gly Ile Asp Ser Pro Val
 180 185 190
 Ala Gly Tyr Leu Ala Leu Lys Arg Gly Val Asp Ile Glu Ala Val His
 195 200 205
 Phe Ala Ser Pro Pro Tyr Thr Ser Pro Gly Ala Leu Lys Lys Ala His
 210 215 220
 Asp Leu Thr Arg Lys Leu Thr Lys Phe Gly Gly Asn Ile Gln Phe Ile
 225 230 235 240
 Glu Val Pro Phe Thr Glu Ile Gln Glu Glu Ile Lys Glu Lys Ala Pro
 245 250 255
 Glu Ala Tyr Leu Met Thr Leu Thr Arg Arg Phe Met Met Arg Ile Thr
 260 265 270

GBS patentin.ST25

Asp Arg Ile Arg Glu Asn Arg Asn Gly Leu Val Ile Ile Asn Gly Glu
275 280 285

Ser Leu Gly Gln Val Ala Ser Gln Thr Leu Glu Ser Met Gln Ala Ile
290 295 300

Asn Ala Val Thr Ala Thr Pro Ile Ile Arg Pro Val Val Thr Met Asp
305 310 315 320

Lys Leu Glu Ile Ile Asp Ile Ala Gln Lys Ile Asp Thr Phe Asp Ile
325 330 335

Ser Ile Gln Pro Phe Glu Asp Cys Cys Thr Ile Phe Ala Pro Asp Arg
340 345 350

Pro Lys Thr Asn Pro Lys Ile Lys Asn Thr Glu Gln Tyr Glu Lys Arg
355 360 365

Met Asp Val Glu Gly Leu Val Glu Arg Ala Val Ala Gly Ile Met Val
370 375 380

Thr Thr Ile Gln Pro Gln Ala Asp Ser Asp Asp Val Asp Asp Leu Ile
385 390 395 400

Asp Asp Leu Leu

<210> 322

<211> 119

<212> PRT

<213> Streptococcus agalactiae

<400> 322

Met Ala Arg Val Lys Gly Gly Val Val Ser Arg Lys Arg Arg Lys Arg
1 5 10 15

Val Leu Lys Leu Ala Lys Gly Tyr Tyr Gly Ala Lys His Ile Leu Phe
20 25 30

Arg Thr Ala Lys Glu Gln Val Met Asn Ser Tyr Tyr Tyr Ala Tyr Arg
35 40 45

Asp Arg Arg Gln Lys Lys Arg Asp Phe Arg Lys Leu Trp Ile Thr Arg
50 55 60

Ile Asn Ala Ala Ala Arg Met Asn Gly Leu Ser Tyr Ser Gln Leu Met
65 70 75 80

GBS patentin.ST25

His Gly Leu Lys Leu Ala Glu Ile Glu Val Asn Arg Lys Met Leu Ala
85 90 95

Asp Leu Ala Val Asn Asp Ala Ala Ala Phe Thr Ala Leu Ala Asp Ala
100 105 110

Ala Lys Ala Lys Leu Gly Lys
115

<210> 323

<211> 341

<212> PRT

<213> Streptococcus agalactiae

<400> 323

Met Phe Lys Ala Ser Lys Lys Leu Val Gln Lys Asn Lys Ser Asn His
1 5 10 15

Phe Trp Leu Val Phe Phe Ile Thr Leu Ile Leu Phe Leu Ile Gly Cys
20 25 30

Tyr Ala Ser Leu Arg Phe Gly Ala Ile Asn Phe Lys Thr Ser Asp Leu
35 40 45

Ile Thr Val Leu Lys Asn Pro Leu Lys Asn Ser Asn Ala Gln Asp Val
50 55 60

Ile Phe Asp Ile Arg Leu Pro Arg Ile Ile Ala Ala Ile Leu Val Gly
65 70 75 80

Ala Ala Met Ser Gln Ala Gly Ala Ile Met Gln Gly Val Thr Arg Asn
85 90 95

Ala Ile Ala Asp Pro Gly Leu Leu Gly Ile Asn Ala Gly Ala Gly Leu
100 105 110

Ala Leu Val Val Ala Tyr Ala Phe Leu Gly Ser Met His Tyr Ser Thr
115 120 125

Ile Leu Ile Val Cys Leu Leu Gly Ser Val Ile Ser Tyr Leu Leu Val
130 135 140

Phe Thr Leu Ser Tyr Thr Lys Gln Lys Gly Tyr His Gln Leu Arg Leu
145 150 155 160

Ile Leu Ala Gly Ala Met Ile Ser Thr Leu Phe Thr Ser Val Gly Gln
165 170 175

GBS patentin.ST25

Val Val Thr Leu Tyr Phe Lys Leu Asn Arg Thr Val Ile Gly Trp Gln
180 185 190

Ala Gly Gly Leu Ser Gln Ile Asn Trp Lys Met Leu Ile Ile Ile Ala
195 200 205

Pro Ile Ile Ile Leu Gly Leu Leu Ile Ser Gln Leu Leu Ala His Gln
210 215 220

Leu Thr Ile Leu Ser Leu Asn Glu Ser Val Ala Lys Ala Leu Gly Gln
225 230 235 240

Lys Thr Gln Leu Met Thr Ala Phe Leu Leu Leu Ile Val Leu Phe Leu
245 250 255

ser Ala Ser Ser Val Ala Leu Ile Gly Thr Val Ser Phe Ile Gly Leu
260 265 270

Ile Ile Pro His Phe Ile Lys Leu Phe Ile Pro Lys Asp Tyr Arg Leu
275 280 285

Leu Leu Pro Leu Ile Gly Phe Ser Gly Ala Thr Phe Met Ile Trp Val
290 295 300

Asp Leu Ser Ser Arg Ile Ile Asn Pro Pro Ser Glu Thr Pro Ile Ser
305 310 315 320

Ser Ile Ile Ser Ile Val Gly Leu Pro Cys Phe Leu Trp Leu Ile Arg
325 330 335

Lys Gly Lys Asn Leu
340

<210> 324

<211> 188

<212> PRT

<213> Streptococcus agalactiae

<400> 324

Met Ile Lys Arg Pro Ile His Leu Ser His Asp Phe Leu Ala Glu Val
1 5 10 15

Ile Asp Lys Glu Ala Ile Thr Leu Asp Ala Thr Met Gly Asn Gly Asn
20 25 30

Asp Thr Val Phe Leu Ala Lys Ser Ser Lys Lys Val Tyr Ala Phe Asp
35 40 45

GBS patentin.ST25

Ile Gln Glu Glu Ala Ile Ala Lys Thr Lys Ala Lys Leu Thr Glu Gln
50 55 60

Gly Ile Ser Asn Ala Glu Leu Ile Leu Asp Gly His Glu Asn Leu Glu
65 70 75 80

Gln Tyr Val His Thr Pro Leu Arg Ala Ala Ile Phe Asn Leu Gly Tyr
85 90 95

Leu Pro Ser Ala Asp Lys Thr Val Ile Thr Lys Pro His Thr Thr Ile
100 105 110

Lys Ala Ile Lys Asn Val Leu Asp Ile Leu Glu Val Gly Gly Arg Leu
115 120 125

Ser Leu Met Val Tyr Tyr Gly His Asp Gly Gly Lys Ser Glu Lys Asp
130 135 140

Ala Val Ile Ala Phe Val Glu Gln Leu Pro Gln Asn Asn Phe Ala Thr
145 150 155 160

Met Leu Tyr Gln Pro Leu Asn Gln Val Asn Thr Pro Pro Phe Leu Ile
165 170 175

Met Val Glu Lys Leu Gln Ser Tyr Glu Asn Glu Val
180 185

<210> 325

<211> 335

<212> PRT

<213> Streptococcus agalactiae

<400> 325

Met Arg Val His Ile Thr Ser Ile Tyr Gly Gln Ser Pro Arg Ser Ile
1 5 10 15

Ala Leu Ile Ser Gln Lys Leu Val Lys Asp Val Gly Arg Gln Leu Gly
20 25 30

Tyr Asp Glu Met Gly Ile Tyr Phe Tyr Asn Asp His Ala Glu Thr His
35 40 45

Gly Glu Arg Ser Thr Arg Met Asp Gly Ile Ile Ala Gly Leu Gly Arg
50 55 60

Gly Asp Ile Val Val Phe Gln Val Pro Thr Trp Asn Ser Thr Glu Phe
65 70 75 80

GBS patentin.ST25

Asp Glu Leu Phe Leu Asp Lys Leu Gln Ala Tyr Gly Ala Arg Ile Ile
85 90 95

Thr Phe Val His Asp Ile Val Pro Leu Met Phe Glu Ser Asn Phe Tyr
100 105 110

Leu Leu Asp Arg Val Ile Asp Met Tyr Asn Arg Ser Asp Val Val Ile
115 120 125

Leu Pro Thr Lys Ala Met His Asp Tyr Leu Ile Glu Lys Gly Met Thr
130 135 140

Thr Ser Lys Val Leu Tyr Gln Glu Val Trp Asp His Pro Val Asn Ile
145 150 155 160

Asp Leu Pro Arg Pro Glu Cys Gln Lys Val Leu Ser Phe Ala Gly Asp
165 170 175

Ile Gln Arg Phe Pro Phe Val Asn Asp Trp Lys Glu Asn Ile Pro Leu
180 185 190

Ile Tyr Tyr Gly Asp Gly Ser Arg Leu Asn Ser Glu Ala Asn Val His
195 200 205

Ala Gln Gly Trp Lys Asp Asp Val Glu Leu Met Leu Ser Leu Ser Lys
210 215 220

Arg Gly Gly Phe Gly Leu Cys Trp Ser Glu Asp Arg Glu Glu Leu Val
225 230 235 240

Glu Arg Arg Tyr Ser Arg Met Asn Ala Ser Tyr Lys Leu Ser Thr Phe
245 250 255

Leu Ala Ala Gly Leu Pro Ile Ile Ala Asn His Asp Ile Ser Ser Arg
260 265 270

Asp Phe Ile Lys Gln His Gly Leu Gly Phe Thr Val Glu Thr Leu Glu
275 280 285

Glu Ala Val Glu Lys Ile Asn Asn Met Glu Lys Glu Thr Tyr Asp Ser
290 295 300

Tyr Val Glu Asn Val Glu Lys Ile Ala Thr Leu Leu Arg Asn Gly Tyr
305 310 315 320

Ile Thr Lys Lys Leu Leu Ile Asp Ala Val His Met Leu Tyr Arg
325 330 335

<210> 326

<211> 1310

<212> PRT

<213> Streptococcus agalactiae

<400> 326

Met Ser Gln Lys Thr Phe Gly Lys Gln Leu Thr Val Val Asp Thr Lys
 1 5 10 15
 Ser Arg Val Lys Met His Lys Ser Gly Lys Asn Trp Val Arg Thr Val
 20 25 30
 Met Ser His Phe Asn Leu Phe Lys Ala Ile Lys Gly Arg Ala Thr Val
 35 40 45
 Glu Ala Asp Val Cys Ile Gln Asp Val Glu Lys Glu Asp Arg Leu Ser
 50 55 60
 Ser Gly Asn Leu Thr Tyr Leu Lys Gly Ile Leu Ala Ala Gly Ala Leu
 65 70 75 80
 Val Gly Gly Ala Ser Leu Thr Ser Arg Val Tyr Ala Asp Glu Thr Pro
 85 90 95
 Val Val Gln Glu Gln Ser Ser Ser Val Pro Thr Leu Ala Glu Gln Thr
 100 105 110
 Glu Val Thr Val Lys Thr Thr Thr Val Gln Asn His Gln Asp Gly Thr
 115 120 125
 Val Ser Lys Asn Ile Ile Asp Ser Asn Ser Val Ser Met Ser Glu Ser
 130 135 140
 Ala Ser Thr Ser Thr Ser Glu Ser Val Ser Met Ser Met Ser Gly Ser
 145 150 155 160
 Thr Leu Thr Ser Val Ser Glu Ser Val Ser Thr Ser Ala Leu Thr Ser
 165 170 175
 Ala Ser Glu Ser Ile Ser Thr Ser Ala Ser Glu Ser Val Ser Lys Ser
 180 185 190
 Thr Ser Ile Ser Glu Val Ser Asn Ile Leu Glu Thr Gln Ala Ser Leu
 195 200 205
 Thr Asp Lys Gly Arg Glu Ser Phe Ser Ala Asn Gln Ile Val Thr Glu
 210 215 220
 Ser Ser Leu Val Thr Asp Ala Gly Lys Asn Ala Ser Val Ser Ser Leu
 225 230 235 240

GBS patentin.ST25

Ile Glu Ile Thr Lys Pro Lys Ser Glu Leu Gln Thr Ser Lys Met Ser
245 250 255

Asn Glu Ser Leu Ile Thr Pro Glu Lys Ser Gln Val Met Ile Ala Ser
260 265 270

Asp Lys Thr Gly Asn Glu Ser Leu Thr Pro Thr Ile Arg Leu Lys Ser
275 280 285

Val Ile Gln Pro Arg Ser Met Asn Leu Met Thr Leu Ser Ser Glu Met
290 295 300

Asp Leu Ile Pro Leu Glu Glu Val Ser Asp Thr Glu Met Leu Gly Lys
305 310 315 320

D Asp Val Ser Ser Glu Leu Gln Lys Val Asn Ile Ala Leu Lys Asp Asn
325 330 335

Thr Leu Ser Glu Pro Gly Thr Val Lys Leu Asp Ser Ser Glu Asn Leu
340 345 350

Val Leu Asn Phe Ala Phe Ser Ile Ala Ser Val Asn Glu Gly Asp Val
355 360 365

Phe Thr Val Lys Leu Ser Asp Asn Leu Asp Thr Gln Gly Ile Gly Thr
370 375 380

Ile Leu Lys Val Gln Asp Ile Met Asp Glu Thr Gly Gln Leu Leu Ala
385 390 395 400

Thr Gly Ser Tyr Ser Pro Leu Thr His Asn Ile Thr Tyr Thr Trp Thr
405 410 415

D Arg Tyr Ala Ser Thr Leu Asn Asn Ile Lys Ala Arg Val Asn Met Pro
420 425 430

Val Trp Pro Asp Gln Arg Ile Ile Ser Lys Thr Thr Ser Asp Lys Gln
435 440 445

Cys Phe Thr Ala Thr Leu Asn Asn Gln Val Ala Ser Ile Glu Glu Arg
450 455 460

Val Gln Tyr Asn Ser Pro Ser Val Thr Glu His Thr Asn Val Lys Thr
465 470 475 480

Asn Val Arg Ser Arg Ile Met Lys Leu Asp Asp Glu Arg Gln Thr Glu
485 490 495

Thr Tyr Ile Thr Gln Ile Asn Pro Glu Gly Lys Glu Met Tyr Phe Ala
500 505 510

GBS patentin.ST25

ser Gly Leu Gly Asn Leu Tyr Thr Ile Ile Gly Ser Asp Gly Thr Ser
 515 520 525
 Gly Ser Pro Val Asn Leu Leu Asn Ala Glu Val Lys Ile Leu Lys Thr
 530 535 540
 Asn Ser Lys Asn Leu Thr Asp Ser Met Asp Gln Asn Tyr Asp Ser Pro
 545 550 555 560
 Glu Phe Glu Asp Val Thr Ser Gln Tyr Ser Tyr Thr Asn Asp Gly Ser
 565 570 575
 Lys Ile Thr Ile Asp Trp Lys Thr Asn Ser Ile Ser Ser Thr Thr Ser
 580 585 590
 Tyr Val Val Leu Val Lys Ile Pro Lys Gln Ser Gly Val Leu Tyr Ser
 595 600 605
 Thr Val Ser Asp Ile Asn Gln Thr Tyr Gly Ser Lys Tyr Ser Tyr Gly
 610 615 620
 His Thr Asn Ile Ser Gly Asp Ser Asp Ala Asn Ala Glu Ile Lys Leu
 625 630 635 640
 Leu Ser Glu Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
 645 650 655
 Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
 660 665 670
 Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
 675 680 685
 Ala Ser Thr Ser Ala Ser Thr Ser Thr Ser Thr Ser Ala Ser Thr Ser
 690 695 700
 Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
 705 710 715 720
 Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
 725 730 735
 Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
 740 745 750
 Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
 755 760 765
 Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Met Ser
 770 775 780

GBS patentin.ST25

Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser
785 790 795 800

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
805 810 815

Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
820 825 830

Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
835 840 845

Ala Ser Thr Ser Ala Ser Thr Ser Thr Ser Thr Ser Ala Ser Thr Ser
850 855 860

D Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
865 870 875 880

Ala Ser Thr Ser Pro Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
885 890 895

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
900 905 910

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
915 920 925

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
930 935 940

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
945 950 955 960

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
965 970 975

Ala Ser Thr Ser Thr Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
980 985 990

Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser
995 1000 1005

Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Ile
1010 1015 1020

Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser
1025 1030 1035

Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala
1040 1045 1050

GBS patentin.ST25

Ser Thr 1055 Ser Ala Ser Thr Ser 1060 Ala Ser Thr Ser Ala 1065 Ser Thr Ser
 Ala Ser 1070 Met Ser Ala Ser Thr 1075 Ser Ala Ser Thr Ser 1080 Ala Ser Thr
 Ser Ala 1085 Ser Thr Ser Ala Ser 1090 Thr Ser Ala Ser Thr 1095 Ser Ala Ser
 Thr Ser 1100 Ala Ser Thr Ser Ser 1105 Ser Thr Ser Ala Ser 1110 Thr Ser Ala
 Ser Thr 1115 Ser Ala Ser Thr Ser 1120 Ala Ser Met Ser Ala 1125 Ser Thr Ser
 Ala Ser 1130 Thr Ser Ala Ser Met 1135 Ser Ala Ser Thr Ser 1140 Ala Ser Thr
 Ser Ala 1145 Ser Thr Ser Ala Ser 1150 Met Ser Ala Ser Thr 1155 Ser Ser Ser
 Thr Ser 1160 Ala Ser Met Ser Ala 1165 Ser Thr Ser Ala Ser 1170 Met Ser Ala
 Ser Thr 1175 Ser Ala Ser Thr Ser 1180 Ala Ser Thr Ser Ala 1185 Ser Met Ser
 Ala Ser 1190 Thr Ser Ser Ser Thr 1195 Ser Ala Ser Met Ser 1200 Ala Ser Thr
 Ser Ala 1205 Ser Met Ser Ala Ser 1210 Thr Ser Ala Ser Thr 1215 Ser Ala Ser
 Thr Ser 1220 Ala Ser Met Ser Ala 1225 Ser Thr Ser Ala Ser 1230 Met Ser Ala
 Thr Thr 1235 Ser Ala Ser Thr Ser 1240 Val Ser Thr Ser Ala 1245 Ser Thr Ser
 Ala Ser 1250 Thr Ser Ala Ser Thr 1255 Ser Ser Ser Ser Ser 1260 Val Thr Ser
 Asn Ser 1265 Ser Lys Glu Lys Val 1270 Tyr Ser Ala Leu Pro 1275 Ser Thr Gly
 Asp Gln 1280 Asp Tyr Ser Val Thr 1285 Ala Thr Ala Leu Gly 1290 Leu Gly Leu
 Met Thr 1295 Gly Ala Thr Leu Leu 1300 Gly Arg Lys Lys Ser 1305 Lys Lys Asp

GBS patentin.ST25

Lys Asp
1310

<210> 327

<211> 663

<212> PRT

<213> Streptococcus agalactiae

<400> 327

Met Ile Asp Arg Lys Asp Thr Asn Arg Phe Lys Leu Val Ser Lys Tyr
1 5 10 15

Ser Pro Ser Gly Asp Gln Pro Gln Ala Ile Glu Thr Leu Val Asp Asn
20 25 30

Ile Glu Gly Gly Glu Lys Ala Gln Ile Leu Lys Gly Ala Thr Gly Thr
35 40 45

Gly Lys Thr Tyr Thr Met Ser Gln Val Ile Ala Gln Val Asn Lys Pro
50 55 60

Thr Leu Val Ile Ala His Asn Lys Thr Leu Ala Gly Gln Leu Tyr Gly
65 70 75 80

Glu Phe Lys Glu Phe Phe Pro Asp Asn Ala Val Glu Tyr Phe Val Ser
85 90 95

Tyr Tyr Asp Tyr Tyr Gln Pro Glu Ala Tyr Val Pro Ser Ser Asp Thr
100 105 110

Tyr Ile Glu Lys Asp Ser Ser Val Asn Asp Glu Ile Asp Lys Leu Arg
115 120 125

His Ser Ala Thr Ser Ser Leu Leu Glu Arg Asn Asp Val Ile Val Val
130 135 140

Ala Ser Val Ser Cys Ile Tyr Gly Leu Gly Ser Pro Lys Glu Tyr Ala
145 150 155 160

Asp Ser Val Val Ser Leu Arg Pro Gly Gln Glu Ile Ser Arg Asp Gln
165 170 175

Leu Leu Asn Asn Leu Val Asp Ile Gln Phe Glu Arg Asn Asp Ile Asp
180 185 190

Phe Gln Arg Gly Lys Phe Arg Val Arg Gly Asp Val Val Glu Val Phe
195 200 205

GBS patentin.ST25

Pro Ala Ser Arg Asp Glu His Ala Phe Arg Ile Glu Phe Phe Gly Asp
210 215 220

Glu Ile Asp Arg Ile Arg Glu Ile Glu Ser Leu Thr Gly Arg Val Leu
225 230 235 240

Gly Glu Val Glu His Leu Ala Ile Phe Pro Ala Thr His Phe Met Thr
245 250 255

Asn Asp Glu His Met Glu Glu Ala Ile Ser Lys Ile Gln Ala Glu Met
260 265 270

Glu Asn Gln Val Glu Leu Phe Glu Lys Glu Gly Lys Leu Ile Glu Ala
275 280 285

Gln Arg Ile Arg Gln Arg Thr Glu Tyr Asp Ile Glu Met Leu Arg Glu
290 295 300

Met Gly Tyr Thr Asn Gly Val Glu Asn Tyr Ser Arg His Met Asp Gly
305 310 315 320

Arg Ser Glu Gly Glu Pro Pro Phe Thr Leu Leu Asp Phe Phe Pro Glu
325 330 335

Asp Phe Leu Ile Met Ile Asp Glu Ser His Met Thr Met Gly Gln Ile
340 345 350

Lys Gly Met Tyr Asn Gly Asp Arg Ser Arg Lys Glu Met Leu Val Asn
355 360 365

Tyr Gly Phe Arg Leu Pro Ser Ala Leu Asp Asn Arg Pro Leu Arg Arg
370 375 380

Glu Glu Phe Glu Ser His Val His Gln Ile Val Tyr Val Ser Ala Thr
385 390 395 400

Pro Gly Asp Tyr Glu Met Glu Gln Thr Asp Thr Val Val Glu Gln Ile
405 410 415

Ile Arg Pro Thr Gly Leu Leu Asp Pro Glu Val Glu Val Arg Pro Ser
420 425 430

Met Gly Gln Met Asp Asp Leu Leu Gly Glu Ile Asn Leu Arg Thr Glu
435 440 445

Lys Gly Glu Arg Thr Phe Ile Thr Thr Leu Thr Lys Arg Met Ala Glu
450 455 460

Asp Leu Thr Asp Tyr Leu Lys Glu Met Gly Val Lys Val Lys Tyr Met
465 470 475 480

GBS patentin.ST25

His Ser Asp Ile Lys Thr Leu Glu Arg Thr Glu Ile Ile Arg Asp Leu
485 490 495

Arg Leu Gly Val Phe Asp Val Leu Ile Gly Ile Asn Leu Leu Arg Glu
500 505 510

Gly Ile Asp Val Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp
515 520 525

Lys Glu Gly Phe Leu Arg Asn Glu Arg Gly Leu Ile Gln Thr Ile Gly
530 535 540

Arg Ala Ala Arg Asn Ser Asn Gly His Val Ile Met Tyr Ala Asp Lys
545 550 555 560

Ile Thr Asp Ser Met Gln Arg Ala Met Asp Glu Thr Ala Arg Arg Arg
565 570 575

Arg Leu Gln Met Asp Tyr Asn Glu Lys His Gly Ile Val Pro Gln Thr
580 585 590

Ile Lys Lys Glu Ile Arg Asp Leu Ile Ala Ile Thr Lys Ser Asn Asp
595 600 605

Ser Asp Lys Pro Glu Lys Val Val Asp Tyr Ser Ser Leu Ser Lys Lys
610 615 620

Glu Arg Gln Ala Glu Ile Lys Ala Leu Gln Gln Gln Met Gln Glu Ala
625 630 635 640

Ala Glu Leu Leu Asp Phe Glu Leu Ala Ala Gln Ile Arg Asp Val Ile
645 650 655

Leu Glu Leu Lys Ala Ile Asp
660

<210> 328

<211> 727

<212> PRT

<213> streptococcus agalactiae

<400> 328

Met Lys His Lys Leu Lys Ala Phe Thr Leu Ala Leu Leu Ser Ile Phe
1 5 10 15

Phe Val Phe Gly Gly Lys Val Ser Ala Glu Thr Val Asn Ile Val Ser
20 25 30

GBS patentin.ST25

Asp Thr Ala Tyr Ala Pro Phe Glu Phe Lys Asp Ser Asp Gln Thr Tyr
 35 40 45
 Lys Gly Ile Asp Val Asp Ile Val Asn Glu Val Ala Lys Arg Ala Gly
 50 55 60
 Trp Asn Val Asn Met Thr Tyr Pro Gly Phe Asp Ala Ala Val Asn Ala
 65 70 75 80
 Val Gln Ser Gly Gln Ala Asp Ala Leu Met Ala Gly Thr Thr Val Thr
 85 90 95
 Glu Ala Arg Lys Lys Val Phe Asn Phe Ser Asp Thr Tyr Tyr Asp Thr
 100 105 110
 Ser Val Ile Leu Tyr Thr Lys Asn Asn Asn Lys Val Thr Asn Tyr Lys
 115 120 125
 Gln Leu Lys Gly Lys Val Val Gly Val Lys Asn Gly Thr Ala Ala Gln
 130 135 140
 Ser Phe Leu Glu Glu Asn Lys Ser Lys Tyr Gly Tyr Lys Val Lys Thr
 145 150 155 160
 Phe Asp Thr Ser Asp Leu Met Asn Asn Ser Leu Asp Ser Gly Ser Ile
 165 170 175
 Tyr Ala Ala Met Asp Asp Gln Pro Val Val Gln Phe Ala Ile Asn Gln
 180 185 190
 Gly Lys Ala Tyr Ala Ile Asn Met Glu Gly Glu Ala Val Gly Ser Phe
 195 200 205
 Ala Phe Ala Val Lys Lys Gly Ser Gly His Asp Asn Leu Ile Lys Glu
 210 215 220
 Phe Asn Thr Ala Phe Ala Gln Met Lys Ser Asp Gly Thr Tyr Asn Asp
 225 230 235 240
 Ile Met Asp Lys Trp Leu Gly Lys Asp Ala Thr Lys Thr Ser Gly Lys
 245 250 255
 Ala Thr Gly Asn Ala Asn Glu Lys Ala Thr Pro Val Lys Pro Ser Tyr
 260 265 270
 Lys Ile Val Ser Asp Ser Ser Phe Ala Pro Phe Glu Tyr Gln Asn Gly
 275 280 285
 Lys Gly Lys Tyr Thr Gly Phe Asp Met Glu Leu Ile Lys Lys Ile Ala
 290 295 300

GBS patentin.ST25

Lys Gln Gln Gly Phe Lys Leu Asp Ile Ser Asn Pro Gly Phe Asp Ala
305 310 315 320

Ala Leu Asn Ala Val Gln Ser Gly Gln Ala Asp Gly Val Ile Ala Gly
325 330 335

Ala Thr Ile Thr Glu Ala Arg Gln Lys Ile Phe Asp Phe Ser Asp Pro
340 345 350

Tyr Tyr Thr Ser Ser Val Ile Leu Ala Val Lys Lys Gly Ser Asn Val
355 360 365

Lys Ser Tyr Gln Asp Leu Lys Gly Lys Thr Val Gly Ala Lys Asn Gly
370 375 380

Thr Ala Ser Tyr Thr Trp Leu Ser Asp His Ala Asp Lys Tyr Asn Tyr
385 390 395 400

His Val Lys Ala Phe Asp Glu Ala Ser Thr Met Tyr Asp Ser Met Asn
405 410 415

Ser Gly Ser Ile Asp Ala Leu Met Asp Asp Glu Ala Val Leu Ala Tyr
420 425 430

Ala Ile Asn Gln Gly Arg Lys Phe Glu Thr Pro Ile Lys Gly Glu Lys
435 440 445

Ser Gly Asp Ile Gly Phe Ala Val Lys Lys Gly Ala Asn Pro Glu Leu
450 455 460

Ile Lys Met Phe Asn Asn Gly Leu Ala Ser Leu Lys Lys Ser Gly Glu
465 470 475 480

Tyr Asp Lys Leu Val Lys Lys Tyr Leu Ser Thr Ala Ser Thr Ser Ser
485 490 495

Asn Asp Lys Ala Ala Lys Pro Val Asp Glu Ser Thr Ile Leu Gly Leu
500 505 510

Ile Ser Asn Asn Tyr Lys Gln Leu Leu Ser Gly Ile Gly Thr Thr Leu
515 520 525

Ser Leu Thr Leu Ile Ser Phe Ala Ile Ala Met Val Ile Gly Ile Ile
530 535 540

Phe Gly Met Met Ser Val Ser Pro Ser Asn Thr Leu Arg Thr Ile Ser
545 550 555 560

Met Ile Phe Val Asp Ile Val Arg Gly Ile Pro Leu Met Ile Val Ala
565 570 575

GBS patentin.ST25

Ala Phe Ile Phe Trp Gly Ile Pro Asn Leu Ile Glu Ser Ile Thr Gly
580 585 590

His Gln Ser Pro Ile Asn Asp Phe Val Ala Ala Thr Ile Ala Leu Ser
595 600 605

Leu Asn Gly Gly Ala Tyr Ile Ala Glu Ile Val Arg Gly Gly Ile Glu
610 615 620

Ala Val Pro Ser Gly Gln Met Glu Ala Ser Arg Ser Leu Gly Ile Ser
625 630 635 640

Tyr Gly Lys Thr Met Gln Lys Val Ile Leu Pro Gln Ala Val Arg Leu
645 650 655

Met Leu Pro Asn Phe Ile Asn Gln Phe Val Ile Ser Leu Lys Asp Thr
660 665 670

Thr Ile Val Ser Ala Ile Gly Leu Val Glu Leu Phe Gln Thr Gly Lys
675 680 685

Ile Ile Ile Ala Arg Asn Tyr Gln Ser Phe Arg Met Tyr Ala Ile Leu
690 695 700

Ala Ile Met Tyr Leu Val Ile Ile Thr Leu Leu Thr Arg Leu Ala Lys
705 710 715 720

Arg Leu Glu Lys Arg Leu Lys
725

<210> 329

<211> 52

<212> PRT

<213> Streptococcus agalactiae

<400> 329

Met Gly Asp Lys Pro Ile Ser Phe Arg Asp Lys Asp Gly Asn Phe Val
1 5 10 15

Ser Ala Ala Asp Val Trp Asn Ala Glu Lys Leu Glu Glu Leu Phe Asn
20 25 30

Thr Leu Asn Pro Asn Arg Lys Leu Arg Leu Glu Arg Glu Lys Leu Ala
35 40 45

Lys Glu Lys Gly
50

GBS patentin.ST25

<210> 330

<211> 280

<212> PRT

<213> Streptococcus agalactiae

<400> 330

Met Glu Thr Tyr Thr Leu Ser Asn Thr Leu Asn Ile Pro Lys Ile Gly
1 5 10 15

Phe Gly Thr Trp Gln Leu Thr Glu Gly Glu Glu Ala Tyr Lys Ala Val
20 25 30

Thr His Ala Leu Lys Val Gly Tyr Thr His Ile Asp Thr Ala Gln Ile
35 40 45

Tyr Gly Asn Glu His Ser Val Gly Arg Ala Ile Arg Asp Ser Gly Leu
50 55 60

Ala Arg Glu Ser Ile Phe Leu Thr Thr Lys Ile Trp Asn Asp Lys His
65 70 75 80

Asp Tyr His Leu Ala Lys Ala Ser Ile Asp Glu Ser Leu Gln Lys Leu
85 90 95

Gly Val Asp Tyr Ile Asp Leu Leu Leu Ile His Trp Pro Asn Pro Lys
100 105 110

Ala Leu Arg Glu Asn Asp Ala Trp Lys Ala Gly Asn Ala Gly Thr Trp
115 120 125

Lys Ala Met Glu Glu Ala Tyr Lys Glu Gly Lys Val Lys Ala Ile Gly
130 135 140

Val Ser Asn Phe Met Lys His His Leu Glu Ala Leu Phe Glu Thr Ala
145 150 155 160

Glu Ile Lys Pro Met Val Asn Gln Ile Ile Leu Ala Pro Gly Cys Ala
165 170 175

Gln Glu Asp Leu Val Arg Phe Cys Lys Gly Asn Asp Ile Leu Leu Glu
180 185 190

Ala Tyr Ser Pro Phe Gly Thr Gly Ala Ile Phe Glu Asn Glu Ser Ile
195 200 205

Lys Ala Ile Ala Glu Lys Tyr Gly Lys Ser Val Ala Gln Val Ala Leu
210 215 220

GBS patentin.ST25

Arg Trp Ser Leu Asp Asn Gly Phe Leu Pro Leu Pro Lys Ser Ala Thr
225 230 235 240

Pro Lys Asn Ile Glu Ala Asn Leu Asp Ile Phe Asp Phe Gln Leu Asn
245 250 255

Glu Asp Asp Ile Thr Thr Leu Ile Gln Leu Asp Ser Gly Ile Lys Pro
260 265 270

Lys Asp Pro Asp Asn Val Ser Phe
275 280

<210> 331

<211> 155

<212> PRT

<213> Streptococcus agalactiae

<400> 331

Met Val Lys Gly Gln Gly Asn Val Val Ala Gln Asn Lys Lys Ala His
1 5 10 15

His Asp Tyr Thr Ile Val Glu Thr Ile Glu Ala Gly Ile Val Leu Thr
20 25 30

Gly Thr Glu Ile Lys Ser Val Arg Ala Ala Arg Ile Thr Leu Lys Asp
35 40 45

Gly Tyr Ala Gln Ile Lys Asn Gly Glu Ala Trp Leu Ile Asn Val His
50 55 60

Ile Thr Pro Tyr Asp Gln Gly Asn Ile Trp Asn Gln Asp Pro Asp Arg
65 70 75 80

Thr Arg Lys Leu Leu Leu Lys Lys Arg Glu Ile Glu Lys Ile Ser Asn
85 90 95

Glu Leu Lys Gly Thr Gly Met Thr Leu Val Pro Leu Lys Val Tyr Leu
100 105 110

Lys Asp Gly Phe Ala Lys Val Leu Leu Gly Leu Ala Lys Gly Lys His
115 120 125

Asp Tyr Asp Lys Arg Glu Ser Ile Lys Arg Arg Glu Gln Asn Arg Asp
130 135 140

Ile Ala Arg Gln Leu Lys Asn Tyr Asn Ser Arg
145 150 155

GBS patentin.ST25

<210> 332

<211> 267

<212> PRT

<213> Streptococcus agalactiae

<400> 332

Met Asp His Phe Thr Lys Leu Trp Gln Asp Phe Ser Lys Leu Pro Asn
1 5 10 15

Val Val Ala Ile Ala Leu Gly Gly Ser Arg Ser Gly Asp Ser Phe Asp
20 25 30

Gln Ser Ser Asp Tyr Asp Leu Tyr Val Tyr Cys Ala Ala Thr Pro Asp
35 40 45

Ile Thr Ser Arg Lys Arg Ile Leu Asn Lys His Cys His Tyr Ile Glu
50 55 60

Leu Asn Asn His Tyr Trp Glu Leu Glu Asp Asn Gly Thr Leu Asn Asp
65 70 75 80

Gly Thr Asp Ile Asp Ile Leu Tyr Arg Asn Ile Asp Asn Phe Leu Ser
85 90 95

Asp Leu Glu Asp Val Val Glu His His Asn Ser Arg Ile Gly Tyr Thr
100 105 110

Thr Cys Phe Trp His Asn Leu Ile Asn Cys Gln Ile Leu Tyr Asp Pro
115 120 125

Glu Asn Gln Leu Gln Ser Leu Lys Glu Arg Phe Glu Val Ser Tyr Pro
130 135 140

Ser Gln Leu Gln Lys Gln Ile Ile Ile Gln Asn Arg Asn Leu Leu Thr
145 150 155 160

Gly Lys Leu Pro Ser Tyr Asp Lys Gln Ile Ile Lys Ala Leu Lys Arg
165 170 175

Gln Asp Phe Val Ser Thr His His Arg Thr Thr Ala Phe Leu Asp Ser
180 185 190

Tyr Phe Asp Ile Ile Phe Ala Leu Asn Lys Leu Thr His Pro Gly Glu
195 200 205

Lys Arg Met Ile Ser Tyr Ala Lys Lys Asn Ala Thr Leu Leu Pro Lys
210 215 220

GBS patentin.ST25

His Phe Glu Glu Asn Ile Ile Lys Leu Cys His His Asn Ser Asn Glu
225 230 235 240

His Thr Val Lys Glu Thr Leu Asn Asp Ile Ile Met His Leu Asp Val
245 250 255

Met Leu Lys Glu Asn Phe Gln His Phe Ile Gly
260 265

<210> 333

<211> 267

<212> PRT

<213> Streptococcus agalactiae

<400> 333

Met Lys Lys Ile Ile Tyr Leu Gly Leu Ala Cys Val Ser Ile Leu Thr
1 5 10 15

Leu Ser Gly Cys Glu Ser Ile Glu Arg Ser Leu Lys Gly Asp Arg Tyr
20 25 30

Val Asp Gln Lys Leu Ala Glu Asn Ser Ser Lys Glu Ala Thr Glu Gln
35 40 45

Leu Asn Lys Lys Thr Lys Gln Ala Leu Lys Ala Asp Lys Lys Ala Phe
50 55 60

Pro Gln Leu Asp Lys Ala Val Ala Lys Asn Glu Ala Gln Val Leu Ile
65 70 75 80

Lys Thr Ser Lys Gly Asp Ile Asn Ile Lys Leu Phe Pro Lys Tyr Ala
85 90 95

Pro Leu Ala Val Glu Asn Phe Leu Thr His Ala Lys Glu Gly Tyr Tyr
100 105 110

Asn Gly Leu Ser Phe His Arg Val Ile Lys Asp Phe Met Ile Gln Ser
115 120 125

Gly Asp Pro Asn Gly Asp Gly Thr Gly Gly Lys Ser Ile Trp Asn Ser
130 135 140

Lys Asp Lys Lys Lys Asp Ser Gly Asn Gly Phe Val Asn Glu Ile Ser
145 150 155 160

Pro Tyr Leu Tyr Asn Ile Arg Gly Ser Leu Ala Met Ala Asn Ala Gly
165 170 175

GBS patentin.ST25

Ala Asp Thr Asn Gly Ser Gln Phe Phe Ile Asn Gln Ser Gln Gln Asp
180 185 190

His Ser Lys Gln Leu Ser Asp Lys Lys Val Pro Lys Val Ile Ile Lys
195 200 205

Ala Tyr Ser Glu Gly Gly Asn Pro Ser Leu Asp Gly Gly Tyr Thr Val
210 215 220

Phe Gly Gln Val Ile Ser Gly Met Glu Thr Val Asp Lys Ile Ala Ser
225 230 235 240

Val Glu Val Thr Lys Ser Asp Gln Pro Lys Glu Lys Ile Thr Ile Thr
245 250 255

Ser Ile Lys Val Ile Lys Asp Tyr Lys Phe Lys
260 265

<210> 334

<211> 229

<212> PRT

<213> Streptococcus agalactiae

<400> 334

Met Lys Ile Gly Ile Ile Ala Ala Met Glu Glu Glu Leu Lys Leu Leu
1 5 10 15

Val Glu Asn Leu Glu Asp Lys Ser Gln Glu Thr Val Leu Ser Asn Val
20 25 30

Tyr Tyr Ser Gly Arg Tyr Gly Glu His Glu Leu Val Leu Val Gln Ser
35 40 45

Gly Val Gly Lys Val Met Ser Ala Met Ser Val Ala Ile Leu Val Glu
50 55 60

Ser Phe Lys Val Asp Ala Ile Ile Asn Thr Gly Ser Ala Gly Ala Val
65 70 75 80

Ala Thr Gly Leu Asn Val Gly Asp Val Val Val Ala Asp Thr Leu Val
85 90 95

Tyr His Asp Val Asp Leu Thr Ala Phe Gly Tyr Asp Tyr Gly Gln Met
100 105 110

Ser Met Gln Pro Leu Tyr Phe His Ser Asp Lys Thr Phe Val Ser Thr
115 120 125

GBS patentin.ST25

Phe Glu Ala Val Leu Ser Lys Glu Glu Met Thr Ser Lys Val Gly Leu
130 135 140

Ile Ala Thr Gly Asp Ser Phe Ile Ala Gly Gln Glu Lys Ile Asp Val
145 150 155 160

Ile Lys Gly His Phe Pro Gln Val Leu Ala Val Glu Met Glu Gly Ala
165 170 175

Ala Ile Ala Gln Ala Ala Gln Ala Thr Gly Lys Pro Phe Val Val Val
180 185 190

Arg Ala Met Ser Asp Thr Ala Ala His Asp Ala Asn Ile Thr Phe Asp
195 200 205

Glu Phe Ile Ile Glu Ala Gly Lys Arg Ser Ala Gln Val Leu Met Ala
210 215 220

Phe Leu Lys Ala Leu
225

<210> 335

<211> 388

<212> PRT

<213> Streptococcus agalactiae

<400> 335

Met Glu Lys Arg Leu Ser Leu Gly Ala Leu Val Leu Ala Ser Thr Val
1 5 10 15

Leu Leu Ala Ala Cys Gly Asn Val Gly Gly Gly Ala Ser Ser Thr Gly
20 25 30

Thr Lys Ile Gly Lys Asp Ile Lys Val Gly Tyr Asn Trp Glu Leu Ser
35 40 45

Gly Asn Val Ser Ser Tyr Gly Asn Ser Met Lys Asn Gly Ala Asp Leu
50 55 60

Ala Val Lys Glu Ile Asn Ala Ala Gly Gly Val Gly Gly Lys Lys Leu
65 70 75 80

Lys Val Leu Ser Gln Asp Asn Lys Ser Glu Asn Ala Glu Ala Ala Thr
85 90 95

Val Ala Thr Asn Leu Val Thr Lys Gly Ala Asn Val Ile Ile Gly Pro
100 105 110

GBS patentin.ST25

Ala Thr Ser Gly Ala Ala Ala Ser Ser Thr Pro Lys Val Asn Ala Ala
115 120 125

Ala Val Pro Met Ile Ala Pro Ala Ala Thr Gln Asp Asn Leu Val Tyr
130 135 140

Gly Ser Asp Gly Lys Thr Leu Asn Gln Tyr Phe Phe Arg Ala Thr Phe
145 150 155 160

Val Asp Asn Tyr Gln Gly Lys Leu Leu Ser Gln Tyr Ala Thr Asp Asn
165 170 175

Leu Lys Ala Lys Lys Val Val Leu Phe Tyr Asp Asn Ser Ser Asp Tyr
180 185 190

Ser Lys Gly Val Ala Lys Ser Phe Lys Glu Ser Tyr Ser Gly Lys Ile
195 200 205

Val Asp Ser Met Thr Phe Ser Ala Gly Asp Thr Asp Phe Gln Ala Ser
210 215 220

Leu Thr Lys Leu Lys Gly Lys Glu Tyr Asp Ala Ile Val Met Pro Gly
225 230 235 240

Tyr Tyr Thr Glu Thr Gly Leu Ile Val Lys Gln Ala Arg Asp Leu Gly
245 250 255

Ile Ser Lys Pro Val Leu Gly Pro Asp Gly Phe Asp Ser Pro Lys Phe
260 265 270

Val Gln Ser Ala Thr Pro Val Gly Ala Ser Asn Val Tyr Tyr Leu Thr
275 280 285

Gly Phe Thr Thr Gln Gly Ser Thr Lys Ala Lys Ala Phe His Asp His
290 295 300

Tyr Val Lys Ala Tyr Gly Glu Glu Pro Ser Met Phe Ser Ala Leu Ser
305 310 315 320

Tyr Asp Ala Val Tyr Met Ala Ala Lys Ser Ala Lys Gly Ala Lys Thr
325 330 335

Ser Ile Asp Leu Lys Lys Ala Leu Ala Lys Leu Lys Asp Phe Lys Gly
340 345 350

Val Thr Gly Lys Met Ser Ile Asp Lys Asn His Asn Val Val Lys Ser
355 360 365

Ala Tyr Val Val Lys Leu Asp Asp Gly Lys Thr Ser Ser Val Asn Ile
370 375 380

Ile Ser Ala Lys
385

<210> 336

<211> 450

<212> PRT

<213> Streptococcus agalactiae

<400> 336

Met Glu Asn His Asn Ser Ile Lys Gln Thr Tyr Gly Leu Met Thr Thr
1 5 10 15

Ile Ala Met Ile Val Gly Val Val Ile Gly Ser Gly Ile Tyr Phe Lys
20 25 30

Val Asp Asp Ile Leu Lys Phe Thr Gly Gly Asp Val Phe Leu Gly Met
35 40 45

Val Ile Leu Val Leu Gly Ser Phe Ser Ile Val Phe Gly Ser Leu Ser
50 55 60

Ile Ser Glu Leu Ala Ile Arg Thr Ser Glu Ser Gly Gly Ile Phe Ser
65 70 75 80

Tyr Tyr Glu Lys Tyr Val Ser Pro Ala Leu Ala Ala Thr Leu Gly Leu
85 90 95

Phe Ala Ser Phe Leu Tyr Leu Pro Thr Leu Thr Ala Ile Val Ser Trp
100 105 110

Val Ala Ala Phe Tyr Thr Leu Gly Glu Ser Ser Ser Leu Glu Ser Gln
115 120 125

Ile Ile Leu Ala Ala Val Tyr Ile Leu Ala Leu Ser Leu Met Asn Ile
130 135 140

Phe Ala Lys Arg Ile Ala Gly Gly Phe Gln Ser Leu Thr Thr Phe Val
145 150 155 160

Lys Met Ile Pro Leu Val Leu Ile Ala Leu Ile Gly Ala Phe Trp Ser
165 170 175

Asp Lys Ala Pro Gln Leu Pro Gln His Leu Thr Ala Ile Gln Pro Ser
180 185 190

Asn Val Gly Trp Ser Trp Val Ser Gly Leu Val Pro Leu Tyr Phe Ala
195 200 205

GBS patentin.ST25

Tyr Asp Gly Trp Thr Ile phe Val Ser Ile Ala Pro Glu Val Lys Asn
210 215 220

Pro Lys Lys Asn Leu Pro Leu Ala Phe Val Ile Gly Pro Ala Leu Ile
225 230 235 240

Leu Leu Ser Tyr Leu Ala Phe Phe Tyr Gly Leu Thr Gln Ile Leu Gly
245 250 255

Ala Ser Phe Ile Met Thr Thr Gly Asn Asp Ala Ile Asn Tyr Ala Ala
260 265 270

Asn Ile Ile Phe Gly Pro Ser Val Gly Arg Leu Leu Ser Phe Ile Val
275 280 285

Ile Leu Ser Val Leu Gly Val Ala Asn Gly Leu Leu Leu Gly Thr Met
290 295 300

Arg Leu Pro Gln Ala Phe Ala Glu Arg Gly Trp Ile Lys Ser Glu Arg
305 310 315 320

Met Ala Asn Ile Asn Leu Lys Tyr Gln Met Ser Leu Pro Ala Ser Leu
325 330 335

Thr Val Thr Ala Val Ala Ile Phe Trp Leu Phe Val His Phe Met Val
340 345 350

Thr Lys Phe Asn Leu Leu Pro Gly Ser Asp Ile Ser Glu Ile Ala Val
355 360 365

Val Phe Asn Asn Thr Ser Leu Ile Ile Leu Tyr Val Leu Val Leu Ser
370 375 380

Leu Tyr Leu Lys Lys Asp Ile Lys Asn Lys Phe Thr Gly Leu Val Ser
385 390 395 400

Pro Ile Leu Ala Ile Leu Gly Gly Leu Ile Leu Phe Ile Gly Ser Leu
405 410 415

Leu Ser Asn Phe Phe Thr Val Leu Ile Phe Gln Cys Phe Cys Leu Leu
420 425 430

phe Cys Leu Ile Cys His Tyr Ile Tyr Gln Lys Asn Asn Pro Lys Thr
435 440 445

His Glu
450

<210> 337

<211> 600

<212> PRT

<213> Streptococcus agalactiae

<400> 337

Leu Thr Glu Phe Asn Asp Asp Gln His Ser Asn His Asp Gln Lys Ser
 1 5 10 15
 Phe Lys Glu Gln Ile Leu Ala Glu Leu Glu Glu Ala Asn Arg Leu Arg
 20 25 30
 Lys Leu Arg Glu Glu Glu Leu Tyr Gln Lys Glu Gln Glu Ala Lys Glu
 35 40 45
 Ala Ala Arg Arg Thr Ala Gln Leu Met Ala Asp Tyr Glu Ala Gln Arg
 50 55 60
 Leu Lys Asp Glu Gln Glu Ala Arg Ala Lys Ala Leu Glu Thr Lys Gln
 65 70 75 80
 Arg Leu Glu Glu Gln Glu Lys Ala Arg Ile Glu Ala Lys Leu Leu Ala
 85 90 95
 Glu Ala Ala Arg Glu Glu Glu Arg Arg Gln Ala Glu Gln Ala Leu Ala
 100 105 110
 Ser Gln Glu Glu Gln Val Ile Asn Gln Gly Met Glu Pro Ser Arg Glu
 115 120 125
 Leu Asp Ser Gly Ser Lys Ser Ser Glu Phe Arg Thr Thr Glu Asn Val
 130 135 140
 Pro Asp Ile Asp Leu Lys Ala Asp Lys Thr Asp Val Ala Thr Ala Val
 145 150 155 160
 Pro Asn Gln Glu Thr Glu Glu Ile Phe Leu Val Arg Ala Thr Asp Ile
 165 170 175
 Pro Thr Glu Gly Glu Asn Val Lys Leu Gly Glu Thr Ser Glu Leu Glu
 180 185 190
 Pro Val Ala Lys Glu Pro Ile Arg Val Glu Asp Leu Ser Lys Glu Glu
 195 200 205
 Glu Asp Ile Ala Leu Ser Ala Lys Asn Lys His Asn Lys Arg Glu Arg
 210 215 220
 Arg Gln Lys Ala Asp Asn Val Ala Lys Arg Ile Ala Arg Ile Leu Ile
 225 230 235 240

GBS patentin.ST25

Ser Ile Ile Ile Leu Val Leu Leu Leu Thr Ala Phe Val Gly Tyr Arg
245 250 255

Phe Val Asp Ser Ala Ile Lys Pro Val Asp Ser Asn Ser Asn Lys Phe
260 265 270

Val Gln Val Glu Ile Pro Ile Gly Ser Gly Asn Lys Leu Ile Gly Gln
275 280 285

Ile Leu Glu Lys Ala Gly Val Ile Lys Ser Ala Thr Val Phe Asn Tyr
290 295 300

Tyr Ser Lys Phe Lys Asn Tyr Ser Asn Phe Gln Ser Gly Tyr Tyr Asn
305 310 315 320

Leu Lys Lys Ser Met Thr Leu Asp Gln Ile Ala Ala Glu Leu Glu Lys
325 330 335

Gly Gly Thr Ala Glu Pro Thr Lys Pro Ala Leu Gly Lys Ile Leu Ile
340 345 350

Thr Glu Gly Tyr Thr Ile Lys Gln Ile Ala Lys Ala Ile Glu Ser Asn
355 360 365

Lys Ile Asp Thr Lys Thr Thr Ser Thr Pro Tyr Lys Ala Asp Asp Phe
370 375 380

Leu Lys Leu Val Gln Asp Glu Thr Phe Ile Lys Lys Met Val Ala Lys
385 390 395 400

Tyr Pro Asn Leu Leu Gly Ser Leu Pro Asp Lys Ser Lys Ala Ile Tyr
405 410 415

Gln Leu Glu Gly Tyr Leu Phe Pro Ala Thr Tyr Asn Tyr Tyr Lys Asp
420 425 430

Thr Thr Leu Glu Gly Leu Val Glu Asp Met Ile Ser Thr Met Asn Thr
435 440 445

Lys Met Ala Pro Tyr Tyr Asn Thr Ile Lys Ala Lys Asn Met Ser Val
450 455 460

Asn Asp Val Leu Thr Leu Ser Ser Leu Val Glu Lys Glu Gly Ser Thr
465 470 475 480

Asp Glu Asp Arg Arg Lys Ile Ala Ser Val Phe Tyr Asn Arg Leu Ser
485 490 495

Ala Gly Gln Ala Leu Gln Ser Asn Ile Ala Ile Leu Tyr Ala Met Gly
500 505 510

GBS patentin.ST25

Lys Leu Gly Asp Lys Thr Ser Leu Ala Glu Asp Ala Gln Ile Asn Thr
515 520 525

Ser Ile Lys Ser Pro Tyr Asn Ile Tyr Thr Asn Thr Gly Leu Met Pro
530 535 540

Gly Pro Val Asp Ser Pro Ser Ile Ser Ala Ile Glu Ala Thr Ile Lys
545 550 555 560

Pro Ala Ser Thr Asp Tyr Leu Tyr Phe Val Ala Asp Val Lys Thr Gly
565 570 575

Asn Val Tyr Tyr Ala Lys Asp Phe Glu Thr His Lys Ala Asn Val Glu
580 585 590

Lys Tyr Ile Asn Ser Gln Ile Asn
595 600

<210> 338

<211> 1032

<212> PRT

<213> Streptococcus agalactiae

<400> 338

Met Ser Arg Met Ile Pro Gly Arg Ile Arg Asn Gln Gly Ile Glu Leu
1 5 10 15

Tyr Glu Gln Gly Leu Val Ser Leu Ile Ser Gln Glu Gly Asn Leu Leu
20 25 30

Lys Ala Lys Val Gly Asp Cys Gln Ile Glu Tyr Ser Leu Val Thr Glu
35 40 45

Glu Thr Lys Cys Ser Cys Asp Phe Phe Ala Arg Lys Gly Tyr Cys Gln
50 55 60

His Leu Ala Ala Leu Glu His Phe Leu Lys Asn Asp Pro Glu Gly Lys
65 70 75 80

Ala Ile Leu Ser Lys Val Gln Val Gln Gln Glu Ser Gln Gln Glu Thr
85 90 95

Lys Lys Lys Thr Ser Phe Gly Ser Val Phe Leu Asp Ser Leu Ile Ile
100 105 110

Asn Glu Asp Asp Thr Ile Lys Tyr Gln Leu Ser Ala Gln Gly Glu Gln
115 120 125

GBS patentin.ST25

Asn Pro Tyr Ala Asn Asp Ile Trp Trp Thr Leu Lys Ile Arg Arg Leu
130 135 140

Pro Asp Asp Arg Ser Tyr Val Ile Arg Asp Ile Lys Ala Phe Leu Asn
145 150 155 160

Thr Val Arg Lys Glu Ala Tyr Tyr Gln Ile Gly Lys Gln Tyr Phe Glu
165 170 175

Thr Leu Ser Leu Ile Gln Phe Asp Glu Thr Ser Gln Glu Leu Ile Glu
180 185 190

Phe Leu Trp Arg Leu Ile Pro Ser His Ser Ser Lys Ile Asp Leu Glu
195 200 205

Phe Ile Leu Pro Asn Gln Gly Arg His Leu Ser Leu Thr Arg Gly Phe
210 215 220

Phe Glu Glu Gly Val Thr Leu Met Asn Ala Leu Glu Asn Phe Ser Phe
225 230 235 240

Glu Ser Asp Phe His Gln Phe Asn His Leu Tyr Phe Lys Glu Leu Glu
245 250 255

Gly Glu Asp His Leu Tyr Gln Phe Lys Val Ile Val His Arg Gln Ser
260 265 270

Ile Glu Leu Glu Ile Lys Glu Lys Asp Leu Lys Pro Leu Phe Ala Asn
275 280 285

Ser Tyr Leu Phe Tyr Arg Asp Thr Phe Tyr His Leu Asn Leu Lys Gln
290 295 300

Glu Lys Met Val Thr Ala Ile Arg Ser Leu Pro Ile Glu Gly Asp Leu
305 310 315 320

Ala Lys His Ile His Phe Asp Leu Asp Asp Gln Asp Lys Leu Ala Ala
325 330 335

His Leu Leu Asp Phe Lys Glu Ile Gly Leu Val Asp Ala Pro Arg Ser
340 345 350

Phe Ser Ile His Asp Phe Lys Val Asn Phe Glu Phe Asp Ile Asn Ser
355 360 365

Gln Asn Glu Ile Leu Leu Gln Met Val Phe Asp Tyr Gly Asn Asp Leu
370 375 380

Thr Val His Asn Arg Gln Glu Leu Glu Gln Leu Thr Phe Ala Ser His
385 390 395 400

GBS patentin.ST25

Phe Lys His Glu Glu Lys Ile Phe Lys Leu Leu Glu Arg Tyr Gly Phe
 405 410 415
 Ala Pro His Phe Ser Thr Ser His Pro Ala Tyr Ser Ala Gln Glu Leu
 420 425 430
 Tyr Asp Phe Tyr Thr Tyr Met Leu Pro Gln Phe Lys Lys Met Gly Thr
 435 440 445
 Val Ser Leu Ser Ala Lys Leu Glu Ser Tyr Arg Leu Ile Glu Arg Pro
 450 455 460
 Gln Ile Asp Ile Glu Ala Lys Gly Ser Leu Leu Asp Ile Ser Phe Asp
 465 470 475 480
 Phe Ser Asp Leu Leu Glu Asn Asp Val Asp Gln Ala Leu Val Ala Leu
 485 490 495
 Phe Asp Asn Asn Pro Tyr Phe Val Asn Lys Ser Gly Gln Leu Val Ile
 500 505 510
 Phe Asp Glu Glu Thr Lys Lys Val Ser Ala Thr Leu Gln Gly Leu Arg
 515 520 525
 Ala Arg Arg Ala Lys Asn Gly His Ile Glu Leu Asp Asn Ile Ala Ala
 530 535 540
 Phe Gln Leu Ser Glu Leu Phe Ala Asn Gln Asp Asn Val Ser Phe Ser
 545 550 555 560
 Gln His Phe Tyr Gln Leu Ile Glu Asp Leu Arg His Pro Glu Lys Phe
 565 570 575
 Lys Ile Pro Gly Leu Ser Val Ser Ala Ser Leu Arg Asp Tyr Gln Leu
 580 585 590
 Thr Gly Val Arg Trp Leu Ser Met Leu Asp His Tyr Gly Phe Ala Gly
 595 600 605
 Ile Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Leu Gln Thr Ile Ser
 610 615 620
 Phe Leu Ser Thr Lys Leu Thr Arg Asp Ser Arg Val Leu Ile Leu Ser
 625 630 635 640
 Pro Ser Ser Leu Ile Tyr Asn Trp Gln Asp Glu Phe His Lys Phe Ala
 645 650 655
 Pro Asp Val Asp Val Ala Val Ala Tyr Gly Ser Lys Ile Arg Arg Asp
 660 665 670

GBS patentin.ST25

Glu Ile Ile Ala Glu Arg His Gln Val Ile Ile Thr Ser Tyr Ser Ser
675 680 685

Phe Arg Gln Asp Phe Glu Thr Tyr Ser Glu Gly Asn Tyr Asp Tyr Leu
690 700

Ile Leu Asp Glu Ala Gln Val Met Lys Asn Ala Gln Thr Lys Ile Ala
705 710 715 720

His Ser Leu Arg Ser Phe Glu Val Lys Asn Cys Phe Ala Leu Ser Gly
725 730 735

Thr Pro Ile Glu Asn Lys Leu Leu Glu Ile Trp Ser Ile Phe Gln Ile
740 745 750

Ile Leu Pro Gly Leu Leu Pro Gly Lys Lys Glu Phe Leu Lys Leu Asn
755 760 765

Pro Lys Gln Val Ala Arg Tyr Ile Lys Pro Phe Val Met Arg Arg Arg
770 775 780

Lys Glu Glu Val Leu Pro Glu Leu Pro Asp Leu Ile Glu Met Asn Tyr
785 790 795 800

Pro Asn Glu Met Thr Asp Ser Gln Lys Val Ile Tyr Leu Ala Gln Leu
805 810 815

Arg Gln Ile Gln Glu Ser Ile Gln His Ser Ser Asp Ala Asp Leu Asn
820 825 830

Arg Arg Lys Ile Glu Ile Leu Ser Gly Ile Thr Arg Leu Arg Gln Ile
835 840 845

Cys Asp Thr Pro Arg Leu Phe Met Asp Tyr Asp Gly Glu Ser Gly Lys
850 855 860

Leu Glu Ser Leu His Gln Leu Leu Thr Gln Ile Lys Glu Asn Gly His
865 870 875 880

Arg Ala Leu Ile Phe Ser Gln Phe Arg Gly Met Leu Asp Ile Ala Glu
885 890 895

Arg Glu Met Val Ala Met Gly Leu Thr Thr Tyr Lys Ile Thr Gly Ser
900 905 910

Thr Pro Ala Asn Glu Arg His Glu Met Thr Arg Ala Phe Asn Ala Gly
915 920 925

Ser Lys Asp Ala Phe Leu Ile Ser Leu Lys Ala Gly Gly Val Gly Leu
930 935 940

GBS patentin.ST25

Asn Leu Thr Gly Ala Asp Thr Val Val Leu Ile Asp Leu Trp Trp Asn
945 950 955 960

Pro Ala Val Glu Met Gln Ala Ile Ser Arg Ala His Arg Leu Gly Gln
965 970 975

Lys Glu Asn Val Glu Val Tyr Arg Leu Ile Thr Arg Gly Thr Ile Glu
980 985 990

Glu Lys Ile Leu Glu Met Gln Glu Thr Lys Lys His Leu Val Thr Thr
995 1000 1005

Val Leu Asp Gly Asn Glu Thr His Ala Ser Met Ser Val Asp Asp
1010 1015 1020

Ile Arg Glu Ile Leu Gly Val Ser Lys
1025 1030

<210> 339

<211> 177

<212> PRT

<213> Streptococcus agalactiae

<400> 339

Val Leu Leu Thr Glu Ile Lys Lys Ser Pro Glu Gly Leu Tyr Phe Asp
1 5 10 15

Lys Lys Ile Asp Ile Lys Glu Ser Leu Met Glu Arg His Ser Glu Ile
20 25 30

Met Asp Ile Ser Asp Ile Gln Val Ser Gly His Val Val Tyr Glu Asp
35 40 45

Gly Leu Tyr Leu Leu Asp Tyr Asn Met Ala Tyr Asp Ile Thr Leu Pro
50 55 60

Ser Ser Arg Ser Met Lys Pro Val Val Leu Ser Glu Lys Gln Thr Ile
65 70 75 80

Asn Glu Val Phe Ile Glu Ala Glu Asn Val Ser Thr Lys Lys Glu Leu
85 90 95

Val Asp Gln Asp Leu Val Leu Ile Leu Glu Glu Asp Asp Ile Asn Leu
100 105 110

Glu Glu Ser Val Ile Asp Asn Ile Leu Leu Asn Ile Pro Leu Arg Val
115 120 125

GBS patentin.ST25

Leu Ala Ala Asp Glu Val Gly Val Glu Ala Asp Leu Ser Gly Lys Asn
130 135 140

Trp Ser Leu Met Thr Glu Lys Gln Tyr Glu Glu Lys Gln Ala Lys Glu
145 150 155 160

Lys Glu Lys Ser Asn Pro Phe Ala Ala Leu Glu Gly Met Phe Asp Ser
165 170 175

Asp

<210> 340

<211> 192

<212> PRT

<213> Streptococcus agalactiae

<400> 340

Met Glu Val Lys Thr Ala Ile Glu Trp Met His Thr Phe Asn Gln Lys
1 5 10 15

Ile Gln Ser Asn Lys Asp Tyr Leu Ser Glu Leu Asp Thr Pro Ile Gly
20 25 30

Asp Gly Asp His Gly Gly Asn Met Ala Arg Gly Met Thr Ala Val Ile
35 40 45

Glu Asn Leu Asp Asn Asn Glu Phe Ser Ser Ala Ala Asp Val Phe Lys
50 55 60

Thr Val Ser Met Gln Leu Leu Ser Lys Val Gly Gly Ala Ser Gly Pro
65 70 75 80

Leu Tyr Gly Ser Ala Phe Met Gly Ile Thr Lys Ala Glu Gln Ser Glu
85 90 95

Ser Thr Ile Ser Glu Ala Leu Gly Ala Gly Leu Glu Met Ile Gln Lys
100 105 110

Arg Gly Lys Ala Glu Leu Asn Glu Lys Thr Met Val Asp Val Trp His
115 120 125

Gly Val Ile Glu Ala Ile Glu Lys Asn Glu Leu Thr Glu Asp Arg Ile
130 135 140

Asp Ser Leu Val Asp Ala Thr Lys Gly Met Lys Ala Thr Lys Gly Arg
145 150 155 160

GBS patentin.ST25

Ala Ser Tyr Val Gly Glu Arg Ser Leu Gly His Ile Asp Pro Gly Ser
165 170 175

Phe Ser Ser Gly Leu Leu Phe Lys Ala Leu Leu Glu Val Gly Gly Val
180 185 190

<210> 341

<211> 942

<212> PRT

<213> Streptococcus agalactiae

<400> 341

Met Gln Asp Lys Leu Met Ile Arg Gly Ala Arg Ala His Asn Leu Lys
1 5 10 15

Asn Ile Ser Val Asp Ile Pro Arg Asp Lys Leu Val Val Val Thr Gly
20 25 30

Leu Ser Gly Ser Gly Lys Ser Ser Leu Ala Phe Asp Thr Ile Tyr Ala
35 40 45

Glu Gly Gln Arg Arg Tyr Val Glu Ser Leu Ser Ala Tyr Ala Arg Gln
50 55 60

Phe Leu Gly Asn Met Glu Lys Pro Asp Val Asp Ser Ile Asp Gly Leu
65 70 75 80

Ser Pro Ala Ile Ser Ile Asp Gln Lys Thr Thr Ser Lys Asn Pro Arg
85 90 95

Ser Thr Val Gly Thr Val Thr Glu Ile Asn Asp Tyr Leu Arg Leu Leu
100 105 110

Tyr Ala Arg Val Gly Thr Pro Tyr Cys Ile Asn Gly His Gly Ala Ile
115 120 125

Thr Ala Ser Ser Val Glu Gln Ile Val Asp Lys Val Leu Ala Leu Pro
130 135 140

Glu Arg Thr Lys Met Gln Ile Leu Ala Pro Ile Ile Arg Arg Lys Lys
145 150 155 160

Gly Gln His Lys Ser Thr Phe Glu Lys Ile Gln Lys Asp Gly Tyr Val
165 170 175

Arg Val Arg Ile Asp Gly Asp Ile His Asp Val Thr Glu Val Pro Glu
180 185 190

GBS patentin.ST25

Leu Ser Lys Ser Lys Met His Asn Ile Asp Ile Val Val Asp Arg Leu
195 200 205

Ile Asn Lys Glu Gly Ile Arg Ser Arg Leu Phe Asp Ser Val Glu Ala
210 215 220

Ala Leu Arg Leu Ser Asp Gly Tyr Val Val Ile Asp Thr Met Asp Gly
225 230 235 240

Asn Glu Leu Leu Phe Ser Glu His Tyr Ser Cys Pro Glu Cys Gly Phe
245 250 255

Thr Val Pro Glu Leu Glu Pro Arg Leu Phe Ser Phe Asn Ala Pro Phe
260 265 270

Gly Ser Cys Thr Thr Cys Asp Gly Leu Gly Ile Lys Leu Glu Val Asp
275 280 285

Ile Asp Leu Val Ile Pro Asp Lys Ser Lys Thr Leu Arg Glu Gly Ala
290 295 300

Leu Val Pro Trp Asn Pro Ile Ser Ser Asn Tyr Tyr Pro Thr Met Leu
305 310 315 320

Glu Gln Ala Met Thr Gln Phe Asp Val Asp Met Asp Thr Pro Phe Glu
325 330 335

Lys Leu Ser Lys Ala Glu Gln Asp Leu Ala Leu Tyr Gly Ser Gly Glu
340 345 350

Arg Glu Phe His Phe His Tyr Ile Asn Asp Phe Gly Gly Glu Arg Asn
355 360 365

Ile Asp Leu Pro Phe Glu Gly Val Val Asn Asn Ile Asn Arg Arg Tyr
370 375 380

His Glu Thr Asn Ser Asp Tyr Thr Arg Asn Val Met Arg Glu Tyr Met
385 390 395 400

Asn Glu Leu Lys Cys Asn Thr Cys His Gly Tyr Arg Leu Asn Asp Gln
405 410 415

Ala Leu Cys Val Arg Val Gly Gly Glu Glu Gly Leu Asn Ile Gly Gln
420 425 430

Val Ser Asp Leu Ser Ile Ala Asp His Leu Glu Leu Leu Glu Thr Leu
435 440 445

Arg Leu Ser Ser Asn Glu Gln Leu Ile Ala Arg Pro Ile Ile Lys Glu
450 455 460

GBS patentin.ST25

Ile His Asp Arg Leu Ser Phe Leu Asn Asn Val Gly Leu Asn Tyr Leu
465 470 475 480

Asn Leu Ser Arg Ser Ala Gly Thr Leu Ser Gly Gly Glu Ser Gln Arg
485 490 495

Ile Arg Leu Ala Thr Gln Ile Gly Ser Asn Leu Ser Gly Val Leu Tyr
500 505 510

Val Leu Asp Glu Pro Ser Ile Gly Leu His Gln Arg Asp Asn Asp Arg
515 520 525

Leu Ile Asp Ser Leu Lys Lys Met Arg Asp Leu Gly Asn Thr Leu Ile
530 535 540

Val Val Glu His Asp Glu Asp Thr Met Met Ala Ala Asp Trp Leu Ile
545 550 555 560

Asp Val Gly Pro Gly Ala Gly Ala Phe Gly Gly Glu Ile Val Ala Ser
565 570 575

Gly Thr Pro Lys Gln Val Ala Lys Asn Thr Lys Ser Ile Thr Gly Gln
580 585 590

Tyr Leu Ser Gly Lys Lys Val Ile Pro Val Pro Ser Glu Arg Arg Val
595 600 605

Gly Asn Gly Arg Phe Leu Glu Ile Lys Gly Ala Ala Glu Asn Asn Leu
610 615 620

Gln Asn Leu Asp Val Lys Phe Pro Leu Gly Lys Phe Ile Ala Val Thr
625 630 635 640

Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Asn Ser Ile Leu Lys
645 650 655

Lys Ala Val Ala Gln Lys Leu Asn Arg Asn Ser Asp Lys Pro Gly Lys
660 665 670

Tyr Val Ser Leu Glu Gly Ile Glu Tyr Val Asp Arg Leu Ile Asp Ile
675 680 685

Asp Gln Ser Pro Ile Gly Arg Thr Pro Arg Ser Asn Pro Ala Thr Tyr
690 695 700

Thr Gly Val Phe Asp Asp Ile Arg Asp Leu Phe Ala Gln Thr Asn Glu
705 710 715 720

Ala Lys Ile Arg Gly Tyr Lys Lys Gly Arg Phe Ser Phe Asn Val Lys
725 730 735

GBS patentin.ST25

Gly Gly Arg Cys Glu Ser Cys Ser Gly Asp Gly Ile Ile Lys Ile Glu
740 745 750

Met His Phe Leu Pro Asp Val Tyr Val Pro Cys Glu Val Cys His Gly
755 760 765

Thr Arg Tyr Asn Ser Glu Thr Leu Glu Val His Tyr Lys Glu Lys Asn
770 775 780

Ile Ala Gln Ile Leu Asp Met Thr Val Asn Asp Ala Val Thr Phe Phe
785 790 795 800

Ala Ala Ile Pro Lys Ile Ala Arg Lys Leu Gln Thr Ile Lys Asp Val
805 810 815

Gly Leu Gly Tyr Val Thr Leu Gly Gln Pro Ala Thr Thr Leu Ser Gly
820 825 830

Gly Glu Ala Gln Arg Met Lys Leu Ala Ser Glu Leu His Lys Arg Ser
835 840 845

Thr Gly Lys Ser Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His
850 855 860

Ala Asp Asp Ile Ala Arg Leu Leu Lys Val Leu Asp Arg Phe Val Asp
865 870 875 880

Asp Gly Asn Thr Val Leu Val Ile Glu His Asn Leu Asp Val Ile Lys
885 890 895

Thr Ala Asp His Ile Ile Asp Leu Gly Pro Glu Gly Gly Ile Gly Gly
900 905 910

Gly Gln Ile Val Ala Ile Gly Thr Pro Glu Glu Val Ala Glu Asn Pro
915 920 925

Lys Ser Tyr Thr Gly Tyr Tyr Leu Lys Glu Lys Leu Ala Arg
930 935 940

<210> 342

<211> 374

<212> PRT

<213> streptococcus agalactiae

<400> 342

Met Trp Pro Glu Asp Arg Ile Ala Ser Phe Arg Arg Thr Leu Leu Gly
1 5 10 15

GBS patentin.ST25

Trp Tyr Asp Gln Glu Lys Arg Asp Leu Pro Trp Arg Arg Thr Thr Asn
20 25 30

Pro Tyr Tyr Ile Trp Val Ser Glu Ile Met Leu Gln Gln Thr Gln Val
35 40 45

Asn Thr Val Ile Pro Tyr Tyr Lys Arg Phe Leu Glu Trp Phe Pro Gln
50 55 60

Ile Lys Asp Leu Ala Asp Ala Pro Glu Glu Gln Leu Leu Lys Ala Trp
65 70 75 80

Glu Gly Leu Gly Tyr Tyr Ser Arg Val Arg Asn Met Gln Lys Ala Ala
85 90 95

Gln Gln Val Met Val Asp Phe Gly Gly Ile Phe Pro His Thr Tyr Asp
100 105 110

Asp Ile Ala Ser Leu Lys Gly Ile Gly Pro Tyr Thr Ala Gly Ala Ile
115 120 125

Ala Ser Ile Ser Phe Asn Leu Pro Glu Pro Ala Val Asp Gly Asn Val
130 135 140

Met Arg Val Met Ala Arg Leu Phe Glu Val Asn Tyr Asp Ile Gly Asp
145 150 155 160

Pro Lys Asn Arg Lys Ile Phe Gln Ala Ile Met Glu Ile Leu Ile Asp
165 170 175

Pro Asp Arg Pro Gly Asp Phe Asn Gln Ala Leu Met Asp Leu Gly Thr
180 185 190

Asp Ile Glu Ser Ala Lys Thr Pro Arg Pro Asp Glu Ser Pro Ile Arg
195 200 205

Phe Phe Asn Ala Ala Tyr Leu Asn Gly Thr Tyr Ser Lys Tyr Pro Ile
210 215 220

Lys Asn Pro Lys Lys Lys Pro Lys Pro Met Arg Ile Gln Ala Phe Val
225 230 235 240

Ile Arg Asn Gln Asn Gly Gln Tyr Leu Leu Glu Lys Asn Thr Lys Gly
245 250 255

Arg Leu Leu Gly Gly Phe Trp Ser Phe Pro Ile Ile Glu Thr Ser Pro
260 265 270

Leu Ser Gln Gln Leu Asp Leu Phe Asp Asp Asn Gln Ser Asn Pro Ile
275 280 285

GBS patentin.ST25

Ile Trp Gln Thr Gln Asn Glu Thr Phe Gln Arg Glu Tyr Gln Leu Lys
290 295 300

Pro Gln Trp Thr Asp Asn His Phe Pro Asn Ile Lys His Thr Phe Ser
305 310 315 320

His Gln Lys Trp Thr Ile Glu Leu Ile Glu Gly Val Val Lys Ala Thr
325 330 335

Asp Leu Pro Asn Ala Pro His Leu Lys Trp Ala Ala Ile Glu Asp Phe
340 345 350

Ser Leu Tyr Pro Phe Ala Thr Pro Gln Lys Lys Met Leu Glu Thr Tyr
355 360 365

Leu Lys Gln Lys Asn Ala
370

<210> 343

<211> 282

<212> PRT

<213> Streptococcus agalactiae

<400> 343

Leu Ile Glu Ile Thr Trp Thr Val Lys Tyr Ile Thr Glu Phe Ile Ala
1 5 10 15

Thr Ala Phe Leu Ile Ile Leu Gly Asn Gly Ala Val Ala Asn Val Asp
20 25 30

Leu Lys Gly Thr Lys Gly Asn Asn Ser Gly Trp Ile Ile Ile Ala Ile
35 40 45

Gly Tyr Gly Leu Gly Val Met Met Pro Ala Leu Met Phe Gly Asn Val
50 55 60

Ser Gly Asn His Ile Asn Pro Ala Phe Thr Leu Gly Leu Ala Phe Ser
65 70 75 80

Gly Leu Phe Pro Trp Ala His Val Gly Gln Tyr Ile Leu Ala Gln Ile
85 90 95

Leu Gly Ala Met Phe Gly Gln Leu Val Val Val Met Val Tyr Gln Pro
100 105 110

Tyr Phe Val Lys Thr Glu Asn Pro Asn His Val Leu Gly Ser Phe Ser
115 120 125

GBS patentin.ST25

Thr Ile Ser Ala Leu Asp Asp Gly Gln Lys Ser Ser Arg Lys Ala Ala
130 135 140

Tyr Ile Asn Gly Phe Leu Asn Glu Phe Val Gly Ser Phe Val Leu Phe
145 150 155 160

Phe Gly Ala Leu Ala Leu Thr Lys Asn Tyr Phe Gly Val Glu Leu Val
165 170 175

Gly Lys Leu Val Gln Ala Gly Tyr Asp Gln Thr Thr Ala Ala Thr Arg
180 185 190

Ile Ser Pro Tyr Val Thr Gly Ser Leu Ala Val Ala His Leu Gly Ile
195 200 205

Gly Phe Leu Val Met Thr Leu Val Ala Ser Leu Gly Gly Pro Thr Gly
210 215 220

Pro Ala Leu Asn Pro Ala Arg Asp Leu Gly Pro Arg Ile Val His Arg
225 230 235 240

Leu Leu Pro Lys Gln Ile Leu Gly Gln Ala Lys Glu Asp Ser Lys Trp
245 250 255

Trp Tyr Ala Trp Val Pro Val Leu Ala Pro Ile Val Ala Ser Ile Leu
260 265 270

Ala Val Ala Leu Phe Lys Leu Leu Tyr Leu
275 280

<210> 344

<211> 326

<212> PRT

<213> Streptococcus agalactiae

<400> 344

Met Ser Ser Tyr Trp Asn Asn Tyr Pro Glu Leu Lys Lys Asn Ile Asp
1 5 10 15

Glu Thr Asn Gln Leu Ile Gln Glu Arg Ile Gln Val Arg Asn Lys Asp
20 25 30

Ile Glu Ala Ala Leu Ser Gln Leu Thr Ala Ala Gly Gly Lys Gln Leu
35 40 45

Arg Pro Ala Phe Phe Tyr Leu Phe Ser Gln Leu Gly Asn Lys Glu Asn
50 55 60

GBS patentin.ST25

Gln Asp Thr Gln Gln Leu Lys Lys Ile Ala Ala Ser Leu Glu Ile Leu
65 70 75 80

His Val Ala Thr Leu Ile His Asp Asp Val Ile Asp Asp Ser Pro Leu
85 90 95

Arg Arg Gly Asn Met Thr Ile Gln Ser Lys Phe Gly Lys Asp Ile Ala
100 105 110

Val Tyr Thr Gly Asp Leu Leu Phe Thr Val Phe Phe Asp Leu Ile Leu
115 120 125

Glu Ser Met Ala Asp Thr Pro Phe Met Arg Ile Asn Ala Lys Ser Met
130 135 140

Arg Lys Ile Leu Met Gly Glu Leu Asp Gln Met His Leu Arg Tyr Asn
145 150 155 160

Gln Gln Gln Gly Ile His His Tyr Leu Arg Ala Ile Ser Gly Lys Thr
165 170 175

Ala Glu Leu Phe Lys Leu Ala Ser Lys Glu Gly Ala Tyr Phe Gly Gly
180 185 190

Ala Glu Lys Glu Val Val Arg Leu Ala Gly His Ile Gly Phe Asn Ile
195 200 205

Gly Met Thr Phe Gln Ile Leu Asp Asp Ile Leu Asp Tyr Thr Ala Asp
210 215 220

Lys Lys Thr Phe Asn Lys Pro Val Leu Glu Asp Leu Thr Gln Gly Val
225 230 235 240

Tyr Ser Leu Pro Leu Leu Leu Ala Ile Glu Glu Asn Pro Asp Ile Phe
245 250 255

Lys Pro Ile Leu Asp Lys Lys Thr Asp Met Ala Thr Glu Asp Met Glu
260 265 270

Lys Ile Ala Tyr Leu Val Val Ser His Arg Gly Val Asp Lys Ala Arg
275 280 285

His Leu Ala Arg Lys Phe Thr Glu Lys Ala Ile Ser Asp Ile Asn Lys
290 295 300

Leu Pro Gln Asn Ser Ala Lys Lys Gln Leu Leu Gln Leu Thr Asn Tyr
305 310 315 320

Leu Leu Lys Arg Lys Ile
325

GBS patentin.ST25

<210> 345

<211> 582

<212> PRT

<213> Streptococcus agalactiae

<400> 345

Met Phe Lys Ile Pro Leu Phe Lys Glu Leu Lys Thr Asp Gln Trp Val
1 5 10 15
Lys Pro Phe Phe Lys Gln Tyr Lys Val Ser Leu Val Ile Ala Leu Phe
20 25 30
Leu Gly Phe Met Thr Phe Phe Ser Ala Ser Ala Leu Met Phe Asn Ser
35 40 45
Gly Tyr Leu Ile Ser Lys Ser Ala Ser Leu Pro Ser Asn Ile Leu Leu
50 55 60
Val Tyr Val Pro Ile Val Leu Thr Arg Ala Phe Gly Ile Gly Arg Pro
65 70 75 80
Val Phe Arg Tyr Ile Glu Arg Leu Thr Ser His Asn Trp Val Leu Arg
85 90 95
Met Thr Ser Gln Leu Arg Leu Lys Leu Tyr His Ser Leu Glu Ser Asn
100 105 110
Ala Ile Phe Met Lys Arg Asp Phe Arg Leu Gly Asp Val Met Gly Leu
115 120 125
Leu Ala Glu Asp Ile Asn Tyr Leu Gln Asn Leu Tyr Leu Arg Thr Ile
130 135 140
Phe Pro Thr Ile Ile Ala Trp Leu Leu Tyr Ser Phe Ile Ile Ile Ala
145 150 155 160
Thr Gly Phe Phe Ser Leu Trp Phe Ala Leu Met Met Leu Leu Tyr Leu
165 170 175
Ala Ile Met Ile Phe Leu Phe Pro Leu Trp Ser Ile Leu Ala Asn Gly
180 185 190
Ala Arg Gln Thr Arg Glu Lys Glu Leu Lys Asn His Leu Tyr Thr Asp
195 200 205
Leu Thr Asp Asn Val Leu Gly Ile Ser Asp Trp Ile Phe Ser Gln Arg
210 215 220

GBS patentin.ST25

Gly Gln Glu Tyr Val Ala Leu His Glu Arg Ser Glu Ser Glu Leu Met
225 230 235 240

Ala Ile Gln Lys Lys Ile Arg Ser Phe Asn Asn Arg Arg Ala Leu Ile
245 250 255

Val Glu Leu Val Phe Gly Phe Leu Ala Ile Leu Val Ile Ile Trp Ala
260 265 270

Ser Asn Gln Phe Ile Gly His Arg Gly Gly Glu Ala Asn Trp Ile Ala
275 280 285

Ala Phe Val Leu Thr Val Phe Pro Leu Ser Glu Ala Phe Ala Gly Leu
290 295 300

Ser Ala Ala Ala Gln Glu Thr Asn Lys Tyr Ser Asp Ser Ile His Arg
305 310 315 320

Leu Asn Glu Leu Ser Glu Thr Tyr Phe Glu Thr Thr Gln Asn Gln Leu
325 330 335

Pro Asn Lys Pro Tyr Asp Phe Ser Val Lys Asn Leu Ser Phe Gln Tyr
340 345 350

Lys Pro Gln Glu Lys Trp Val Leu His His Leu Asp Leu Asp Ile Lys
355 360 365

Glu Gly Glu Lys Ile Ala Ile Leu Gly Arg Ser Gly Ser Gly Lys Ser
370 375 380

Thr Leu Ala Ser Leu Leu Arg Gly Asp Leu Lys Ala Ser Gln Gly Lys
385 390 395 400

Ile Thr Leu Gly Gly Ala Asp Val Ser Ile Val Gly Asp Cys Ile Ser
405 410 415

Asn Tyr Ile Gly Val Ile Gln Gln Ala Pro Tyr Leu Phe Asn Thr Thr
420 425 430

Leu Leu Asn Asn Ile Arg Ile Gly Asn Gln Asp Ala Ser Glu Glu Asp
435 440 445

Val Trp Lys Val Leu Glu Arg Val Gly Leu Lys Glu Met Val Thr Asp
450 455 460

Leu Ser Asp Gly Leu Tyr Thr Met Val Asp Glu Ala Gly Leu Arg Phe
465 470 475 480

Ser Gly Gly Glu Arg His Arg Ile Ala Leu Ala Arg Ile Leu Leu Lys
485 490 495

GBS patentin.ST25

Asp Val Pro Ile Val Ile Leu Asp Glu Pro Thr Val Gly Leu Asp Pro
500 505 510

Ile Thr Glu Gln Ala Leu Leu Arg Val Phe Met Lys Glu Leu Glu Gly
515 520 525

Lys Thr Leu Val Trp Ile Thr His His Leu Lys Gly Ile Glu His Ala
530 535 540

Asp Arg Ile Leu Phe Ile Glu Asn Gly Gln Leu Glu Leu Glu Gly Ser
545 550 555 560

Pro Gln Glu Leu Ser Gln Ser Ser Gln Arg Tyr Arg Gln Leu Lys Ala
565 570 575

Ala Asp Asp Gly Asp Leu
580

<210> 346

<211> 148

<212> PRT

<213> Streptococcus agalactiae

<400> 346

Met Lys Lys Leu Ile Thr Glu Lys Lys Val Asn Asn Val Ser Thr Val
1 5 10 15

Asn Tyr Leu Lys Leu Gly Leu Val Ser Ala Met Phe Ala Gly Gly Ala
20 25 30

Phe Val Ala Leu Gly Ser Thr Gln Gly Val Ser Ala Ser Thr Phe Thr
35 40 45

Ala Pro Gln Ala Thr His Pro Lys Ala Glu Arg Gln Leu Thr Asp Ser
50 55 60

Glu Ile Tyr Glu Arg Ala Gln Lys Gln Val Leu Pro Lys Tyr Ile Gln
65 70 75 80

Gly Ser Leu Ser Gly Ile Leu Asn Gln His Ser Thr Leu Tyr Lys Gln
85 90 95

Gln Asn Ala Ala Val Thr Pro Gln Val Ser Ser Pro Lys Ala Glu Arg
100 105 110

Gln Leu Thr Asp Ser Glu Ile Tyr Glu Arg Ala Gln Lys Gln Val Leu
115 120 125

GBS patentin.ST25

Pro Lys Tyr Ile Gln Gly Ser Leu Ser Gly Ile Leu Asn Gln His Ser
130 135 140

Thr Leu Asn Ala
145

<210> 347

<211> 169

<212> PRT

<213> Streptococcus agalactiae

<400> 347

Met Glu Glu Asn Met Asn Ile Lys Gln Leu Lys Ser Lys Thr Met Leu
1 5 10 15

Gly Thr Val Ala Leu Val Ser Ala Phe Ser Phe Ala Ser Thr Asn Ala
20 25 30

Asp Ala Asn Thr Tyr Asn Tyr Ala Val Asp Val Asp Tyr Leu Ala Ser
35 40 45

Ala Glu Glu Ile Ala Gln Ala His Pro Ala Ser Asn Thr Phe Pro Leu
50 55 60

Gly Gln Cys Thr Trp Gly Val Lys Glu Met Ala Thr Trp Ala Gly Asn
65 70 75 80

Trp Trp Gly Asn Gly Gly Asp Trp Ala Ala Ser Ala Ala Ser Ala Gly
85 90 95

Tyr Thr Val Gly Thr Gln Pro Arg Val Gly Ser Ile Val Cys Trp Thr
100 105 110

Asp Gly Ser Tyr Gly His Val Ala Tyr Val Thr Ala Val Asp Pro Val
115 120 125

Thr Asn Lys Ile Gln Val Leu Glu Ser Asn Tyr Ala Gly His Gln Trp
130 135 140

Ile Asp Asn Tyr Arg Gly Trp Phe Asp Pro Gln Asn Thr Ala Thr Pro
145 150 155 160

Gly Val Val Ser Tyr Ile Tyr Pro Asn
165

<210> 348

<211> 313

<212> PRT

<213> Streptococcus agalactiae

<400> 348

Met Lys Ile Asn Gln Met Lys Lys Asp Glu Leu Phe Glu Gly Phe Tyr
 1 5 10 15
 Leu Ile Lys Lys Ala Glu Val Arg Lys Thr Arg Ala Gly Lys Asp Phe
 20 25 30
 Ile Ala Phe Thr Phe Arg Asp Asp Thr Gly Glu Ile Ser Gly Asn Met
 35 40 45
 Trp Asp Ala Gln Thr Tyr Asn Val Glu Glu Phe Val Ala Gly Lys Ile
 50 55 60
 Val His Met Lys Gly Arg Arg Glu Val Tyr Asn Gly Thr Pro Gln Val
 65 70 75 80
 Asn Gln Ile Thr Leu Arg Asn Ile Lys Asp Gly Glu Pro Asn Asp Pro
 85 90 95
 Arg Asp Phe Lys Glu Lys Pro Pro Ile Asn Val Asp Asn Val Arg Glu
 100 105 110
 Tyr Met Glu Gln Met Leu Phe Lys Ile Glu Asn Ala Thr Trp Gln Arg
 115 120 125
 Val Val Arg Ala Leu Tyr Arg Lys Tyr Asn Lys Glu Phe Phe Thr Tyr
 130 135 140
 Pro Ala Ala Lys Thr Asn His His Ala Phe Glu Ser Gly Leu Ala Tyr
 145 150 155 160
 His Thr Ala Thr Met Val Arg Leu Ala Asp Ser Ile Gly Asp Ile Tyr
 165 170 175
 Pro Glu Leu Asn Lys Ser Leu Met Phe Ala Gly Ile Met Leu His Asp
 180 185 190
 Leu Ala Lys Val Ile Glu Leu Ser Gly Pro Asp Asn Thr Glu Tyr Thr
 195 200 205
 Ile Arg Gly Asn Leu Ile Gly His Ile Ser Leu Ile Asp Glu Glu Leu
 210 215 220
 Thr Lys Ile Leu Ala Glu Leu Asn Ile Asp Asp Thr Lys Glu Glu Val
 225 230 235 240

GBS patentin.ST25

Thr Val Leu Arg His val Ile Leu Ser His His Gly Gln Leu Glu Tyr
245 250 255

Gly Ser Pro Val Arg Pro Arg Ile Met Glu Ala Glu Ile Ile His Met
260 265 270

Ile Asp Asn Ile Asp Ala Asn Met Met Met Met Thr Thr Ala Leu Asn
275 280 285

Arg Val Asn Glu Gly Glu Met Thr Asn Arg Ile Phe Ala Met Asp Asn
290 295 300

Arg Ser Phe Tyr Lys Pro Asn Ile Lys
305 310

<210> 349

<211> 283

<212> PRT

<213> streptococcus agalactiae

<400> 349

Met Leu Val Asp Lys Lys Trp Arg Phe Glu Asp Ser Ala Ser Tyr Phe
1 5 10 15

Ala Cys Pro Lys Cys Gln Asn Pro Leu Ile Lys Glu Ser Asn Ser Leu
20 25 30

Lys Cys Ser Asp Asn His Cys Phe Asp Leu Ser Lys Phe Gly Tyr Val
35 40 45

Asn Leu Leu Gly Gly Lys Lys Ile Asp Glu His Tyr Asp Lys Lys Ser
50 55 60

Phe Glu Asn Arg Gln Leu Val Leu Glu Asn Gly Tyr Tyr Asn His Ile
65 70 75 80

Leu Glu Ala Ile Ser Lys Val Leu Glu Asn Asn ser Gln Phe His Ser
85 90 95

Val Leu Asp Ile Gly Cys Gly Glu Gly Phe Tyr ser Arg Gln Leu Val
100 105 110

Asn Lys Tyr Glu Lys Thr Phe Leu Ala Phe Asp Ile Ser Lys Asp Ser
115 120 125

Ile Gln Leu Ala Ala Lys Ser Asp Gln ser Arg Leu Val Lys Trp Phe
130 135 140

GBS patentin.ST25

Val Ser Asp Leu Ala Asn Leu Pro Ile Gln Asp Ser Ser Ile Asp Ile
145 150 155 160

Ile Leu Asp Ile Phe Ser Pro Ala Asn Tyr Lys Glu Phe Arg Arg Val
165 170 175

Leu Ser Asp Asp Gly Ile Leu Val Lys Val Val Pro Val Ala Glu His
180 185 190

Val Gln Glu Leu Arg Glu Lys Ala Ser Gln Tyr Leu Lys Gln Lys Asp
195 200 205

Tyr Ser Asn Gln Lys Ile Leu Asp His Phe Arg Glu Asn Phe Glu Ile
210 215 220

Ile Ser Glu Gln Lys Val Val Gln Ser Tyr Asn Cys Ser Gln Gln Glu
225 230 235 240

Arg Gln Ala Phe Ile Asp Met Thr Pro Leu Leu Phe Ser Val Asp Lys
245 250 255

Thr Thr Ile Asp Trp Ala Ser Ile Ser Glu Ile Thr Val Gly Ala Leu
260 265 270

Ile Val Ile Gly Lys Lys Arg Ser Val Ser Lys
275 280

<210> 350

<211> 149

<212> PRT

<213> streptococcus agalactiae

<400> 350

Met Cys Leu Ile Cys Gln Arg Ile Glu Met Ile Glu Arg Asn Glu Asn
1 5 10 15

Pro Tyr Phe Val Lys Glu Tyr Glu Thr Gly Tyr Leu Val Leu Gly Asp
20 25 30

His Gln Tyr Phe Gln Gly Tyr Cys Leu Phe Leu Ser Lys Lys His Val
35 40 45

Thr Glu Leu His Glu Leu Pro Arg Asp Trp Arg Asn Gln Tyr Leu Ser
50 55 60

Glu Met Ala Asp Ala Ser Glu Ile Val Ala Lys Ala Phe Arg Ala Asp
65 70 75 80

GBS patentin.ST25

Lys Met Asn Ile Glu Ser Leu Gly Asn Gly Asp Ala His Leu His Phe
85 90 95

His Leu Phe Pro Arg Lys Thr Gly Asp Leu Arg Asn Tyr Gly His Asn
100 105 110

Gly Lys Gly Pro Val Trp Trp Tyr Pro Phe Glu Lys Met Tyr Ala Asp
115 120 125

Ser Val Arg Ala Thr Gly Ala Glu Ile Glu Lys Leu Lys Glu Lys Leu
130 135 140

Leu Asp Val Leu Gly
145

<210> 351

<211> 395

<212> PRT

<213> streptococcus agalactiae

<400> 351

Met Phe Ser Asp Leu Arg Lys Lys Phe Val Phe Leu Thr Met Ser Ile
1 5 10 15

Leu Ile Val Val Val Leu Phe Leu Phe Ala Val Ser Asn Arg Tyr Asn
20 25 30

Gln Tyr Trp Asp Glu Tyr Asp Ala Tyr Arg Ile Val Lys Leu Val Ala
35 40 45

Lys Asn Asp Tyr Leu Gly Ile Pro Gly Asp Glu Pro Ile Ala Leu Val
50 55 60

Thr Ile Asp Asn Gln Lys Met Val Lys Ile Gln Ser Asn Asn Thr Asp
65 70 75 80

Leu Thr Asn Asp Val Ile Glu Lys Ser Ser Leu Lys Leu Leu Glu Gln
85 90 95

Gly Lys Lys Ser Arg Lys Trp Lys Ser Phe Ile Tyr Ser Ile Lys Glu
100 105 110

Tyr Lys Asp Lys Thr Tyr Thr Ile Ala Ile Met Asp Leu Ala Ser Tyr
115 120 125

Glu Val Pro Tyr Ala Arg Arg Phe Leu Ile Leu Val Phe Thr Ile Phe
130 135 140

GBS patentin.ST25

Gly Phe Cys Leu Leu Ala Ala Val Ser Leu Tyr Leu Ser Arg Phe Ile
145 150 155 160

Val Gly Pro Val Glu Thr Glu Met Thr Arg Glu Lys Gln Phe Val Ser
165 170 175

Asp Ala Ser His Glu Leu Lys Thr Pro Ile Ala Ala Ile Arg Ala Asn
180 185 190

Val Gln Val Leu Glu Gln Gln Ile Pro Gly Asn Arg Tyr Leu Asp His
195 200 205

Val Val Ser Glu Thr Lys Arg Met Glu Phe Leu Ile Glu Asp Leu Leu
210 215 220

Asn Leu Ser Arg Leu Asp Glu Lys Arg Ser Lys Val Asn Phe Lys Lys
225 230 235 240

Leu Asn Leu Ser Val Leu Cys Gln Glu Val Leu Leu Thr Tyr Glu Ser
245 250 255

Leu Ala Tyr Glu Glu Glu Lys Cys Leu Asn Asp Thr Ile Glu Asp Asp
260 265 270

Val Trp Ile Val Gly Glu Glu Ser Gln Ile Lys Gln Ile Leu Ile Ile
275 280 285

Leu Leu Asp Asn Ala Ile Arg His Ser Leu Ser Lys Ser Glu Ile Gln
290 295 300

Phe Ser Leu Lys Gln Ala Arg Arg Lys Ala Ile Leu Thr Ile Ser Asn
305 310 315 320

Pro Ser Ala Ile Tyr Ser Lys Glu Val Met Asp Asn Leu Phe Glu Arg
325 330 335

Phe Tyr Gln Ala Lys Asp Asp His Ala Asp Ser Leu Ser Phe Gly Leu
340 345 350

Gly Leu Ser Ile Ala Lys Ala Ile Val Glu Arg His Lys Gly Arg Ile
355 360 365

Arg Ala Tyr Gln Glu Lys Asp Gln Leu Arg Leu Glu Val Gln Leu Pro
370 375 380

Ile Asp Gly Phe Trp Thr Asn Thr Met Ile Asn
385 390 395

<210> 352

GBS patentin.ST25

<211> 559

<212> PRT

<213> Streptococcus agalactiae

<400> 352

Leu Ile Ile Leu Asp Lys Lys Ser Tyr Asp Leu Leu Phe Tyr Leu Leu
1 5 10 15

Lys Leu Glu Glu Pro Glu Thr Val Met Ala Ile Ala Asn Ala Leu Asn
20 25 30

Gln Ser Arg Arg Lys Val Tyr Tyr His Leu Glu Lys Ile Asn Asp Ala
35 40 45

Leu Pro Ser Asp Val Pro Gln Ile Val Ser Tyr Pro Arg Val Gly Ile
50 55 60

Leu Leu Thr Glu Lys Gln Lys Ala Ala Cys Arg Leu Leu Leu Asp Glu
65 70 75 80

Val Thr Asp Tyr Ser Tyr Val Met Lys Ser Ser Glu Arg Leu Gln Leu
85 90 95

Ser Leu Val Ser Ile Val Val Ala Lys Asp Arg Ile Thr Ile Asp Arg
100 105 110

Leu Met Gln Leu Asn Asp Val Ser Arg Asn Thr Ile Leu Asn Asp Leu
115 120 125

Asn Glu Leu Arg Ser Glu Leu Ala Glu Lys Glu Tyr Asn Leu Gln Leu
130 135 140

Gln Ser Thr Lys Cys Arg Gly Tyr Phe Leu Asp Gly His Pro Leu Ser
145 150 155 160

Ile Ile Gln Tyr Leu Tyr Lys Leu Leu Asp Asp Ile Tyr His Asn Gly
165 170 175

Ser Ser Ser Phe Ile Asp Leu Phe Asn His Lys Leu Ser Gln Ala Phe
180 185 190

Gly Ala Ser Thr Tyr Phe Ser Lys Glu Val Leu Asp Tyr Phe His His
195 200 205

Tyr Leu Phe Ile Ser Gln Arg Ser Leu Gly Lys Lys Ile Asn Ser Gln
210 215 220

Asp Gly Gln Phe Met Ile Gln Ile Leu Pro Phe Ile Leu Met Ala Tyr
225 230 235 240

GBS patentin.ST25

Arg Lys Met Arg Leu Ser Pro Glu Val Gln Thr Ser Leu Asn Ser Asp
245 250 255

Phe Ser Leu Val Trp Gln Arg Lys Glu Tyr Glu Ile Ala Lys Glu Leu
260 265 270

Ala Asp Glu Leu Glu Glu Asn Phe Gln Leu Ser Leu Asp Glu Ile Glu
275 280 285

Val Gly Leu Val Ala Met Leu Met Leu Ser Phe Arg Lys Asp Arg Asp
290 295 300

Asn His Leu Glu Ser Gln Asp Tyr Asp Asp Met Arg Ala Thr Leu Thr
305 310 315 320

Ser Phe Leu Lys Glu Leu Glu Glu Arg Tyr His Leu His Phe Val His
325 330 335

Lys Lys Asp Leu Leu Arg Gln Leu Leu Thr His Cys Lys Ala Leu Leu
340 345 350

Tyr Arg Lys Arg Tyr Gly Ile Phe Ser Val Asn Pro Leu Thr Glu His
355 360 365

Ile Lys Asp Lys Tyr Glu Glu Leu Phe Ala Ile Thr Ser Ser Ser Val
370 375 380

Lys Leu Leu Glu Lys Ala Trp Gln Ile Lys Leu Thr Asp Asp Asp Val
385 390 395 400

Ala Tyr Leu Thr Ile His Leu Gly Gly Glu Leu Arg Asn Ser Gln Gln
405 410 415

Ser Pro Asn Lys Leu Lys Leu Val Ile Val Ser Asp Glu Gly Ile Ala
420 425 430

Ile Gln Lys Leu Leu Leu Lys Gln Cys Gln Arg Tyr Leu Thr Asn Ser
435 440 445

Asp Ile Glu Ala Val Phe Thr Thr Glu Gln Tyr Gln Ser Val Ser Asp
450 455 460

Leu Met His Val Asp Met Val Val Ser Thr Ser Asp Ala Leu Glu Ser
465 470 475 480

Arg Phe Pro Met Leu Val Val His Pro Val Leu Thr Asp Asp Asp Ile
485 490 495

Ile Arg Leu Ile Arg Phe Ser Lys Lys Gly Asn Cys Ala Asn Ser Asn
500 505 510

GBS patentin.ST25

Gln Phe Thr Asn Glu Leu Glu Lys Thr Ile Ala Gln Tyr Val Lys Glu
515 520 525

Asp Ser Glu Arg Tyr Val Leu Lys Ser Lys Ile Glu Lys Leu Ile His
530 535 540

Gln Glu Leu Leu Gln Asp Val Leu Pro Leu Gln Ser Thr Val Cys
545 550 555

<210> 353

<211> 215

<212> PRT

<213> Streptococcus agalactiae

<400> 353

Met Lys Tyr Phe Leu Asp Thr Ala Asp Val Ser Glu Ile Arg Arg Leu
1 5 10 15

Asn Arg Leu Gly Ile Val Asp Gly Val Thr Thr Asn Pro Thr Ile Ile
20 25 30

Ser Arg Glu Gly Arg Asp Phe Lys Glu Val Ile Asn Glu Ile Cys Gln
35 40 45

Ile Val Asp Gly Pro Val Ser Ala Glu Val Thr Gly Leu Thr Cys Asp
50 55 60

Glu Met Val Thr Glu Ala Arg Glu Ile Ala Lys Trp Ser Pro Asn Val
65 70 75 80

Val Val Lys Ile Pro Met Thr Glu Glu Gly Leu Ala Ala Val Ser Gln
85 90 95

Leu Ser Lys Glu Gly Ile Lys Thr Asn Val Thr Leu Ile Phe Thr Val
100 105 110

Ala Gln Gly Leu Ser Ala Met Lys Ala Gly Ala Thr Phe Ile Ser Pro
115 120 125

Phe Val Gly Arg Leu Glu Asp Ile Gly Thr Asp Ala Tyr Ala Leu Ile
130 135 140

Arg Asp Leu Arg His Ile Ile Asp Phe Tyr Gly Phe Gln Ser Glu Ile
145 150 155 160

Ile Ala Ala Ser Ile Arg Gly Leu Ala His Val Glu Gly Val Ala Lys
165 170 175

GBS patentin.ST25

Cys Gly Ala His Ile Ala Thr Ile Pro Asp Lys Thr Phe Ala Ser Leu
180 185 190

Phe Thr His Pro Leu Thr Asp Lys Gly Ile Glu Thr Phe Leu Lys Asp
195 200 205

Trp Asp Ser Phe Lys Lys Lys
210 215

<210> 354

<211> 815

<212> PRT

<213> Streptococcus agalactiae

<400> 354

Met Ser His Tyr Ser Ile Lys Leu Gln Glu Val Phe Arg Leu Ala Gln
1 5 10 15

Phe Gln Ala Ala Arg Tyr Glu Ser His Tyr Leu Glu Ser Trp His Leu
20 25 30

Leu Leu Ala Met Val Leu Val His Asp Ser Val Ala Gly Leu Thr Phe
35 40 45

Ala Glu Tyr Glu Ser Glu Val Ala Ile Glu Glu Tyr Glu Ala Ala Thr
50 55 60

Ile Leu Ala Leu Gly Arg Ala Pro Lys Glu Glu Ile Thr Asn Tyr Gln
65 70 75 80

Phe Leu Glu Gln Ser Pro Ala Leu Lys Lys Ile Leu Lys Leu Ala Glu
85 90 95

Asn Ile Ser Ile Val Val Gly Ala Glu Asp Val Gly Thr Glu His Val
100 105 110

Leu Leu Ala Met Leu Val Asn Lys Asp Leu Leu Ala Thr Arg Ile Leu
115 120 125

Glu Leu Val Gly Phe Arg Gly Gln Asp Asp Gly Glu Ser Val Arg Met
130 135 140

Val Asp Leu Arg Lys Ala Leu Glu Arg His Ala Gly Phe Thr Lys Asp
145 150 155 160

Asp Ile Lys Ala Ile Tyr Glu Leu Arg Asn Pro Lys Lys Ala Lys Ser
165 170 175

GBS patentin.ST25

Gly Ala Ser Phe Ser Asp Met Met Lys Pro Pro Ser Thr Ala Gly Asp
180 185 190

Leu Ala Asp Phe Thr Arg Asp Leu Ser Gln Met Ala Val Asp Gly Glu
195 200 205

Ile Glu Pro Val Ile Gly Arg Asp Lys Glu Ile Ser Arg Met Val Gln
210 215 220

Val Leu Ser Arg Lys Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala
225 230 235 240

Gly Val Gly Lys Thr Ala Leu Ala Tyr Gly Leu Ala Gln Arg Ile Ala
245 250 255

Asn Gly Asn Ile Pro Tyr Glu Leu Arg Asp Met Arg Val Leu Glu Leu
260 265 270

Asp Met Met Ser Val Val Ala Gly Thr Arg Phe Arg Gly Asp Phe Glu
275 280 285

Glu Arg Met Asn Gln Ile Ile Ala Asp Ile Glu Glu Asp Gly His Ile
290 295 300

Ile Leu Phe Ile Asp Glu Leu His Thr Ile Met Gly Ser Gly Ser Gly
305 310 315 320

Ile Asp Ser Thr Leu Asp Ala Ala Asn Ile Leu Lys Pro Ala Leu Ala
325 330 335

Arg Gly Thr Leu Arg Thr Val Gly Ala Thr Thr Gln Glu Glu Tyr Gln
340 345 350

Lys His Ile Glu Lys Asp Ala Ala Leu Ser Arg Arg Phe Ala Lys Val
355 360 365

Leu Val Glu Glu Pro Asn Leu Glu Asp Ala Tyr Glu Ile Leu Leu Gly
370 375 380

Leu Lys Pro Ala Tyr Glu Ala Phe His Asn Val Thr Ile Ser Asp Glu
385 390 395 400

Ala Val Met Thr Ala Val Lys Val Ala His Arg Tyr Leu Thr Ser Lys
405 410 415

Asn Leu Pro Asp Ser Ala Ile Asp Leu Leu Asp Glu Ala Ser Ala Thr
420 425 430

Val Gln Met Met Ile Lys Lys Asn Ala Pro Ser Leu Leu Thr Glu Val
435 440 445

GBS patentin.ST25

Asp Gln Ala Ile Leu Asp Asp Asp Met Lys Ser Ala Ser Lys Ala Leu
 450 455 460
 Lys Ala Ser Tyr Lys Gly Lys Lys Arg Lys Pro Ile Ala Val Thr Glu
 465 470 475 480
 Asp His Ile Met Ala Thr Leu Ser Arg Leu Ser Gly Ile Pro Val Glu
 485 490 495
 Lys Leu Thr Gln Ala Asp Ser Lys Lys Tyr Leu Asn Leu Glu Lys Glu
 500 505 510
 Leu His Lys Arg Val Ile Gly Gln Asp Asp Ala Val Thr Ala Ile Ser
 515 520 525
 Arg Ala Ile Arg Arg Asn Gln Ser Gly Ile Arg Thr Gly Lys Arg Pro
 530 535 540
 Ile Gly Ser Phe Met Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Glu
 545 550 555 560
 Leu Ala Lys Ala Leu Ala Glu Val Leu Phe Asp Asp Glu Ser Ala Leu
 565 570 575
 Ile Arg Phe Asp Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Ser His
 580 585 590
 Leu Asn Gly Ala Pro Pro Gly Tyr Val Gly Tyr Asp Glu Gly Gly Glu
 595 600 605
 Leu Thr Glu Lys Val Arg Asn Lys Pro Tyr Ser Val Leu Leu Phe Asp
 610 615 620
 Glu Val Glu Lys Ala His Pro Asp Ile Phe Asn Val Leu Leu Gln Val
 625 630 635 640
 Leu Asp Asp Gly Val Leu Thr Asp Ser Arg Gly Arg Lys Val Asp Phe
 645 650 655
 Ser Asn Thr Ile Ile Ile Met Thr Ser Asn Leu Gly Ala Thr Ala Leu
 660 665 670
 Arg Asp Asp Lys Thr Val Gly Phe Gly Ala Lys Asp Ile Ser His Asp
 675 680 685
 Tyr Thr Ala Met Gln Lys Arg Ile Met Glu Glu Leu Lys Lys Ala Tyr
 690 695 700
 Arg Pro Glu Phe Ile Asn Arg Ile Asp Glu Lys Val Val Phe His Ser
 705 710 715 720

GBS patentin.ST25

Leu Ser Gln Asp Asn Met Arg Glu Val Val Lys Ile Met Val Lys Pro
725 730 735

Leu Ile Leu Ala Leu Lys Asp Lys Gly Met Asp Leu Lys Phe Gln Pro
740 745 750

Ser Ala Leu Lys His Leu Ala Glu Asp Gly Tyr Asp Ile Glu Met Gly
755 760 765

Ala Arg Pro Leu Arg Arg Thr Ile Gln Thr Gln Val Glu Asp His Leu
770 775 780

Ser Glu Leu Leu Leu Ala Asn Gln Val Lys Glu Gly Gln Val Ile Lys
785 790 795 800

Ile Gly Val Ser Lys Gly Lys Leu Lys Phe Asp Ile Ala Lys Ser
805 810 815

<210> 355

<211> 510

<212> PRT

<213> Streptococcus agalactiae

<400> 355

Met Val Leu Asp Lys Glu Ile Lys Ala Gln Leu Ala Gln Tyr Leu Asp
1 5 10 15

Leu Leu Glu Ser Asp Ile Val Leu Gln Ala Asp Leu Gly Asp Asn Asp
20 25 30

Asn Ser Gln Lys Val Lys Asp Phe Leu Asp Glu Ile Val Ala Met Ser
35 40 45

Asp Arg Ile Ser Leu Glu Ser Thr His Leu Lys Arg Gln Pro Ser Phe
50 55 60

Gly Ile Ala Lys Lys Gly His Glu Ser Arg Val Ile Phe Ser Gly Leu
65 70 75 80

Pro Met Gly His Glu Phe Thr Ser Phe Ile Leu Ala Leu Leu Gln Val
85 90 95

Ser Gly Arg Ala Pro Lys Val Asp Glu Asp Ile Ile Lys Arg Ile Lys
100 105 110

Gly Ile Glu Lys Thr Ile Asn Leu Glu Thr Tyr Val Ser Leu Thr Cys
115 120 125

GBS patentin.ST25

His Asn Cys Pro Asp Val Val Gln Ala Phe Asn Ile Met Ala Val Leu
130 135 140

Asn Pro Asn Ile Thr His Thr Met Ile Glu Gly Gly Met Tyr Gln Asp
145 150 155 160

Glu Val Lys Ser Lys Gly Ile Met Ser Val Pro Thr Val Tyr Lys Asp
165 170 175

Gln Glu Glu Phe Thr Ser Gly Arg Ala Thr Ile Glu Gln Leu Leu Glu
180 185 190

Gln Leu Asp Gly Pro Leu Asp Ala Glu Ala Phe Ala Asp Lys Gly Val
195 200 205

Tyr Asp Val Leu Val Ile Gly Gly Gly Pro Ala Gly Asn Ser Ala Ala
210 215 220

Ile Tyr Ala Ala Arg Lys Gly Leu Lys Thr Gly Ile Leu Ala Glu Thr
225 230 235 240

Phe Gly Gly Gln Val Ile Glu Thr Val Gly Ile Glu Asn Met Ile Gly
245 250 255

Thr Leu Tyr Thr Glu Gly Pro Lys Leu Met Ala Gln Ile Glu Glu His
260 265 270

Thr Lys Ser Tyr Asp Ile Asp Ile Ile Lys Ser Gln Leu Ala Thr Gly
275 280 285

Ile Glu Lys Lys Glu Leu Val Glu Val Thr Leu Ala Asn Gly Ala Ile
290 295 300

Leu Gln Ala Lys Thr Ala Ile Leu Ala Leu Gly Ala Lys Trp Arg Asn
305 310 315 320

Ile Asn Val Pro Gly Glu Glu Glu Phe Arg Asn Lys Gly Val Thr Tyr
325 330 335

Cys Pro His Cys Asp Gly Pro Leu Phe Glu Gly Lys Asp Val Ala Val
340 345 350

Ile Gly Gly Gly Asn Ser Gly Met Glu Ala Ala Leu Asp Leu Ala Gly
355 360 365

Val Thr Lys His Val Thr Val Leu Glu Phe Leu Pro Glu Leu Lys Ala
370 375 380

Asp Gln Val Leu Gln Glu Arg Ala Ala Lys Thr Asp Asn Leu Thr Ile
385 390 395 400

GBS patentin.ST25

Leu Lys Asn Val Ala Thr Lys Asp Ile Val Gly Glu Asp His Val Thr
405 410 415

Gly Leu Asn Tyr Thr Asp Arg Asp Thr Asn Glu Glu Lys His Ile Asp
420 425 430

Leu Glu Gly Val Phe Val Gln Ile Gly Leu Val Pro Ser Thr Ser Trp
435 440 445

Leu Lys Asp Ser Gly Ile Glu Leu Asn Glu Arg Gln Glu Ile Val Val
450 455 460

Asp Lys Phe Gly Ser Thr Asn Ile Pro Gly Ile Phe Ala Ala Gly Asp
465 470 475 480

Cys Thr Asp Ala Ala Tyr Lys Gln Ile Ile Ile Ser Met Gly Ser Gly
485 490 495

Ala Thr Ala Ala Ile Gly Ala Phe Asp Tyr Leu Ile Arg Gln
500 505 510

<210> 356

<211> 631

<212> PRT

<213> Streptococcus agalactiae

<400> 356

Met Ile Lys Tyr Gln Asp Asp Phe Tyr Gln Ala Val Asn Gly Glu Trp
1 5 10 15

Ala Lys Thr Ala Val Ile Pro Asp Asp Lys Pro Arg Thr Gly Gly Phe
20 25 30

Ser Asp Leu Ala Asp Asp Ile Glu Ala Leu Met Leu Ser Thr Thr Asp
35 40 45

Lys Trp Leu Ala Asp Glu Asn Lys Pro Ser Asp Thr Ile Leu Asn His
50 55 60

Phe Ile Ala Phe His Lys Met Thr Ala Asp Tyr Gln Lys Arg Glu Glu
65 70 75 80

Val Gly Val Ser Pro Val Leu Pro Leu Ile Glu Glu Tyr Lys Gly Leu
85 90 95

Gln Ser Phe Ser Glu Phe Ala Ser Lys Val Ala Glu Tyr Glu Leu Glu
100 105 110

GBS patentin.ST25

Gly Lys Pro Asn Glu Phe Pro Phe Gly Val Ala Pro Asp Phe Met Asn
115 120 125

Ala Gln Leu Asn Val Leu Trp Ala Glu Ala Pro Gly Ile Ile Leu Pro
130 135 140

Asp Thr Thr Tyr Tyr Ser Glu Asp Asn Glu Lys Gly Lys Glu Leu Leu
145 150 155 160

Ala Phe Trp Arg Lys Ser Gln Glu Asp Leu Leu Pro Leu Phe Gly Leu
165 170 175

Ser Glu Gln Glu Ile Lys Asp Ile Leu Asp Lys Val Leu Ala Leu Asp
180 185 190

Ala Lys Leu Ala Gln Tyr Val Leu Ser Arg Glu Glu Ser Ser Glu Tyr
195 200 205

Val Lys Leu Tyr His Pro Tyr Asn Trp Glu Asp Phe Thr Lys Leu Ala
210 215 220

Pro Glu Leu Pro Leu Asp Ala Ile Phe Gln Lys Ile Leu Gly Gln Lys
225 230 235 240

Pro Asp Lys Val Ile Val Pro Glu Glu Arg Phe Trp Thr Glu Phe Ala
245 250 255

Ser Asp Tyr Tyr Ser Glu Ser Asn Trp Glu Leu Leu Lys Ala Asp Leu
260 265 270

Ile Leu Ser Ala Ala Asn Ala Tyr Asn Ala Tyr Leu Thr Asp Asp Ile
275 280 285

Arg Ile Lys Ser Gly Val Tyr Ser Arg Ala Leu Ser Gly Thr Pro Gln
290 295 300

Ala Met Asp Lys Lys Lys Ala Ala Tyr Tyr Leu Ala Ser Gly Pro Tyr
305 310 315 320

Asn Gln Ala Leu Gly Leu Trp Tyr Ala Gly Glu Lys Phe Ser Pro Glu
325 330 335

Ala Lys Ala Asp Val Glu His Lys Ile Ala Thr Met Ile Asp Val Tyr
340 345 350

Lys Ser Arg Leu Glu Lys Ala Asp Trp Leu Ala Gln Ser Thr Arg Glu
355 360 365

Lys Ala Ile Met Lys Leu Asn Val Ile Thr Pro His Ile Gly Tyr Pro
370 375 380

GBS patentin.ST25

Glu Lys Leu Pro Glu Thr Tyr Thr Lys Lys Ile Ile Asp Pro Lys Leu
385 390 395 400

Ser Leu Val Glu Asn Ala Thr Asn Leu Asp Lys Ile Ser Ile Ala Tyr
405 410 415

Gly Trp Ser Lys Trp Asn Lys Pro Val Asp Arg Ser Glu Trp His Met
420 425 430

Pro Ala His Met Val Asn Ala Tyr Tyr Asp Pro Gln Gln Asn Gln Ile
435 440 445

Val Phe Pro Ala Ala Ile Leu Gln Glu Pro Phe Tyr Ala Leu Glu Gln
450 455 460

Ser Ser Ser Ala Asn Tyr Gly Gly Ile Gly Ala Val Ile Ala His Glu
465 470 475 480

Ile Ser His Ala Phe Asp Thr Asn Gly Ala Ser Phe Asp Glu His Gly
485 490 495

Ser Leu Asn Asn Trp Trp Thr Asp Glu Asp Phe Glu Ala Phe Lys Lys
500 505 510

Leu Thr Asp Lys Val Val Glu Gln Phe Asp Gly Leu Glu Ser Tyr Gly
515 520 525

Ala Lys Val Asn Gly Lys Leu Thr Val Ser Glu Asn Val Ala Asp Leu
530 535 540

Gly Gly Val Ala Cys Ala Leu Glu Ala Ala Gln Arg Glu Ser Asp Phe
545 550 555 560

Ser Ala Arg Asp Phe Phe Ile Asn Phe Ala Thr Ile Trp Arg Met Lys
565 570 575

Ala Arg Asp Glu Tyr Met Gln Met Leu Ala Ser Val Asp Val His Ala
580 585 590

Pro Ala Gln Trp Arg Thr Asn Ile Thr Val Thr Asn Phe Glu Glu Phe
595 600 605

His Lys Glu Phe Asp Val Lys Asp Gly Asp Asn Met Trp Arg Pro Val
610 615 620

Glu Lys Arg Val Ile Ile Trp
625 630

<210> 357

GBS patentin.ST25

<211> 335

<212> PRT

<213> Streptococcus agalactiae

<400> 357

```

Met Ser Lys Ile Leu Phe Phe Gly Glu Pro Leu Ile Arg Ile Thr Pro
1      5      10      15
Lys Glu Asn Asp Tyr Phe Ala Asp Ser Ile Ser Thr Lys Leu Phe Tyr
20      25      30
Gly Gly Ser Glu Val Asn Thr Ala Arg Ala Leu Gln Gly Phe Gly Gln
35      40      45
Asp Thr Lys Leu Leu Ser Ala Leu Pro Asn Asn Pro Ile Gly Asn Ser
50      55      60
Phe Leu Gln Phe Leu Lys Ala Gln Gly Ile Asp Thr His Ser Ile Gln
65      70      75      80
Trp Val Gly Glu Arg Val Gly Leu Tyr Phe Leu Glu Asp Ser Phe Ala
85      90      95
Cys Arg Lys Gly Glu Val Val Tyr Asp Arg Asp His Ser Ser Leu His
100     105     110
Asp Phe Arg Ile Asn Gln Ile Asp Phe Asp Gln Leu Phe Glu Gly Val
115     120     125
Ser Leu Phe His Phe Ser Gly Ile Thr Leu Ser Leu Asp Glu Ser Ile
130     135     140
Gln Glu Ile Thr Leu Leu Leu Leu Lys Glu Ala Lys Lys Arg Glu Ile
145     150     155     160
Thr Ile Ser Leu Asp Leu Asn Phe Arg Ser Lys Leu Ile Ser Pro Lys
165     170     175
Asn Ala Lys Ile Leu Phe Ser Gln Phe Ala Thr Phe Ala Asp Ile Cys
180     185     190
Phe Gly Ile Glu Pro Leu Met Val Asp Ser Gln Asp Thr Thr Phe Phe
195     200     205
Asn Arg Asp Glu Ala Thr Ile Glu Asp Val Lys Glu Arg Met Ile Ser
210     215     220
Leu Ile Asn His Phe Asp Phe Gln Val Ile Phe His Thr Lys Arg Leu
225     230     235     240

```

GBS patentin.ST25

Gln Asp Glu Trp Gly Arg Asn His Tyr Gln Ala Tyr Ile Ala Asn Arg
245 250 255

Lys Gln Glu Phe Val Thr Ser Lys Glu Ile Thr Thr Ala Val Asn Gln
260 265 270

Arg Ile Gly Ser Gly Asp Ala Phe Val Ala Gly Ala Leu Tyr Gln Leu
275 280 285

Leu Gln His Ser Asp Ser Lys Thr Val Ile Asp Phe Ala Val Ala Ser
290 295 300

Ala Ser Leu Lys Cys Ala Leu Glu Gly Asp Asn Met Phe Glu Thr Val
305 310 315 320

Thr Ala Val Asn Lys Val Leu Asn Gln Ser Lys Asp Ile Ile Arg
325 330 335

<210> 358

<211> 194

<212> PRT

<213> Streptococcus agalactiae

<400> 358

Met Lys Ser Arg Lys Lys Asp Lys Leu Val Leu Arg Leu Thr Thr Thr
1 5 10 15

Leu Leu Val Phe Gly Leu Gly Gly Val Trp Phe Tyr Asn Tyr Lys Asn
20 25 30

Asp Asn Val Glu Pro Thr Val Thr Ser Ala Ser Asp Gln Thr Thr Thr
35 40 45

Phe Ile Gln Thr Ile Ser Pro Thr Ala Ile Glu Ile Ser Lys Thr Tyr
50 55 60

Asp Leu Tyr Ala Ser Val Leu Leu Ala Gln Ala Ile Leu Glu Ser Ser
65 70 75 80

Ser Gly Gln Ser Asp Leu Ser Lys Ala Pro Asn Tyr Asn Leu Phe Gly
85 90 95

Ile Lys Gly Glu Tyr Lys Gly Lys Ser Val Gln Met Pro Thr Leu Glu
100 105 110

Asp Asp Gly Lys Gly Asn Met Thr Gln Ile Gln Ala Pro Phe Arg Ala
115 120 125

GBS patentin.ST25

Tyr Pro Asn Tyr Ser Ala Ser Leu Tyr Asp Tyr Ala Glu Leu Val Ser
130 135 140

Ser Gln Lys Tyr Ala Ser Val Trp Lys Ser Asn Thr Ser Ser Tyr Lys
145 150 155 160

Asp Ala Thr Ala Ala Leu Thr Gly Leu Tyr Ala Thr Asp Thr Ala Tyr
165 170 175

Ala Ser Lys Leu Asn Gln Ile Ile Glu Thr Tyr Ser Leu Asp Ala Tyr
180 185 190

Asp Lys

<210> 359

<211> 445

<212> PRT

<213> Streptococcus agalactiae

<400> 359

Met Ala Asp Val Lys Val Val Asn Asn Glu Asp Ser Arg Gly Gln Lys
1 5 10 15

Gln Asp Leu Lys Ala Lys Leu Phe His Ile Lys Ile Gly Ser Val Pro
20 25 30

Leu Pro Val Tyr Val Cys Leu Ala Leu Leu Ile Leu Leu Ala Gly Phe
35 40 45

Leu Gln Lys Leu Pro Val Asn Met Leu Gly Gly Phe Ala Val Ile Leu
50 55 60

Thr Met Gly Trp Phe Leu Gly Thr Ile Gly Ala Ser Ile Pro Gly Phe
65 70 75 80

Lys Asn Phe Gly Gly Pro Ala Ile Leu Ser Leu Leu Val Pro Ser Ile
85 90 95

Leu Val Phe Phe Asn Leu Ile Asn Lys Asn Val Leu Glu Ser Thr Asn
100 105 110

Met Leu Met Lys Gln Ala Asn Phe Leu Tyr Phe Tyr Ile Ala Cys Leu
115 120 125

Val Ser Gly Ser Ile Leu Gly Met Asn Arg Lys Met Leu Ile Gln Gly
130 135 140

GBS patentin.ST25

Leu Leu Arg Met Ile Phe Pro Met Leu Leu Gly Met Val Cys Ala Met
145 150 155 160

Met Val Gly Thr Phe Val Gly Val Ile Leu Gly Leu Glu Trp Arg His
165 170 175

Thr Leu Phe Tyr Ile Val Thr Pro Val Leu Ala Gly Gly Ile Gly Glu
180 185 190

Gly Ile Leu Pro Leu Ser Leu Gly Tyr Ser Ser Ile Thr Gly Val Ala
195 200 205

Ser Glu Gln Leu Val Ala Gln Leu Ile Pro Ala Thr Ile Ile Gly Asn
210 215 220

Phe Phe Ala Ile Leu Cys Thr Ala Leu Leu Asn Arg Leu Gly Glu Lys
225 230 235 240

Lys Pro His Leu Ser Gly Gln Gly Gln Leu Val Arg Leu Asn Lys Gly
245 250 255

Glu Asp Met Ser Asp Ile Ile Ala Asp His Ser Gly Pro Ile Asp Val
260 265 270

Lys Lys Met Gly Gly Gly Val Leu Thr Ala Cys Ser Leu Phe Ile Phe
275 280 285

Gly His Leu Leu Gln Gln Leu Thr Gly Phe Pro Gly Pro Val Leu Met
290 295 300

Ile Val Ala Ala Ala Ile Leu Lys Tyr Ile Asn Val Ile Pro Arg Glu
305 310 315 320

Thr Gln Asn Gly Ala Lys Gln Leu Tyr Lys Phe Ile Ser Gly Asn Phe
325 330 335

Thr Phe Pro Leu Met Ala Gly Leu Gly Leu Leu Tyr Ile Pro Leu Lys
340 345 350

Asp Val Val Ala Thr Leu Ser Ile Gln Tyr Phe Ile Val Val Ile Ser
355 360 365

Val Val Phe Thr Val Ile Ser Val Gly Phe Phe Val Ser Arg Phe Leu
370 375 380

Asn Met Asn Pro Val Glu Ala Gly Ile Ile Ser Ala Cys Gln Ser Gly
385 390 395 400

Met Gly Gly Thr Gly Asp Val Ala Ile Leu Ser Thr Ala Asp Arg Met
405 410 415

GBS patentin.ST25

Asn Leu Met Pro Phe Ala Gln Val Ala Thr Arg Leu Gly Gly Ala Ile
420 425 430

Thr Val Ile Thr Met Thr Ala Ile Leu Arg Met Leu Phe
435 440 445

<210> 360

<211> 412

<212> PRT

<213> Streptococcus agalactiae

<400> 360

Arg Gly Lys Lys Ala Gly Lys Tyr Thr Thr Ser Asp Gly Tyr Ile Phe
1 5 10 15

Asp Ala Lys Asp Ile Lys Lys Asp Thr Gly Thr Gly Tyr Val Ile Pro
20 25 30

His Met Thr His Glu His Trp Val Pro Lys Lys Asp Leu Ser Glu Ser
35 40 45

Glu Leu Lys Ala Ala Gln Glu Phe Leu Ser Gly Lys Ser Glu Ala Asn
50 55 60

Gln Asp Lys Pro Lys Thr Gly Lys Thr Ala Gln Glu Ile Tyr Glu Ala
65 70 75 80

Ile Glu Pro Lys Ala Ile Val Lys Pro Glu Asp Leu Leu Phe Gly Ile
85 90 95

Ala Gln Ala Thr Asp Tyr Lys Asn Gly Thr Phe Val Ile Pro His Lys
100 105 110

Asp His Tyr His Tyr Val Glu Leu Lys Trp Phe Asp Glu Glu Lys Asp
115 120 125

Leu Leu Ala Asp Ser Asp Lys Thr Tyr Ser Leu Glu Asp Tyr Leu Ala
130 135 140

Thr Ala Lys Tyr Tyr Met Met His Pro Glu Lys Arg Pro Lys Val Glu
145 150 155 160

Gly Trp Gly Lys Asp Ala Glu Ile Tyr Lys Glu Lys Asp Ser Asn Lys
165 170 175

Ala Asp Lys Pro Ser Pro Ala Pro Thr Asp Asn Lys Ser Thr Ser Asn
180 185 190

GBS patentin.ST25

Ser Ser Asp Lys Asn Leu Ser Ala Ala Glu Val Phe Lys Gln Ala Lys
195 200 205

Pro Glu Lys Ile Val Pro Leu Asp Lys Ile Ala Ala His Met Ala Tyr
210 215 220

Ala Val Gly Phe Glu Asp Asp Gln Leu Ile Val Pro His His Asp His
225 230 235 240

Tyr His Asn Val Pro Met Ala Trp Phe Asp Lys Gly Gly Leu Trp Lys
245 250 255

Ala Pro Glu Gly Tyr Thr Leu Gln Gln Leu Phe Ser Thr Ile Lys Tyr
260 265 270

Tyr Met Glu His Pro Asn Glu Leu Pro Lys Glu Lys Gly Trp Gly His
275 280 285

Asp Ser Asp His Asn Lys Gly Ser Asn Lys Asp Asn Lys Ala Lys Asn
290 295 300

Tyr Ala Pro Asp Glu Glu Pro Glu Asp Ser Gly Lys Val Thr His Asn
305 310 315 320

Tyr Gly Phe Tyr Asp Val Asn Lys Gly Ser Asp Glu Glu Glu Pro Glu
325 330 335

Lys Gln Glu Asp Glu Ser Glu Leu Asp Glu Tyr Glu Leu Gly Met Ala
340 345 350

Gln Asn Ala Lys Lys Tyr Gly Met Asp Arg Gln Ser Phe Glu Lys Gln
355 360 365

Leu Ile Gln Leu Ser Asn Lys Tyr Ser Val Ser Phe Glu Ser Phe Asn
370 375 380

Tyr Ile Asn Gly Ser Gln Val Gln Val Thr Lys Lys Asp Gly Ser Lys
385 390 395 400

Val Leu Val Asp Ile Lys Thr Leu Thr Glu Val Lys
405 410

<210> 361

<211> 481

<212> PRT

<213> streptococcus agalactiae

<400> 361

Met Asn Arg Lys Lys Thr Val Ile Ile Ser Ala Leu Ser Val Ala Leu
 1 5 10 15
 Phe Gly Thr Gly Val Gly Ala Tyr Gln Leu Gly Ser Tyr Asn Ala Gln
 20 25 30
 Lys Ser Asp Asn Ser Val Ser Tyr Val Lys Thr Asp Lys Ser Asp Ser
 35 40 45
 Lys Ala Gln Ala Thr Ala Val Asn Lys Thr Pro Asp Gln Ile Ser Lys
 50 55 60
 Glu Glu Gly Ile Ser Ala Glu Gln Ile Val Val Lys Ile Thr Asp Asp
 65 70 75 80
 Gly Tyr Val Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys
 85 90 95
 Val Pro Tyr Asp Ala Ile Ile Ser Glu Glu Leu Ile Met Lys Asp Pro
 100 105 110
 Ser Tyr Val Phe Asn Lys Ala Asp Val Ile Asn Glu Val Lys Asp Gly
 115 120 125
 Tyr Ile Ile Lys Val Asn Gly Lys Tyr Tyr Leu Tyr Leu Lys Glu Gly
 130 135 140
 Ser Lys Arg Thr Asn Val Arg Thr Lys Glu Gln Ile Gln Lys Gln Arg
 145 150 155 160
 Glu Glu Trp Ser Lys Gly Gly Ser Lys Gly Glu Ser Gly Lys His Ser
 165 170 175
 Ser Ala Lys Thr Gln Ala Leu Ser Ala Ser Val Arg Glu Ala Lys Ala
 180 185 190
 Ser Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Val Phe Ser Pro Thr Asp
 195 200 205
 Val Ile Asp Asp Met Gly Asp Ala Phe Leu Val Pro His Gly Asp His
 210 215 220
 Phe His Tyr Ile Pro Lys Ala Asp Leu Ser Pro Ser Glu Leu Ser Ala
 225 230 235 240
 Ala Gln Ala Tyr Trp Asn Arg Lys Thr Gly Arg Ser Gly Asn Ser Ser
 245 250 255
 Lys Pro Ser Asn Ser Ser Ser Tyr Ile His Ala Ser Ala Pro Ser Gly
 260 265 270

GBS patentin.ST25

Asn Val Ser Thr Gly Arg His Ala Asn Ala Pro Ile Ser Ile Pro Arg
275 280 285

Val Thr His Ala Asn His Trp Ser Lys Pro Ala Gly Asn His Ala Thr
290 295 300

Ala Pro Lys His His Ala Pro Thr Thr Lys Pro Ile Asn Lys Asp Ser
305 310 315 320

Ala Leu Asp Lys Met Leu Lys Arg Leu Tyr Ala Gln Pro Leu Tyr Ala
325 330 335

Arg His Val Glu Ser Asp Gly Leu Val Tyr Asp Pro Ala Gln Val Asn
340 345 350

Ala Phe Thr Ala Ile Gly Val Ser Ile Pro His Gly Asn His Phe His
355 360 365

Phe Ile His Tyr Lys Asp Met Ser Pro Leu Glu Leu Glu Ala Thr Arg
370 375 380

Met Val Ala Glu His Arg Gly His His Ile Asp Ala Leu Gly Lys Lys
385 390 395 400

Asp Ser Thr Glu Lys Pro Lys His Ile Ser His Glu Pro Asn Lys Glu
405 410 415

Pro His Thr Glu Glu Glu His His Ala Val Thr Pro Lys Asp Gln Arg
420 425 430

Lys Gly Lys Pro Asn Ser Gln Ile Val Tyr Ser Ala Gln Glu Ile Glu
435 440 445

Glu Ala Lys Lys Leu Val Asn Thr Gln His Leu Met Val Thr Phe Leu
450 455 460

Met Pro Lys Ile Leu Lys Lys Ile Gln Val Gln Val Met Ser Phe His
465 470 475 480

Ile

<210> 362

<211> 156

<212> PRT

<213> streptococcus agalactiae

GBS patentin.ST25

<400> 362

Met Ala Lys Phe Gly Phe Leu Ser Val Leu Glu Glu Glu Leu Asp Lys
 1 5 10 15
 His Leu Gln Tyr Asp Phe Ala Met Asp Trp Asp Lys Lys Asn His Thr
 20 25 30
 Val Glu Val Thr Phe Ile Leu Glu Ala Gln Asn Ser Ser Ala Ile Glu
 35 40 45
 Thr Val Asp Asp Gln Gly Glu Thr Ser Ser Glu Asp Ile Val Phe Glu
 50 55 60
 Asp Tyr Val Leu Phe Tyr Asn Pro Val Lys Ser Arg Phe Asp Ala Glu
 65 70 75 80
 Asp Tyr Leu Val Thr Ile Pro Tyr Glu Pro Lys Lys Gly Leu Ser Arg
 85 90 95
 Glu Phe Leu Ala Tyr Phe Ala Glu Thr Leu Asn Glu Val Ala Thr Glu
 100 105 110
 Gly Leu Ser Asp Leu Met Asp Phe Leu Thr Asp Asp Ser Ile Glu Glu
 115 120 125
 Phe Gly Leu Ser Trp Asp Thr Asp Ala Phe Glu Asn Gly Arg Ala Glu
 130 135 140
 Leu Lys Glu Thr Glu Phe Tyr Pro Tyr Pro Arg Tyr
 145 150 155

<210> 363

<211> 1570

<212> PRT

<213> Streptococcus agalactiae

<400> 363

Met Asn Thr Lys Gln Arg Phe Ser Ile Arg Lys Tyr Lys Leu Gly Ala
 1 5 10 15
 Val Ser Val Leu Leu Gly Thr Leu Phe Phe Leu Gly Gly Ile Thr Asn
 20 25 30
 Val Ala Ala Asp Ser Val Ile Asn Lys Pro Ser Asp Ile Ala Val Glu
 35 40 45
 Gln Gln Val Lys Asp Ser Pro Thr Ser Ile Ala Asn Glu Thr Pro Thr
 50 55 60

GBS patentin.ST25

Asn Asn Thr Ser Ser Ala Leu Ala Ser Thr Ala Gln Asp Asn Leu Val
65 70 75 80

Thr Lys Ala Asn Asn Ser Pro Thr Glu Thr Gln Pro Val Ala Glu Ser
85 90 95

His Ser Gln Ala Thr Glu Thr Phe Ser Pro Val Ala Asn Gln Pro Val
100 105 110

Glu Ser Thr Gln Glu Val Ser Lys Thr Pro Leu Thr Lys Gln Asn Leu
115 120 125

Ala Val Lys Ser Thr Pro Ala Ile Ser Lys Glu Thr Pro Gln Asn Ile
130 135 140

Asp Ser Asn Lys Ile Ile Thr Val Pro Lys Val Trp Asn Thr Gly Tyr
145 150 155 160

Lys Gly Glu Gly Thr Val Val Ala Ile Ile Asp Ser Gly Leu Asp Ile
165 170 175

Asn His Asp Ala Leu Gln Leu Asn Asp Ser Thr Lys Ala Lys Tyr Gln
180 185 190

Asn Glu Gln Gln Met Asn Ala Ala Lys Ala Lys Ala Gly Ile Asn Tyr
195 200 205

Gly Lys Trp Tyr Asn Asn Lys Val Ile Phe Gly His Asn Tyr Val Asp
210 215 220

Val Asn Thr Glu Leu Lys Glu Val Lys Ser Thr Ser His Gly Met His
225 230 235 240

Val Thr Ser Ile Ala Thr Ala Asn Pro Ser Lys Lys Asp Thr Asn Glu
245 250 255

Leu Ile Tyr Gly Val Ala Pro Glu Ala Gln Val Met Phe Met Arg Val
260 265 270

Phe Ser Asp Glu Lys Arg Gly Thr Gly Pro Ala Leu Tyr Val Lys Ala
275 280 285

Ile Glu Asp Ala Val Lys Leu Gly Ala Asp Ser Ile Asn Leu Ser Leu
290 295 300

Gly Gly Ala Asn Gly Ser Leu Val Asn Ala Asp Asp Arg Leu Ile Lys
305 310 315 320

Ala Leu Glu Met Ala Arg Leu Ala Gly Val Ser Val Val Ile Ala Ala
325 330 335

GBS patentin.ST25

Gly Asn Asp Gly Thr Phe Gly Ser Gly Ala Ser Lys Pro Ser Ala Leu
340 345 350

Tyr Pro Asp Tyr Gly Leu Val Gly Ser Pro Ser Thr Ala Arg Glu Ala
355 360 365

Ile Ser Val Ala Ser Tyr Asn Asn Thr Thr Leu Val Asn Lys Val Phe
370 375 380

Asn Ile Ile Gly Leu Glu Asn Asn Arg Asn Leu Asn Asn Gly Leu Ala
385 390 395 400

Ala Tyr Ala Asp Pro Lys Val Ser Asp Lys Thr Phe Glu Val Gly Lys
405 410 415

Gln Tyr Asp Tyr Val Phe Val Gly Lys Gly Asn Asp Asn Asp Tyr Lys
420 425 430

Asp Lys Thr Leu Asn Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile
435 440 445

Thr Phe Thr Lys Lys Val Val Asn Ala Ile Asn His Gly Ala Val Gly
450 455 460

Ala Ile Ile Phe Asn Asn Lys Ala Gly Glu Ala Asn Leu Thr Met Ser
465 470 475 480

Leu Asp Pro Glu Ala Ser Ala Ile Pro Ala Ile Phe Thr Gln Lys Glu
485 490 495

Phe Gly Asp Val Leu Ala Lys Asn Asn Tyr Lys Ile Val Phe Asn Asn
500 505 510

Ile Lys Asn Lys Gln Ala Asn Pro Asn Ala Gly Val Leu Ser Asp Phe
515 520 525

Ser Ser Trp Gly Leu Thr Ala Asp Gly Gln Leu Lys Pro Asp Leu Ser
530 535 540

Ala Pro Gly Gly Ser Ile Tyr Ala Ala Ile Asn Asp Asn Glu Tyr Asp
545 550 555 560

Met Met Ser Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Thr
565 570 575

Ala Leu Val Lys Gln Tyr Leu Leu Lys Glu His Pro Glu Leu Lys Lys
580 585 590

Gly Asp Ile Glu Arg Thr Val Lys Tyr Leu Leu Met Ser Thr Ala Lys
595 600 605

GBS patentin.ST25

Ala His Leu Asn Lys Asp Thr Gly Ala Tyr Thr Ser Pro Arg Gln Gln
610 615 620

Gly Ala Gly Ile Ile Asp Val Ala Ala Ala Val Gln Thr Gly Leu Tyr
625 630 635 640

Leu Thr Gly Gly Glu Asn Asn Tyr Gly Ser Val Thr Leu Gly Asn Ile
645 650 655

Lys Asp Lys Ile Ser Phe Asp Val Thr Val His Asn Ile Asn Lys Val
660 665 670

Ala Lys Asp Leu His Tyr Thr Thr Tyr Leu Asn Thr Asp Gln Val Lys
675 680 685

Asp Gly Phe Val Thr Leu Ala Pro Gln Gln Leu Gly Thr Phe Thr Gly
690 695 700

Lys Thr Ile Arg Ile Glu Pro Gly Gln Thr Gln Thr Ile Thr Ile Asp
705 710 715 720

Ile Asp Val Ser Lys Tyr His Asp Met Leu Lys Lys Val Met Pro Asn
725 730 735

Gly Tyr Phe Leu Glu Gly Tyr Val Arg Phe Thr Asp Pro Val Asp Gly
740 745 750

Gly Glu Val Leu Ser Ile Pro Tyr Val Gly Phe Lys Gly Glu Phe Gln
755 760 765

Asn Leu Glu Val Leu Glu Lys Ser Ile Tyr Lys Leu Val Ala Asn Lys
770 775 780

Glu Lys Gly Phe Tyr Phe Gln Pro Lys Gln Thr Asn Glu Val Pro Gly
785 790 795 800

Ser Glu Asp Tyr Thr Ala Leu Met Thr Thr Ser Ser Glu Pro Ile Tyr
805 810 815

Ser Thr Asp Gly Thr Ser Pro Ile Gln Leu Lys Ala Leu Gly Ser Tyr
820 825 830

Lys Ser Ile Asp Gly Lys Trp Ile Leu Gln Leu Asp Gln Lys Gly Gln
835 840 845

Pro His Leu Ala Ile Ser Pro Asn Asp Asp Gln Asn Gln Asp Ala Val
850 855 860

Ala Val Lys Gly Val Phe Leu Arg Asn Phe Asn Asn Leu Arg Ala Lys
865 870 875 880

GBS patentin.ST25

Val Tyr Arg Ala Asp Asp Val Asn Leu Gln Lys Pro Leu Trp Val Ser
 885 890 895
 Ala Pro Gln Ala Gly Asp Lys Asn Tyr Tyr Ser Gly Asn Thr Glu Asn
 900 905 910
 Pro Lys Ser Thr Phe Leu Tyr Asp Thr Glu Trp Lys Gly Thr Thr Thr
 915 920 925
 Asp Gly Ile Pro Leu Glu Asp Gly Lys Tyr Lys Tyr Val Leu Thr Tyr
 930 935 940
 Tyr Ser Asp Val Pro Gly Ser Lys Pro Gln Gln Met Val Phe Asp Ile
 945 950 955 960
 Thr Leu Asp Arg Gln Ala Pro Thr Leu Thr Thr Ala Thr Tyr Asp Lys
 965 970 975
 Asp Arg Arg Ile Phe Lys Ala Arg Pro Ala Val Glu His Gly Glu Ser
 980 985 990
 Gly Ile Phe Arg Glu Gln Val Cys Tyr Leu Lys Lys Asp Lys Asp Gly
 995 1000 1005
 His Tyr Asn Ser Val Leu Arg Gln Gln Gly Glu Asp Gly Ile Leu
 1010 1015 1020
 Val Glu Asp Asn Lys Val Phe Ile Lys Gln Glu Lys Asn Gly Ser
 1025 1030 1035
 Phe Ile Leu Pro Lys Glu Val Asn Asp Phe Ser His Val Tyr Tyr
 1040 1045 1050
 Thr Val Glu Asp Tyr Ala Gly Asn Leu Val Ser Ala Lys Leu Glu
 1055 1060 1065
 Asp Leu Ile Asn Ile Gly Asn Lys Asn Gly Leu Val Asn Val Lys
 1070 1075 1080
 Val Phe Ser Pro Glu Leu Asn Ser Asn Val Asp Ile Asp Phe Ser
 1085 1090 1095
 Tyr Ser Val Lys Asp Asp Lys Gly Asn Ile Ile Lys Lys Gln His
 1100 1105 1110
 His Gly Lys Asp Leu Asn Leu Leu Lys Leu Pro Phe Gly Thr Tyr
 1115 1120 1125
 Thr Phe Asp Leu Phe Leu Tyr Asp Glu Glu Arg Ala Asn Leu Ile
 1130 1135 1140

GBS patentin.ST25

Ser Pro Lys Ser Val Thr Val Thr Ile Ser Glu Lys Asp Ser Leu
1145 1150 1155

Lys Asp Val Leu Phe Lys Val Asn Leu Leu Lys Lys Ala Ala Leu
1160 1165 1170

Leu Val Glu Phe Asp Lys Leu Leu Pro Lys Gly Ala Thr Val Gln
1175 1180 1185

Leu Val Thr Lys Thr Asn Thr Val Val Asp Leu Pro Lys Ala Thr
1190 1195 1200

Tyr Ser Pro Thr Asp Tyr Gly Lys Asn Ile Pro Val Gly Asp Tyr
1205 1210 1215

Arg Leu Asn Val Thr Leu Pro Ser Gly Tyr Ser Thr Leu Glu Asn
1220 1225 1230

Leu Asp Asp Leu Leu Val Ser Val Lys Glu Asp Gln Val Asn Leu
1235 1240 1245

Thr Lys Leu Thr Leu Ile Asn Lys Ala Pro Leu Ile Asn Ala Leu
1250 1255 1260

Ala Glu Gln Thr Asp Ile Ile Thr Gln Pro Val Phe Tyr Asn Ala
1265 1270 1275

Gly Thr His Leu Lys Asn Asn Tyr Leu Ala Asn Leu Glu Lys Ala
1280 1285 1290

Gln Thr Leu Ile Lys Asn Arg Val Glu Gln Thr Ser Ile Asp Asn
1295 1300 1305

Ala Ile Ala Ala Leu Arg Glu Ser Arg Gln Ala Leu Asn Gly Lys
1310 1315 1320

Glu Thr Asp Thr Ser Leu Leu Ala Lys Ala Ile Leu Ala Glu Thr
1325 1330 1335

Glu Ile Lys Gly Asn Tyr Gln Phe Val Asn Ala Ser Pro Leu Ser
1340 1345 1350

Gln Ser Thr Tyr Ile Asn Gln Val Gln Leu Ala Lys Asn Leu Leu
1355 1360 1365

Gln Lys Pro Asn Val Thr Gln Ser Glu Val Asp Lys Ala Leu Glu
1370 1375 1380

Asn Leu Asp Ile Ala Lys Asn Gln Leu Asn Gly His Glu Thr Asp
1385 1390 1395

GBS patentin.ST25

Tyr Ser Gly Leu His His Met Ile Ile Lys Ala Asn Val Leu Lys
 1400 1405 1410
 Gln Thr Ser Ser Lys Tyr Gln Asn Ala Ser Gln Phe Ala Lys Glu
 1415 1420 1425
 Asn Tyr Asn Asn Leu Ile Lys Lys Ala Glu Leu Leu Leu Ser Asn
 1430 1435 1440
 Arg Gln Ala Thr Gln Ala Gln Val Glu Glu Leu Leu Asn Gln Ile
 1445 1450 1455
 Lys Ala Thr Glu Gln Glu Leu Asp Gly Arg Asp Arg Val Ser Ser
 1460 1465 1470
 Ala Glu Asn Tyr Ser Gln Ser Leu Asn Asp Asn Asp Ser Leu Asn
 1475 1480 1485
 Thr Thr Pro Ile Asn Pro Pro Asn Gln Pro Gln Ala Leu Ile Phe
 1490 1495 1500
 Lys Lys Gly Met Thr Lys Glu Ser Glu Val Ala Gln Lys Arg Val
 1505 1510 1515
 Leu Gly Val Thr Ser Gln Thr Asp Asn Gln Lys Val Lys Thr Asn
 1520 1525 1530
 Lys Leu Pro Lys Thr Gly Glu Ser Thr Pro Lys Ile Thr Tyr Thr
 1535 1540 1545
 Ile Leu Leu Phe Ser Leu Ser Met Leu Gly Leu Ala Thr Ile Lys
 1550 1555 1560
 Leu Lys Ser Ile Lys Arg Glu
 1565 1570

<210> 364

<211> 643

<212> PRT

<213> Streptococcus agalactiae

<400> 364

Met Asn Asn Asn Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Thr Ala
 1 5 10 15
 Tyr Gly Leu Ala Ser Met Ser Ala Ala Phe Ala Val Cys Ser Gly Ile
 20 25 30

GBS patentin.ST25

Val His Ala Asp Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys
35 40 45

Lys Gln Val Asn Leu Gly Ala Val Thr Leu Lys Asn Leu Ile Ser Lys
50 55 60

Tyr Arg Gly Asn Asp Lys Ala Ile Ala Ile Leu Leu Ser Arg Val Asn
65 70 75 80

Asp Phe Asn Arg Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser
85 90 95

Thr Glu Ala Glu Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys
100 105 110

Gln Asn Lys Pro Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu
115 120 125

Leu Gly Lys Gln Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly
130 135 140

Phe Leu Ser Ser Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser
145 150 155 160

Ser Lys Asp Ser Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln
165 170 175

Leu Asn Asn Ala Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp
180 185 190

Val Ala Leu Ile Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys
195 200 205

Glu Lys Ile Gln Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val
210 215 220

Ala Glu Ala Lys Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn
225 230 235 240

Gln Ala Asn Gly Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser
245 250 255

Asn Asp Glu Met Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys
260 265 270

Gln Tyr Asn Glu Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu
275 280 285

Asn Ser Ile Lys Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln
290 295 300

GBS patentin.ST25

Lys Gln Tyr Ala Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala
305 310 315 320

Leu Ser Lys Lys Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu
325 330 335

Pro Thr Pro Gly Tyr Tyr Ala Asp Ser Val Gly Thr Tyr Leu Asn Arg
340 345 350

Phe Arg Asp Lys Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln
355 360 365

Ser Gly Leu Asp Glu Ala Lys Lys Met Leu Asp Glu Val Lys Lys Leu
370 375 380

Leu Lys Glu Leu Gln Asp Leu Thr Arg Gly Thr Lys Glu Asp Lys Lys
385 390 395 400

Pro Asp Val Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Asn Ile Gln
405 410 415

Val Pro Lys Gln Ala Pro Thr Glu Ala Ala Lys Pro Ala Leu Ser Pro
420 425 430

Glu Ala Leu Thr Arg Leu Thr Thr Trp Tyr Asn Gln Ala Lys Asp Leu
435 440 445

Leu Lys Asp Asp Gln Val Lys Asp Lys Tyr Val Asp Ile Leu Ala Val
450 455 460

Gln Lys Ala Val Asp Gln Ala Tyr Asp His Val Glu Glu Gly Lys Phe
465 470 475 480

Ile Thr Thr Asp Gln Ala Asn Gln Leu Ala Asn Lys Leu Arg Asp Ala
485 490 495

Leu Gln Ser Leu Glu Leu Lys Asp Lys Lys Val Ala Lys Pro Glu Ala
500 505 510

Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Glu Ala
515 520 525

Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Asp Val
530 535 540

Lys Pro Glu Ala Lys Pro Asp Val Lys Pro Glu Ala Lys Pro Glu Ala
545 550 555 560

Lys Pro Glu Ala Lys Ser Glu Ala Lys Pro Glu Ala Lys Leu Glu Ala
565 570 575

GBS patentin.ST25

Lys Pro Glu Ala Lys Pro Ala Thr Lys Lys Ser Val Asn Thr Ser Gly
580 585 590

Asn Leu Ala Ala Lys Lys Ala Ile Glu Asn Lys Lys Tyr Ser Lys Lys
595 600 605

Leu Pro Ser Thr Gly Glu Ala Ala Ser Pro Leu Leu Ala Ile Val Ser
610 615 620

Leu Ile Val Met Leu Ser Ala Gly Leu Ile Thr Ile Val Leu Lys His
625 630 635 640

Lys Lys Asn

<210> 365

<211> 540

<212> PRT

<213> streptococcus agalactiae

<400> 365

Met Ala Lys Asp Ile Lys Phe Ser Ala Asp Ala Arg Ser Ala Met Val
1 5 10 15

Arg Gly Val Asp Ile Leu Ala Asp Thr Val Lys Val Thr Leu Gly Pro
20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Ala Phe Gly Ser Pro Leu Ile
35 40 45

Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His
50 55 60

Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val Ala Ser Lys Thr
65 70 75 80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Gln
85 90 95

Ala Ile Val Arg Glu Gly Leu Lys Asn Val Thr Ala Gly Ala Asn Pro
100 105 110

Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Val Ser Ala Ala Val Glu
115 120 125

Glu Leu Lys Glu Ile Ala Gln Pro Val Ser Gly Lys Glu Ala Ile Ala
130 135 140

GBS patentin.ST25

Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val Gly Glu Tyr Ile
145 150 155 160

Ser Glu Ala Met Gly Arg Val Gly Asn Asp Gly Val Ile Thr Ile Glu
165 170 175

Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val Glu Gly Met Gln
180 185 190

Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr Asp Asn Glu Lys
195 200 205

Met Val Ser Glu Leu Glu Asn Pro Tyr Ile Leu Ile Thr Asp Lys Lys
210 215 220

Ile Ser Asn Ile Gln Glu Ile Leu Pro Leu Leu Glu Glu Val Leu Lys
225 230 235 240

Thr Asn Arg Pro Leu Leu Ile Ile Ala Asp Asp Val Asp Gly Glu Ala
245 250 255

Leu Pro Thr Leu Val Leu Asn Lys Ile Arg Gly Thr Phe Asn Val Val
260 265 270

Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Glu
275 280 285

Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Val Thr Glu Asp Leu Gly
290 295 300

Leu Asp Leu Lys Asp Ala Thr Met Gln Val Leu Gly Gln Ser Ala Lys
305 310 315 320

Val Thr Val Asp Lys Asp Ser Thr Val Ile Val Glu Gly Ala Gly Asp
325 330 335

Ser Ser Ala Ile Ala Asn Arg Val Ala Ile Ile Lys Ser Gln Met Glu
340 345 350

Ala Thr Thr Ser Asp Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
355 360 365

Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu
370 375 380

Thr Glu Leu Lys Glu Met Lys Leu Arg Ile Glu Asp Ala Leu Asn Ala
385 390 395 400

Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ser Gly Gly Gly Thr Ala
405 410 415

GBS patentin.ST25

Leu Val Asn Val Ile Glu Lys Val Ala Ala Leu Lys Leu Asn Gly Asp
420 425 430

Glu Glu Thr Gly Arg Asn Ile Val Leu Arg Ala Leu Glu Glu Pro Val
435 440 445

Arg Gln Ile Ala Tyr Asn Ala Gly Tyr Glu Gly Ser Val Ile Ile Glu
450 455 460

Arg Leu Lys Gln Ser Glu Ile Gly Thr Gly Phe Asn Ala Ala Asn Gly
465 470 475 480

Glu Trp Val Asp Met Val Thr Thr Gly Ile Ile Asp Pro Val Lys Val
485 490 495

Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu Ile Leu
500 505 510

Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro Glu Ala Pro Thr
515 520 525

Ala Pro Ala Met Asp Pro Ser Met Met Gly Gly Phe
530 535 540

<210> 366

<211> 513

<212> PRT

<213> Streptococcus agalactiae

<400> 366

Val Val Glu Asn Leu Glu Lys Pro Ile Gly Val Ser Tyr Lys Asn Ser
1 5 10 15

Pro Ser Met Ser Lys Arg Thr Ala Ile Arg Met Lys Lys Ser Ser Arg
20 25 30

Phe Ser Ile Leu Leu Tyr Ser Val Leu Ser Thr Leu Leu Ala Ile Ala
35 40 45

Asn Pro Leu Leu Thr Tyr Phe Ala Asn Gly Leu Gln Thr Gln Asn Leu
50 55 60

Tyr Thr Gly Leu Met Met Thr Lys Gly Gln Ile Pro Tyr Ser Asp Val
65 70 75 80

Phe Ala Thr Gly Gly Phe Leu Tyr Tyr Val Thr Ile Ala Leu Ser Tyr
85 90 95

GBS patentin.ST25

Leu Leu Gly Ser Ser Ile Trp Leu Leu Ile Val Gln Phe Ile Ala Tyr
 100 105 110
 Tyr Val Ser Gly Ile Tyr Phe Tyr Lys Leu Val Tyr Tyr Val Ala Gln
 115 120 125
 Ser Glu Ile val Ser Ile Gly Met Thr Leu Ile Phe Tyr Ile Met Asn
 130 135 140
 Ile Val Leu Gly Phe Gly Gly Met Tyr Pro Ile Gln Trp Ala Leu Pro
 145 150 155 160
 Phe Met Leu Ile Ser Leu Trp Phe Leu Ile Lys Phe Cys Val Asp Asn
 165 170 175
 Ile Val Asp Glu Ala Phe Ile Phe Tyr Gly Ile Leu Ala Ala Phe Ser
 180 185 190
 Leu Phe Ile Asp Pro Gln Thr Leu Ile Phe Trp Leu Cys Ser Phe Val
 195 200 205
 Leu Leu Thr Ala Thr Asn Ile Lys Gln Lys Gln Ser Leu Arg Gly Phe
 210 215 220
 Tyr Gln Phe Leu Cys val val Phe Gly Met Ile Leu Ile Ala Tyr Thr
 225 230 235 240
 val Gly Tyr Phe Met Phe Asn Leu Gln Ile Ile Ser Ser Tyr Ile Asp
 245 250 255
 Lys Ala Ile Phe Tyr Pro Phe Thr Tyr Phe Ala Arg Thr Asn His Ser
 260 265 270
 Phe Leu Leu Ser Leu Ala Ile Gln Ile Val Val Leu Leu Gly Ser Gly
 275 280 285
 Cys Leu Phe Gly Leu Trp Asp Phe Ile Gln Asn Arg Lys Lys Ala Ser
 290 295 300
 Tyr Gln Ile Gly Leu Asn Phe Ile Ala Cys Ile Phe Ile Ile Tyr Ala
 305 310 315 320
 Ile Met Ala Ile Phe Ser Arg Asp Phe Asn Leu Tyr His Phe Leu Pro
 325 330 335
 Ala Leu Pro Phe Gly Leu Leu Leu Thr Ser Asn Lys Ile Thr Ile Leu
 340 345 350
 Tyr Gln Lys val Ile Asp Arg Arg Ser His Arg Arg Gln Tyr Phe Ser
 355 360 365

GBS patentin.ST25

Gly Lys Ser Leu Ile Val Asp Leu Phe Val Lys Lys Thr Tyr Tyr Leu
370 375 380

Pro Leu Leu Leu Val Ser Leu Ser Ile Gly Leu Leu Val Tyr Asn Thr
385 390 395 400

Tyr Gln Asn Val Thr Leu Ser Lys Glu Arg Arg Asp Ile Ser His Tyr
405 410 415

Leu Thr Thr Lys Ile Asp Arg Asp Gly Lys Ile Tyr Val Trp Asp Lys
420 425 430

Val Ala Ser Ile Tyr Ser Gln Thr Arg Leu Lys Ser Ala Ser Gln Phe
435 440 445

Val Leu Pro His Ile Asn Thr Ala Gln Lys Asn Asn Glu Lys Ile Leu
450 455 460

Lys Asp Glu Leu Leu Gln His Gly Ala Lys Tyr Phe Ile Leu Asn Lys
465 470 475 480

Asn Glu Lys Leu Pro Asn Glu Leu Lys Ser Asp Ile Lys Lys His Tyr
485 490 495

Gln Glu Val Pro Leu Ser Asn Ile Thr His Phe Val Leu Tyr Arg Phe
500 505 510

Lys

<210> 367

<211> 858

<212> PRT

<213> Streptococcus agalactiae

<400> 367

Met Ala Lys Pro Thr Ile Ser Pro Gly Met Gln Gln Tyr Leu Asp Ile
1 5 10 15

Lys Glu Asn Tyr Pro Asp Ala Phe Leu Leu Phe Arg Met Gly Asp Phe
20 25 30

Tyr Glu Leu Phe Tyr Asp Asp Ala Val Lys Ala Ala Gln Ile Leu Glu
35 40 45

Ile Ser Leu Thr Ser Arg Asn Lys Asn Ala Glu Lys Pro Ile Pro Met
50 55 60

GBS patentin.ST25

Ala Gly Val Pro Tyr His Ser Ala Gln Gln Tyr Ile Asp Val Leu Val
65 70 75 80

Glu Leu Gly Tyr Lys Val Ala Ile Ala Glu Gln Met Glu Asp Pro Lys
85 90 95

Lys Ala Val Gly Val Val Lys Arg Glu Val Val Gln Val Val Thr Pro
100 105 110

Gly Thr Val Val Glu Ser Thr Lys Pro Asp Ser Ala Asn Asn Phe Leu
115 120 125

Val Ala Ile Asp Ser Gln Asp Gln Gln Thr Phe Gly Leu Ala Tyr Met
130 135 140

Asp Val Ser Thr Gly Glu Phe Gln Ala Thr Leu Leu Thr Asp Phe Glu
145 150 155 160

Ser Val Arg Ser Glu Ile Leu Asn Leu Lys Ala Arg Glu Ile Val Val
165 170 175

Gly Tyr Gln Leu Thr Asp Glu Lys Asn His Leu Leu Thr Lys Gln Met
180 185 190

Asn Leu Leu Leu Ser Tyr Glu Asp Glu Arg Leu Asn Asp Ile His Leu
195 200 205

Ile Asp Glu Gln Leu Thr Asp Leu Glu Ile Ser Ala Ala Glu Lys Leu
210 215 220

Leu Gln Tyr Val His Arg Thr Gln Lys Arg Glu Leu Ser His Leu Gln
225 230 235 240

Lys Val Val His Tyr Glu Ile Lys Asp Tyr Leu Gln Met Ser Tyr Ala
245 250 255

Thr Lys Asn Ser Leu Asp Leu Leu Glu Asn Ala Arg Thr Ser Lys Lys
260 265 270

His Gly Ser Leu Tyr Trp Leu Leu Asp Glu Thr Lys Thr Ala Met Gly
275 280 285

Thr Arg Met Leu Arg Thr Trp Ile Asp Arg Pro Leu Val Ser Met Asn
290 295 300

Arg Ile Lys Glu Arg Gln Asp Ile Ile Gln Val Phe Leu Asp Tyr Phe
305 310 315 320

Phe Glu Arg Asn Asp Leu Thr Glu Ser Leu Lys Gly Val Tyr Asp Ile
325 330 335

GBS patentin.ST25

Glu Arg Leu Ala Ser Arg Val Ser Phe Gly Lys Ala Asn Pro Lys Asp
340 345 350

Leu Leu Gln Leu Gly Gln Thr Leu Ser Gln Ile Pro Arg Ile Lys Met
355 360 365

Ile Leu Gln Ser Phe Asn Gln Pro Glu Leu Asp Ile Ile Val Asn Lys
370 375 380

Ile Asp Thr Met Pro Glu Leu Glu Ser Leu Ile Asn Thr Ala Ile Ala
385 390 395 400

Pro Glu Ala Gln Ala Thr Ile Thr Glu Gly Asn Ile Ile Lys Ser Gly
405 410 415

Phe Asp Lys Gln Leu Asp Asn Tyr Arg Thr Val Met Arg Glu Gly Thr
420 425 430

Gly Trp Ile Ala Asp Ile Glu Ala Lys Glu Arg Ala Ala Ser Gly Ile
435 440 445

Gly Thr Leu Lys Ile Asp Tyr Asn Lys Lys Asp Gly Tyr Tyr Phe His
450 455 460

Val Thr Asn Ser Asn Leu Ser Leu Val Pro Glu His Phe Phe Arg Lys
465 470 475 480

Ala Thr Leu Lys Asn Ser Glu Arg Tyr Gly Thr Ala Glu Leu Ala Lys
485 490 495

Ile Glu Gly Glu Met Leu Glu Ala Arg Glu Gln Ser Ser Asn Leu Glu
500 505 510

Tyr Asp Ile Phe Met Arg Val Arg Ala Gln Val Glu Ser Tyr Ile Lys
515 520 525

Arg Leu Gln Glu Leu Ala Lys Thr Ile Ala Thr Val Asp Val Leu Gln
530 535 540

Ser Leu Ala Val Val Ala Glu Asn Tyr His Tyr Val Arg Pro Lys Phe
545 550 555 560

Asn Asp Gln His Gln Ile Lys Ile Lys Asn Gly Arg His Ala Thr Val
565 570 575

Glu Lys Val Met Gly Val Gln Glu Tyr Ile Pro Asn Ser Ile Tyr Phe
580 585 590

Asp ser Gln Thr Asp Ile Gln Leu Ile Thr Gly Pro Asn Met Ser Gly
595 600 605

GBS patentin.ST25

Lys Ser Thr Tyr Met Arg Gln Leu Ala Leu Thr Val Ile Met Ala Gln
 610 615 620
 Met Gly Gly Phe Val Ser Ala Asp Glu Val Asp Leu Pro Val Phe Asp
 625 630 635 640
 Ala Ile Phe Thr Arg Ile Gly Ala Ala Asp Asp Leu Ile Ser Gly Gln
 645 650 655
 Ser Thr Phe Met Val Glu Met Met Glu Ala Asn Gln Ala Val Lys Arg
 660 665 670
 Ala Ser Asp Lys Ser Leu Ile Leu Phe Asp Glu Leu Gly Arg Gly Thr
 675 680 685
 Ala Thr Tyr Asp Gly Met Ala Leu Ala Gln Ser Ile Ile Glu Tyr Ile
 690 695 700
 His Asp Arg Val Arg Ala Lys Thr Met Phe Ala Thr His Tyr His Glu
 705 710 715 720
 Leu Thr Asp Leu Ser Glu Gln Leu Thr Arg Leu Val Asn Val His Val
 725 730 735
 Ala Thr Leu Glu Arg Asp Gly Glu Val Thr Phe Leu His Lys Ile Glu
 740 745 750
 Ser Gly Pro Ala Asp Lys Ser Tyr Gly Ile His Val Ala Lys Ile Ala
 755 760 765
 Gly Leu Pro Ile Asp Leu Leu Asp Arg Ala Thr Asp Ile Leu Ser Gln
 770 775 780
 Leu Glu Ala Asp Ala Val Gln Leu Ile Val Ser Pro Ser Gln Glu Ala
 785 790 795 800
 Val Thr Ala Asp Leu Asn Glu Glu Leu Asp Ser Glu Lys Gln Gln Gly
 805 810 815
 Gln Leu Ser Leu Phe Glu Glu Pro Ser Asn Ala Gly Arg Val Ile Glu
 820 825 830
 Glu Leu Glu Ala Ile Asp Ile Met Asn Leu Thr Pro Met Gln Ala Met
 835 840 845
 Asn Ala Ile Phe Asp Leu Lys Lys Leu Leu
 850 855

<210> 368

GBS patentin.ST25

<211> 290

<212> PRT

<213> Streptococcus agalactiae

<400> 368

Met Leu Lys Leu Asp Leu Lys Thr Lys Ile Lys Glu Ala Ile Leu Ile
1 5 10 15

Ala Phe Gly Val Ala Leu Tyr Thr Phe Gly Phe Val Lys Phe Asn Met
20 25 30

Ala Asn His Leu Ala Glu Gly Gly Ile Ser Gly Val Thr Leu Ile Ile
35 40 45

His Ala Leu Phe Gly Val Asn Pro Ala Leu Ser Ser Leu Leu Leu Asn
50 55 60

Ile Pro Leu Phe Ile Leu Gly Ala Arg Ile Leu Gly Lys Lys Ser Leu
65 70 75 80

Leu Leu Thr Ile Tyr Gly Thr Val Leu Met Ser Phe Phe Met Trp Phe
85 90 95

Trp Gln Gln Ile Pro Val Thr Val Pro Leu Lys Asn Asp Met Met Leu
100 105 110

Val Ala Val Ala Ala Gly Ile Leu Ala Gly Thr Gly Ser Gly Leu Val
115 120 125

Phe Arg Tyr Gly Ala Thr Thr Gly Gly Ala Asp Ile Ile Gly Arg Ile
130 135 140

Val Glu Glu Lys Ser Gly Ile Lys Leu Gly Gln Thr Leu Leu Phe Ile
145 150 155 160

Asp Ala Ile Val Leu Thr Ser Ser Leu Val Tyr Ile Asn Leu Gln Gln
165 170 175

Met Leu Tyr Thr Leu Val Ala Ser Phe Val Phe Ser Gln Val Leu Thr
180 185 190

Asn Val Glu Asn Gly Gly Tyr Thr Val Arg Gly Met Ile Ile Ile Thr
195 200 205

Lys Glu Ser Glu Ser Ala Ala Ala Thr Ile Leu His Glu Ile Asn Arg
210 215 220

Gly Val Thr Phe Leu Arg Gly Gln Gly Ala Tyr Ser Gly Arg Glu His
225 230 235 240

GBS patentin.ST25

Asp Val Leu Tyr Val₂₄₅ Ala Leu Asn Pro Ser₂₅₀ Glu Val Arg Asp Val₂₅₅ Lys

Glu Ile Met Ala₂₆₀ Asp Leu Asp Pro Asp₂₆₅ Ala Phe Ile Ser Val₂₇₀ Ile Asn

Val Asp Glu₂₇₅ Val Ile Ser Ser Asp₂₈₀ Phe Lys Ile Arg Arg₂₈₅ Arg Asn Tyr

Asp Lys₂₉₀

<210> 369

<211> 583

<212> PRT

<213> Streptococcus agalactiae

<400> 369

Met Lys Arg Ser Met₅ Tyr Ala Gly Arg Val₁₀ Arg Ser Glu His Ile₁₅ Gly

Thr Ser Ile Thr₂₀ Leu Lys Gly Trp Val₂₅ Gly Arg Arg Arg Asp₃₀ Leu Gly

Gly Leu Ile₃₅ Phe Ile Asp Leu Arg Asp Arg Glu Gly Ile₄₅ Met Gln Leu

Val Ile₅₀ Asn Pro Glu Glu Val₅₅ Ala Ala Ser Val Met₆₀ Ala Thr Ala Glu

Ser Leu Arg Ser Glu Phe₇₀ Val Ile Glu Val Ser₇₅ Gly Val Val Thr Ala₈₀

Arg Glu Gln Ala Asn₈₅ Asp Asn Leu Pro Thr₉₀ Gly Glu Val Glu Leu₉₅ Lys

Val Gln Glu Leu₁₀₀ Ser Val Leu Asn Thr₁₀₅ Ser Lys Thr Thr Pro₁₁₀ Phe Glu

Ile Lys Asp₁₁₅ Gly Ile Glu Ala Asn₁₂₀ Asp Asp Thr Arg Met₁₂₅ Arg Tyr Arg

Tyr Leu Asp Leu Arg Arg Pro₁₃₅ Glu Met Leu Glu Asn₁₄₀ Phe Lys Leu Arg

Ala Lys Val Thr His Ser₁₅₀ Ile Arg Asn Tyr Leu₁₅₅ Asp Asn Leu Glu Phe₁₆₀

GBS patentin.ST25

Ile Asp Val Glu Thr Pro Met Leu Thr Lys Ser Thr Pro Glu Gly Ala
165 170 175

Arg Asp Tyr Leu Val Pro Ser Arg Val Asn Gln Gly His Phe Tyr Ala
180 185 190

Leu Pro Gln Ser Pro Gln Ile Thr Lys Gln Leu Leu Met Asn Ala Gly
195 200 205

Phe Asp Arg Tyr Tyr Gln Ile Val Lys Cys Phe Arg Asp Glu Asp Leu
210 215 220

Arg Gly Asp Arg Gln Pro Glu Phe Thr Gln Val Asp Leu Glu Thr Ser
225 230 235 240

Phe Leu Ser Asp Gln Glu Ile Gln Asp Ile Val Glu Gly Met Ile Ala
245 250 255

Lys Val Met Lys Asp Thr Lys Gly Leu Glu Val Ser Leu Pro Phe Pro
260 265 270

Arg Met Ala Tyr Asp Asp Ala Met Asn Asn Tyr Gly Ser Asp Lys Pro
275 280 285

Asp Thr Arg Phe Asp Met Leu Leu Gln Asp Leu Thr Glu Ile Val Lys
290 295 300

Glu Val Asp Phe Lys Val Phe Ser Glu Ala Ser Val Val Lys Ala Ile
305 310 315 320

Val Val Lys Asp Lys Ala Asp Lys Tyr Ser Arg Lys Asn Ile Asp Lys
325 330 335

Leu Thr Glu Ile Ala Lys Gln Tyr Gly Ala Lys Gly Leu Ala Trp Leu
340 345 350

Lys Tyr Val Asp Asn Thr Ile Ser Gly Pro Val Ala Lys Phe Leu Thr
355 360 365

Ala Ile Glu Gly Arg Leu Thr Glu Ala Leu Gln Leu Glu Asn Asn Asp
370 375 380

Leu Ile Leu Phe Val Ala Asp Ser Leu Glu Val Ala Asn Glu Thr Leu
385 390 395 400

Gly Ala Leu Arg Thr Arg Ile Ala Lys Glu Leu Glu Leu Ile Asp Tyr
405 410 415

Ser Lys Phe Asn Phe Leu Trp Val Val Asp Trp Pro Met Phe Glu Trp
420 425 430

GBS patentin.ST25

Ser Glu Glu Glu Gly Arg Tyr Met Ser Ala His His Pro Phe Thr Leu
435 440 445

Pro Thr Ala Glu Thr Ala His Glu Leu Glu Gly Asp Leu Ala Lys Val
450 455 460

Arg Ala Val Ala Tyr Asp Ile Val Leu Asn Gly Tyr Glu Leu Gly Gly
465 470 475 480

Gly Ser Leu Arg Ile Asn Gln Lys Asp Thr Gln Glu Arg Met Phe Lys
485 490 495

Ala Leu Gly Phe Ser Ala Glu Ser Ala Gln Glu Gln Phe Gly Phe Leu
500 505 510

Leu Glu Ala Met Asp Tyr Gly Phe Pro Pro His Gly Gly Leu Ala Ile
515 520 525

Gly Leu Asp Arg Phe Val Met Leu Leu Ala Gly Lys Asp Asn Ile Arg
530 535 540

Glu Val Ile Ala Phe Pro Lys Asn Asn Lys Ala Ser Asp Pro Met Thr
545 550 555 560

Gln Ala Pro Ser Leu Val Ser Glu Gln Gln Leu Glu Glu Leu Ser Leu
565 570 575

Thr Val Glu Ser Tyr Glu Asn
580

<210> 370

<211> 151

<212> PRT

<213> Streptococcus agalactiae

<400> 370

Lys Glu Lys Gly Lys Leu Ile Lys Lys Lys Ile Leu Glu Asn Asn Thr
1 5 10 15

Asp Ile Ile Pro Lys Ile Ile Glu Lys Ser Pro Gln Asn Leu Ile Leu
20 25 30

Thr Ser Asn Tyr Asn Arg Val Asn Ile Asp Lys Ile Lys Asn Ile Lys
35 40 45

Asn Phe Asp Lys Gly Phe Glu Leu Gly Phe Pro Leu Phe Glu Lys Gly
50 55 60

GBS patentin.ST25

Glu Ile Leu Arg Lys Glu Gly Glu Ile Thr Ser Ala Ile Glu Leu Phe
65 70 75 80

Asp Lys Ala Arg Glu Leu Gly Tyr Phe Val Pro Ala Leu Tyr Asn Ser
85 90 95

Tyr Ala Met Ala Phe Arg Lys Ile Lys Asn Tyr Asp Asp Glu Ile Leu
100 105 110

Ile Leu Gln Glu Gly Ile Glu Arg Phe Lys Lys Ser Thr Leu Ser Ser
115 120 125

Asn Ile Asn Pro Lys Thr Ile Asp Arg Trp Ser Thr Arg Ile Ser Arg
130 135 140

Ala Lys Asp Leu Lys Cys Lys
145 150

<210> 371

<211> 225

<212> PRT

<213> Streptococcus agalactiae

<400> 371

Leu Asn Val Lys Lys His His Leu Ala Tyr Gly Ala Ile Thr Leu Val
1 5 10 15

Ala Leu Phe Ser Cys Ile Leu Ala Val Met Val Ile Phe Lys Ser Ser
20 25 30

Gln Val Thr Thr Glu Ser Leu Ser Lys Ala Asp Lys Val Arg Val Ala
35 40 45

Lys Lys Ser Lys Met Thr Lys Ala Thr Ser Lys Ser Lys Val Glu Asp
50 55 60

Val Lys Gln Ala Pro Lys Pro Ser Gln Ala Ser Asn Glu Ala Pro Lys
65 70 75 80

Ser Ser Ser Gln Ser Thr Glu Ala Asn Ser Gln Gln Gln Val Thr Ala
85 90 95

Ser Glu Glu Ala Ala Val Glu Gln Ala Val Val Thr Glu Asn Thr Pro
100 105 110

Ala Thr Ser Gln Ala Gln Gln Ala Tyr Ala Val Thr Glu Thr Thr Tyr
115 120 125

GBS patentin.ST25

Arg Pro Ala Gln His Gln Thr Ser Gly Gln Val Leu Ser Asn Gly Asn
130 135 140

Thr Ala Gly Ala Ile Gly Ser Ala Ala Ala Ala Gln Met Ala Ala Ala
145 150 155 160

Thr Gly Val Pro Gln Ser Thr Trp Glu His Ile Ile Ala Arg Glu Ser
165 170 175

Asn Gly Asn Pro Asn Val Ala Asn Ala Ser Gly Ala Ser Gly Leu Phe
180 185 190

Gln Thr Met Pro Gly Trp Gly Ser Thr Ala Thr Val Gln Asp Gln Val
195 200 205

Asn Ser Ala Ile Lys Ala Tyr Arg Ala Gln Gly Leu Ser Ala Trp Gly
210 215 220

Tyr
225

<210> 372

<211> 493

<212> PRT

<213> Streptococcus agalactiae

<400> 372

Met Ser Asn Trp Asp Thr Lys Phe Leu Lys Lys Gly Phe Thr Phe Asp
1 5 10 15

Asp Val Leu Leu Ile Pro Ala Glu Ser His Val Leu Pro Asn Glu Val
20 25 30

Asp Met Lys Thr Lys Leu Ala Asp Asn Leu Thr Leu Asn Ile Pro Ile
35 40 45

Ile Thr Ala Ala Met Asp Thr Val Thr Asp Ser Lys Met Ala Ile Ala
50 55 60

Ile Ala Arg Ala Gly Gly Leu Gly Ile Ile His Lys Asn Met Ser Ile
65 70 75 80

Val Asp Gln Ala Glu Glu Val Arg Lys Val Lys Arg Ser Glu Asn Gly
85 90 95

Val Ile Ile Asp Pro Phe Phe Leu Thr Pro Asp Asn Thr Val Ser Glu
100 105 110

GBS patentin.ST25

Ala Glu Glu Leu Met Gln Asn Tyr Arg Ile Ser Gly Val Pro Ile Val
115 120 125

Glu Thr Leu Glu Asn Arg Lys Leu Val Gly Ile Ile Thr Asn Arg Asp
130 135 140

Met Arg Phe Ile Ser Asp Tyr Lys Gln Leu Ile Ser Glu His Met Thr
145 150 155 160

Ser Gln Asn Leu Val Thr Ala Pro Ile Gly Thr Asp Leu Glu Thr Ala
165 170 175

Glu Arg Ile Leu His Glu His Arg Ile Glu Lys Leu Pro Leu Val Asp
180 185 190

Asp Glu Gly Arg Leu Ser Gly Leu Ile Thr Ile Lys Asp Ile Glu Lys
195 200 205

Val Ile Glu Phe Pro Lys Ala Ala Lys Asp Glu Phe Gly Arg Leu Leu
210 215 220

Val Ala Gly Ala Val Gly Val Thr Ser Asp Thr Phe Glu Arg Ala Glu
225 230 235 240

Ala Leu Phe Glu Ala Gly Ala Asp Ala Ile Val Ile Asp Thr Ala His
245 250 255

Gly His Ser Ala Gly Val Leu Arg Lys Ile Ala Glu Ile Arg Ala His
260 265 270

Phe Pro Asn Arg Thr Leu Ile Ala Gly Asn Ile Ala Thr Ala Glu Gly
275 280 285

Ala Arg Ala Leu Tyr Asp Ala Gly Val Asp Val Val Lys Val Gly Ile
290 295 300

Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val Gly Val
305 310 315 320

Pro Gln Ile Thr Ala Ile Tyr Asp Ala Ala Ala Val Ala Arg Glu Tyr
325 330 335

Gly Lys Thr Ile Ile Ala Asp Gly Gly Ile Lys Tyr Ser Gly Asp Ile
340 345 350

Val Lys Ala Leu Ala Ala Gly Gly Asn Ala Val Met Leu Gly Ser Met
355 360 365

Phe Ala Gly Thr Asp Glu Ala Pro Gly Glu Thr Glu Ile Phe Gln Gly
370 375 380

GBS patentin.ST25

Arg Lys Phe Lys Thr Tyr Arg Gly Met Gly Ser Ile Ala Ala Met Lys
385 390 395 400

Lys Gly Ser Ser Asp Arg Tyr Phe Gln Gly Ser Val Asn Glu Ala Asn
405 410 415

Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Ala Tyr Lys Gly Ser
420 425 430

Val Ala Asp Ile Val Phe Gln Met Leu Gly Gly Ile Arg Ser Gly Met
435 440 445

Gly Tyr Val Gly Ala Ala Asn Ile Lys Glu Leu His Asp Asn Ala Gln
450 455 460

Phe Val Glu Met Ser Gly Ala Gly Leu Lys Glu Ser His Pro His Asp
465 470 475 480

Val Gln Ile Thr Asn Glu Ala Pro Asn Tyr Ser Val His
485 490

<210> 373

<211> 859

<212> PRT

<213> Streptococcus agalactiae

<400> 373

Met Thr Ile Asn His Tyr Lys Leu Arg Ile Pro Tyr Tyr Thr Ile Ser
1 5 10 15

Phe Leu Leu Pro Phe Ile Ile Ile Val Cys Ile Leu Phe Thr Lys Asn
20 25 30

Ile Tyr Trp Gly Ser Pro Thr Thr Ile Leu Ala Ser Asp Gly Phe His
35 40 45

Gln Tyr Val Ile Phe Asn Gln Ala Leu Arg Asn Ile Leu His Gly Ser
50 55 60

Asn Ser Leu Phe Tyr Thr Phe Thr Ser Gly Leu Gly Leu Asn Phe Tyr
65 70 75 80

Ala Leu Ser Ser Tyr Tyr Leu Gly Ser Phe Leu Ser Pro Ile Val Tyr
85 90 95

Phe Phe Asn Leu Lys Asn Met Pro Asp Ala Ile Tyr Leu Leu Thr Ile
100 105 110

GBS patentin.ST25

Cys Lys Ile Gly Leu Ile Gly Leu Ser Met Phe Val Thr Leu Cys Lys
115 120 125

Arg His Cys Lys Val Asn Arg Val Leu Leu Leu Val Ile Ser Thr Cys
130 135 140

Tyr Ser Leu Met Ser Phe Ser Ile Ser Gln Ile Glu Ile Asn Met Trp
145 150 155 160

Leu Asp Val Phe Ile Leu Ile Pro Leu Val Val Leu Gly Val Asp Gln
165 170 175

Leu Leu Trp Glu Arg Lys Pro Ile Leu Tyr Phe Leu Ser Leu Thr Ala
180 185 190

Leu Phe Ile Gln Asn Tyr Tyr Phe Gly Phe Met Thr Ala Ile Phe Thr
195 200 205

Ser Leu Tyr Phe Ile Val Gln Ile Thr Arg Asn Thr Asp Ser Lys Val
210 215 220

Ala Phe Lys Gln Phe Leu His Phe Thr Phe Leu Ser Leu Leu Ala Gly
225 230 235 240

Met Thr Ser Ser Ile Met Ile Leu Pro Thr Tyr Phe Asp Leu Thr Thr
245 250 255

His Gly Glu Lys Leu Thr Lys Val Ser Lys Met Phe Thr Glu Asn Ser
260 265 270

Trp Tyr Met Asp Leu Phe Ala Lys Asn Met Ile Gly Ala Tyr Asp Thr
275 280 285

Thr Lys Phe Gly Ser Ile Pro Met Ile Tyr Val Gly Leu Leu Pro Leu
290 295 300

Leu Leu Ser Leu Leu Tyr Phe Thr Ile Lys Glu Val Pro Arg Arg Thr
305 310 315 320

Arg Leu Ala Tyr Gly Phe Leu Ile Ile Phe Val Ile Ala Ser Phe Tyr
325 330 335

Ile Thr Pro Leu Asp Leu Phe Trp Gln Gly Met His Ala Pro Asn Met
340 345 350

Phe Leu His Arg Tyr Ser Trp Val Leu Ser Val Leu Ile Cys Leu Leu
355 360 365

Ala Ala Glu Cys Leu Glu Tyr Leu Asp Asn Ile Ser Trp Lys Lys Ile
370 375 380

GBS patentin.ST25

Leu Gly Val Asn Leu Ile Leu Val Ser Gly Phe Ile Ile Thr Phe Leu
 385 390 395 400
 Phe Lys Lys His Tyr His Tyr Leu Asn Leu Glu Leu Leu Leu Leu Thr
 405 410 415
 Leu Thr Phe Leu Ser Ala Tyr Ile Ile Leu Thr Ile Ser Phe Val Ser
 420 425 430
 Lys Gln Ile Pro Lys Leu Val Phe Tyr Pro Phe Leu Ile Gly Phe Val
 435 440 445
 Val Leu Glu Met Thr Leu Asn Thr Phe Tyr Gln Leu Asn Ser Leu Asn
 450 455 460
 Asp Glu Trp Ile Phe Pro Ser Arg Gln Gly Tyr Ala Lys Tyr Asn His
 465 470 475 480
 Ser Ile Ser Lys Leu Val Arg Lys Thr Glu Arg Asn Asn Ser Thr Phe
 485 490 495
 Phe Arg Thr Glu Arg Trp Leu Gly Gln Thr Gly Asn Asp Ser Met Lys
 500 505 510
 Tyr Asn Tyr Asn Gly Ile Ser Gln Phe Ser Ser Ile Arg Asn Arg Ser
 515 520 525
 Ser Ser Gln Val Leu Asp Arg Leu Gly Phe Lys Ser Asp Gly Thr Asn
 530 535 540
 Leu Asn Leu Arg Tyr Gln Asn Asn Thr Leu Ile Ala Asp Ser Leu Phe
 545 550 555 560
 Gly Val Lys Tyr Asn Leu Thr Glu Tyr Pro Phe Asp Lys Phe Gly Phe
 565 570 575
 Ile Lys Lys Ala Gln Asp Lys Gln Thr Ile Leu Tyr Lys Asn Gln Phe
 580 585 590
 Ala Ser Gln Leu Ala Ile Leu Thr Asn Gln Val Tyr Gln Asp Lys Pro
 595 600 605
 Phe Thr Val Asn Thr Leu Asp Asn Gln Thr Thr Leu Leu Asn Gln Leu
 610 615 620
 Ser Gly Leu Lys Glu Thr Tyr Phe Glu His Leu Ile Pro Asn Ser Val
 625 630 635 640
 Ser Gly Gln Thr Thr Leu Asn Lys Gln Val Phe Val Lys Lys Asn Lys
 645 650 655

GBS patentin.ST25

Gln Gly Asn Thr Glu Ile Thr Tyr Asn Ile Thr Ile Pro Lys Asn Ser
660 665 670

Gln Leu Tyr Val Ser Met Pro Phe Ile Asn Phe Asn Asn Glu Glu Asn
675 680 685

Lys Ile Val Gln Ile Ser Val Asn Asn Gly Pro Phe Val Pro Asn Thr
690 695 700

Leu Asp Asn Ala Tyr Ser Phe Phe Asn Ile Gly Ser Phe Ala Glu Asn
705 710 715 720

Ser Arg Ile Lys Val Lys Phe Gln Phe Pro His Asn Asp Gln Val Ser
725 730 735

Phe Pro Ile Pro His Phe Tyr Gly Leu Lys Leu Glu Ala Tyr Gln Lys
740 745 750

Ala Met Thr Val Ile Asn Lys Arg Lys Val Lys Val Arg Thr Asp His
755 760 765

Asn Lys Val Ile Ala Asn Tyr Thr Ser Pro Asn Arg Ser Ser Leu Phe
770 775 780

Phe Thr Ile Pro Tyr Asp Arg Gly Trp Lys Ala Tyr Gln Asn Asn Lys
785 790 795 800

Glu Ile Lys Ile Phe Lys Ala Gln Lys Gly Phe Met Lys Ile Asn Ile
805 810 815

Pro Lys Gly Lys Gly Lys Val Thr Leu Ile Phe Ile Pro Tyr Gly Phe
820 825 830

Lys Phe Gly Val Gly Leu Ser Ile Thr Gly Ile Val Leu Phe Thr Val
835 840 845

Tyr Tyr Phe Lys Phe Gly Lys Asn Lys Ile Gly
850 855

<210> 374

<211> 15

<212> PRT

<213> Streptococcus agalactiae

<400> 374

Trp Phe Met Lys His Ser Val Gly Lys Arg His Asn Leu Val Thr
1 5 10 15

GBS patentin.ST25

<210> 375

<211> 30

<212> PRT

<213> Streptococcus agalactiae

<400> 375

Met Lys Asp His Leu Arg Cys Phe Leu His Tyr Arg Ser Lys Asn Val
1 5 10 15

Gly Lys Asn Gly Thr Arg Leu Lys Gly Gly Lys Pro Asn Asp
20 25 30

<210> 376

<211> 33

<212> PRT

<213> Streptococcus agalactiae

<400> 376

Asp Lys Gln Leu Phe Gln Cys Val Gln Gly Phe Gln Ile Arg Asn Leu
1 5 10 15

Asn Gly Lys Lys His Gly Ile Lys Leu Ile Phe Ile Lys Asn Val Lys
20 25 30

His

<210> 377

<211> 26

<212> PRT

<213> Streptococcus agalactiae

<400> 377

Asn Glu Glu Ala Ile Asp Gly Val Ser Lys Leu Gly Lys Lys Ile Thr
1 5 10 15

Ile Leu Gly Asn Asn Ser Tyr Leu Ser Ser
20 25

<210> 378

GBS patentin.ST25

<211> 31

<212> PRT

<213> Streptococcus agalactiae

<400> 378

Ile Lys Gln Trp Leu Leu Val Met Lys Lys Met Thr Val Leu Cys Leu
1 5 10 15

Lys Leu Leu Glu Ile Leu Leu Leu Cys Lys Thr Ala Ile Leu Asn
20 25 30

<210> 379

<211> 19

<212> PRT

<213> Streptococcus agalactiae

<400> 379

Arg Arg Ile Ser Asn Asn Leu Gly Val Leu Lys Glu Ala Thr Val Ile
1 5 10 15

His Ala Val

<210> 380

<211> 36

<212> PRT

<213> Streptococcus agalactiae

<400> 380

Glu Leu Cys Leu Lys Leu Ser Asn Val Lys Pro Ile Tyr Met Pro Trp
1 5 10 15

His Phe Glu Gln Ile Ser Leu Lys Lys Gln Val Ser Arg Val Tyr His
20 25 30

Ala Leu Phe Glu
35

<210> 381

<211> 32

<212> PRT

<213> Streptococcus agalactiae

<400> 381

Arg Ser Cys Phe Ser Arg Cys Tyr Pro Arg Phe Asn Arg Phe Arg Tyr
 1 5 10 15
 His Phe Leu Lys Pro Pro Trp Thr Arg Thr Asn Tyr Cys Lys Arg Tyr
 20 25 30

<210> 382

<211> 19

<212> PRT

<213> Streptococcus agalactiae

<400> 382

Arg Trp Phe Gly Phe Arg Tyr Asp Asp Gly Arg Lys Phe Ser Phe Thr
 1 5 10 15

Asn Leu Leu

<210> 383

<211> 22

<212> PRT

<213> Streptococcus agalactiae

<400> 383

Pro Leu Lys Ser Leu Ser Met Thr Ser Arg Met Lys Leu Leu Arg Leu
 1 5 10 15

Ser Gln Arg Lys Ala Met
 20

<210> 384

<211> 30

<212> PRT

<213> Streptococcus agalactiae

<400> 384

Arg His Leu Arg Lys Arg Gln Lys Gln Asn His Leu Met Asn Leu Cys
 1 5 10 15

GBS patentin.ST25

Phe Leu Cys Ala Val Lys Lys Leu Lys Lys Asp Asn Leu Ile
20 25 30

<210> 385

<211> 30

<212> PRT

<213> Streptococcus agalactiae

<400> 385

Lys Leu Phe Ile Gln Pro Ile Gln Glu Asn Met Lys Gln Pro Ile Glu
1 5 10 15

Ile Ile Ser Asn Tyr Tyr Ala Lys Leu Gly Leu Met Lys Ile
20 25 30

<210> 386

<211> 19

<212> PRT

<213> Streptococcus agalactiae

<400> 386

Tyr Gln Thr Tyr Ser Lys Lys Ala Arg Lys Phe Gly Ser Val Trp Leu
1 5 10 15

Lys Pro Lys

<210> 387

<211> 28

<212> PRT

<213> Streptococcus agalactiae

<400> 387

Thr Leu Leu Phe Gln Ile Leu Leu Leu Leu Ser His Leu Lys Lys Asn
1 5 10 15

Ile Phe Leu Glu Trp Asn Met His Ala Thr Tyr Asn
20 25

<210> 388

<211> 70

<212> PRT

<213> Streptococcus agalactiae

<400> 388

Lys Lys Phe Tyr Glu Ile Ile Leu Ala Thr Lys Tyr His Thr Ser Val
 1 5 10 15

Phe Lys Trp Ser Leu Lys Leu Lys Asn Lys Leu Thr Asn Thr Lys Lys
 20 25 30

Ile Ser Glu Ala Ser Ser Gly Lys Leu Glu Ile His Leu Glu Gln Gln
 35 40 45

Leu Asn Ser Met Pro Lys Val Thr Leu Ala Leu Ile Leu Leu Val Asp
 50 55 60

Lys Ser Asn Ala Leu Leu
 65 70

<210> 389

<211> 111

<212> PRT

<213> Streptococcus agalactiae

<400> 389

Leu Lys Gln Met Phe Arg Arg Val Leu His Leu Leu Phe Gln Val Val
 1 5 10 15

Leu Ile Ala Val Arg Ser Leu Met Lys Met Val Leu Lys Ser Ser Trp
 20 25 30

Asp Gly Val Thr Cys Ser Leu Ser Leu Leu Met Arg Ile Ile Gln Tyr
 35 40 45

Asp Tyr Lys Val Pro Leu Phe Gln Met Met Met Leu Lys Gly Ser Leu
 50 55 60

Val Leu Ser Lys Thr Lys Pro Arg Leu Thr Met Met Met Pro Leu Ile
 65 70 75 80

Leu Glu Lys Tyr Leu Lys Gln Ile Thr Ala Leu Val Val Ala Ala Glu
 85 90 95

Tyr Leu Lys Val Ile Leu Phe Leu Lys Lys Pro Arg Asp Ser Phe
 100 105 110

<210> 390

<211> 13

<212> PRT

<213> Streptococcus agalactiae

<400> 390

Gly Arg Lys Ile Asn Phe Ser Arg Pro Ser Arg Phe Glu
1 5 10

<210> 391

<211> 27

<212> PRT

<213> Streptococcus agalactiae

<400> 391

Arg Val Lys Tyr Lys Lys Trp Glu Pro Leu Ser Ile Ser Arg Ser Cys
1 5 10 15

Tyr Glu Lys Ser Ser Ser Thr Ser Ser Arg Ile
20 25

<210> 392

<211> 31

<212> PRT

<213> Streptococcus agalactiae

<400> 392

Thr Trp Ser Arg Cys Cys Ile Pro Arg Cys Tyr Ser Trp Cys Lys Ile
1 5 10 15

Arg Arg Ser Asn Gln Cys Phe Gly Arg Trp Thr Ser Ser Phe Gly
20 25 30

<210> 393

<211> 33

<212> PRT

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 393

Lys Glu Asn Phe Val Gln Arg Leu Arg Ser Leu Leu Lys Ala Ile Ser
1 5 10 15

Lys Asn Ile Ile Ile Tyr Ser Leu Val Ser Leu Pro Leu Ala Arg His
20 25 30

Leu

<210> 394

<211> 59

<212> PRT

<213> Streptococcus agalactiae

<400> 394

Ser Ile Ile Asn Ile Lys Leu Glu Ile Tyr Asp Ile Cys Pro Lys Thr
1 5 10 15

Ile Ser Asn Arg Glu Ser Ile His Gly Tyr Arg Lys Leu Leu Pro Arg
20 25 30

Leu Leu Phe Gly Asp Tyr Leu Ser Lys Thr Leu Phe Gln Gly Phe Thr
35 40 45

Ser Asn His Pro Asn Cys Arg Pro Ile Arg Leu
50 55

<210> 395

<211> 16

<212> PRT

<213> Streptococcus agalactiae

<400> 395

Leu Ser Phe Arg Arg Ser Arg Arg Ile Gly Ser Ser His Ser Gln Ile
1 5 10 15

<210> 396

<211> 14

<212> PRT

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 396

Phe Ile Phe Lys Asp Arg Phe Lys Met Arg His Phe Thr Asp
1 5 10

<210> 397

<211> 74

<212> PRT

<213> Streptococcus agalactiae

<400> 397

Gly Leu Ile Cys Ala Cys Lys Ala Phe Ile Ser Ala Ile Leu Ala Asn
1 5 10 15

Leu Phe Cys Ser Ser Val Ile Pro Ile Ala Ser Cys Pro Glu Asn Ile
20 25 30

Cys Ala Lys Pro Arg Thr Arg Phe Ser Ser Thr Ser Asp Ile Val Leu
35 40 45

Ser Pro Ala Lys Tyr Ile Phe Lys Ala Pro Thr Val Leu Ser Phe Ile
50 55 60

Phe Arg Gly Thr Thr Ile Ala Glu Phe Asn
65 70

<210> 398

<211> 33

<212> PRT

<213> Streptococcus agalactiae

<400> 398

Ser Ser Ser Leu Asp Thr His Tyr Lys His Arg Glu Leu Phe Leu Val
1 5 10 15

Ala Asp Ser Leu Gly Ser Leu Trp Leu Ile Leu Leu Val Ala Tyr Phe
20 25 30

val

<210> 399

<211> 25

<212> PRT

GBS patentin.ST25
<213> Streptococcus agalactiae

<400> 399

His Leu Val Pro Thr Gln Tyr His Lys Gln Asn Leu Pro Leu Glu Tyr
1 5 10 15

Lys Arg Leu Asn Ala Leu Val His Lys
20 25

<210> 400

<211> 24

<212> PRT

<213> Streptococcus agalactiae

<400> 400

Ala His Leu His Glu Gly Tyr His Lys Tyr Pro Leu Lys Arg Arg Asn
1 5 10 15

Leu Tyr Glu Phe Leu Arg Lys Leu
20

<210> 401

<211> 23

<212> PRT

<213> Streptococcus agalactiae

<400> 401

Pro Leu Lys Glu Leu Arg Glu His Tyr Ile Ile Pro Arg Lys Ile Arg
1 5 10 15

Leu Gln Asn Phe Pro His Arg
20

<210> 402

<211> 21

<212> PRT

<213> Streptococcus agalactiae

<400> 402

Lys Tyr Thr Ile Ala Gly Ser Arg Val Thr Gln Arg Arg Pro Ser Phe
1 5 10 15

Ser Val Thr Lys Val
20

<210> 403

<211> 19

<212> PRT

<213> Streptococcus agalactiae

<400> 403

Ala Ala Phe Ser Ser Pro Ala Ala Lys Asn Arg Ala Phe Ile Thr Thr
1 5 10 15

Arg Ser Ser

<210> 404

<211> 47

<212> PRT

<213> Streptococcus agalactiae

<400> 404

Ser Met Val Lys Gln Ile Ser Phe Ser Asp His Leu Ile Ser Arg Phe
1 5 10 15

Glu Gly Leu Cys Leu Arg Arg Phe Ser Val Arg Phe Arg Leu Arg Arg
20 25 30

Ser Leu Ser Ser Val Ser Asn Ser Thr Asn Asn Thr Ser Trp Leu
35 40 45

<210> 405

<211> 43

<212> PRT

<213> Streptococcus agalactiae

<400> 405

Tyr His Val Leu Ser Arg Tyr His Leu Asn Pro Leu His Val Leu Gln
1 5 10 15

Ala Leu Tyr Ala His Gln Glu Tyr Val Ile Val Leu Ile Ile His Gln
20 25 30

GBS patentin.ST25

Arg Glu Leu Phe Tyr Arg Gly Gln Arg Gly Gln
35 40

<210> 406

<211> 18

<212> PRT

<213> Streptococcus agalactiae

<400> 406

Ala Gln Pro Ser Ser Thr Arg Ile Ser Pro Lys Ile Asp Arg Phe Thr
1 5 10 15

Pro Lys

<210> 407

<211> 38

<212> PRT

<213> Streptococcus agalactiae

<400> 407

Trp Asn Arg Thr Ile Asn Tyr Phe Leu Asn Asn Leu Gln Leu Val Thr
1 5 10 15

Asn Ile Lys Leu Pro Thr Arg Lys Ile Phe Gln Ser Gln Asn Lys Phe
20 25 30

Leu Ser Phe Ile Lys Asn
35

<210> 408

<211> 12

<212> PRT

<213> Streptococcus agalactiae

<400> 408

Val Gln Glu Gly His Lys Ile Phe Pro Leu Gln Arg
1 5 10

<210> 409

GBS patentin.ST25

<211> 29

<212> PRT

<213> Streptococcus agalactiae

<400> 409

Gln Gln Ser Asn Asn Thr Ala Asn Tyr Ser Arg Pro Tyr Lys Pro Trp
1 5 10 15

His Lys Lys Lys Asn Gly Leu Ser Cys Arg Cys Phe Ser
20 25

<210> 410

<211> 83

<212> PRT

<213> Streptococcus agalactiae

<400> 410

Phe Phe Asp Asp Thr Lys Val Asn Ile His Trp Leu Glu Met Phe Ala
1 5 10 15

Val Cys Met Cys Asn Ile Met Trp Gln Cys Thr Asn Ser Ser Ser Leu
20 25 30

Trp Glu Asn Tyr Phe Thr Leu Pro Ile Lys Ala Thr Gly Ser Ile Asp
35 40 45

Ser Arg Tyr Lys Thr Thr Cys Cys Arg Phe Tyr Ile Thr Phe Asn Thr
50 55 60

Gly His Leu Ser Ser Lys Glu Lys Ile Trp Val Leu Thr Cys Ser Lys
65 70 75 80

Gly Leu Val

<210> 411

<211> 81

<212> PRT

<213> Streptococcus agalactiae

<400> 411

Val Tyr Ser Leu Arg Ile Ala Thr Leu Glu Leu Glu Arg Asn Leu Ile
1 5 10 15

GBS patentin.ST25

Asp Lys Arg Arg Gly Lys Pro Thr Asp Ser Arg Ser Ile Glu Phe Leu
20 25 30

Glu Val Ser Leu Ala Ile Leu Ser Cys Lys Asn Lys Leu Ile Pro Asp
35 40 45

Ile Met Leu Glu Lys Thr Phe Pro Leu Val Ser Ser Glu Ala Lys Ser
50 55 60

Glu Asp Leu Lys Phe Lys Ser Ala Ile Ser Leu Asn Leu Glu Asn Cys
65 70 75 80

Ser

<210> 412

<211> 56

<212> PRT

<213> Streptococcus agalactiae

<400> 412

Gly His Ser Asn Gly Ile Lys Glu Gly Asn Gly Gly Ile Phe Pro Val
1 5 10 15

Phe Cys Ile Ala Ile Thr Ala Thr Arg Phe Arg Phe Thr Ile Asn Gly
20 25 30

Phe Cys Asn Arg Ile Asn Pro Cys Leu Cys His Phe Ile Val Thr Leu
35 40 45

Leu Ser Cys Cys Asn Arg Lys Ser
50 55

<210> 413

<211> 163

<212> PRT

<213> Streptococcus agalactiae

<400> 413

Arg Ile Glu Lys Ala Ile Val Pro Lys Pro Ala Ile Ser Val Leu Met
1 5 10 15

Ile Ile Ser Arg Met Val Leu Gly Thr Pro Glu Lys Glu Pro Val Ile
20 25 30

GBS patentin.ST25

Cys Ser Ala Asn Gly Ile Ile Ser Ile Val Ile Ala Thr Pro Ala Asp
35 40 45
Ile Glu Ile Gln Met Ser Lys Ala Asp Ile Ile Lys Ala Lys Pro Val
50 55 60
Glu Lys Leu Phe Cys Glu Asn Ser Leu Thr Glu Leu Thr Lys Ala Ala
65 70 75 80
Pro Gly Thr Ile Thr Ile Ser Ala Pro Asn Ile Ile Met Leu Arg Cys
85 90 95
Ser Pro Asn Pro Glu Lys Tyr Asn Lys Leu Ala Leu Lys Ala Thr Thr
100 105 110
Glu Leu Pro Arg Met Val Lys Arg Asn Pro Val Cys Ile Arg Leu Ser
115 120 125
Ile Lys Phe Arg Lys Tyr Pro Lys Ile Lys Pro Val Thr Ala Ala Glu
130 135 140
Asn Glu Ser Asn Lys Glu Leu Pro Lys Ala Lys Glu Lys Leu Pro Ala
145 150 155 160
Pro Gln Lys

<210> 414

<211> 89

<212> PRT

<213> Streptococcus agalactiae

<400> 414

Pro Tyr Ser Val Thr Tyr Ala Ala Pro Val Ile Cys Asn Gly Ala Asp
1 5 10 15
Leu Ala Arg Arg Thr Ala Tyr Ala Met Ser Ser Ser Val Thr Lys Pro
20 25 30
Ser Asp Val Glu Glu Leu Val Thr Ile Gly Asp Arg Thr Lys Arg Phe
35 40 45
Ser Arg Leu Asn Pro Leu Gly Ser Ile Asn Gly Arg Asn Lys Leu Pro
50 55 60
Trp Thr Leu Phe Ile Ser Ala His Arg Pro Leu Ile Ser His Arg Leu
65 70 75 80

GBS patentin.ST25

Ser Leu Lys Ser Ile Lys Leu Cys Asn
85

<210> 415

<211> 18

<212> PRT

<213> Streptococcus agalactiae

<400> 415

Ala Asn His Asn Asp Lys Asn Asn Thr Ile Ser Val Asn Lys Phe Ser
1 5 10 15

Ala Lys

<210> 416

<211> 51

<212> PRT

<213> Streptococcus agalactiae

<400> 416

Ser Phe Cys Val Phe Cys Cys His Ser Lys Lys Gly Ser Tyr Pro His
1 5 10 15

Pro Lys Gln Ser Ser Trp Ser Ser Arg Phe Asn Ser Arg Ser His Thr
20 25 30

Asn Asp Ile Thr Cys Pro Tyr Arg Cys Ser Lys Ser Ser Cys Lys Gly
35 40 45

Ser Ile Thr
50

<210> 417

<211> 30

<212> PRT

<213> Streptococcus agalactiae

<400> 417

Thr Leu Gly Ile Ser Phe Lys Ile Arg Gly Cys His Phe Ser Ala Lys
1 5 10 15

GBS patentin.ST25

Pro Phe Leu Gly Gly Lys Ser Pro Asp Phe Pro Leu Pro Gly
20 25 30

<210> 418

<211> 60

<212> PRT

<213> Streptococcus agalactiae

<400> 418

Phe Asn Ile Ser Asn Ser Ser Leu Gly Phe Gly Thr Ser Ala Lys Ser
1 5 10 15

Ala Ser Thr Ser Ser Ala Asn Ser Ser Leu Ile Ile Ser Cys Asp Lys
20 25 30

Ala Thr His Ser Leu Gln Met Lys Thr Pro Leu Pro Ala Ile Ile Phe
35 40 45

Phe Thr Ser Ser Trp Leu Leu Pro Gln Asn Glu Gln
50 55 60

<210> 419

<211> 35

<212> PRT

<213> Streptococcus agalactiae

<400> 419

Gly Val Tyr Lys Lys Gln Ser Leu Ser Leu Ile Phe His Gln Ile His
1 5 10 15

Leu Ile Val Tyr His Phe Asp Phe Leu His Asp Arg Phe Val Pro Tyr
20 25 30

Tyr Arg Glu
35

<210> 420

<211> 87

<212> PRT

<213> Streptococcus agalactiae

<400> 420

Ile Phe Leu Arg Ser Val Cys Gly Asn Ser Arg Gln Ala Leu Gly Leu
 1 5 10 15

Thr Ser Tyr Ile Leu His Lys Leu Ser Ser Pro Lys Asn Gly Gln Gly
 20 25 30

Ile Ala Leu Asn Thr Leu Ser Pro Ser Ser Ser Thr Ser Lys Asn Lys
 35 40 45

Ser Ser Lys Ala Asp Asn Phe Ile Arg Lys Cys Leu Glu Ile Leu Glu
 50 55 60

Ile Ser Ala Ser Val Asn Arg Gly Pro Lys Val Leu Gln Gln Leu Ala
 65 70 75 80

His Ala Val Gln Ser Ile Ser
 85

<210> 421

<211> 130

<212> PRT

<213> Streptococcus agalactiae

<400> 421

Ser Arg Ile Ser Thr Ile Thr Ile Pro Ile Arg Ile Ser Pro Thr Phe
 1 5 10 15

Leu Tyr Arg Glu Asp Phe Ser Ser Gly Leu Lys Gly Ser Phe Gly Leu
 20 25 30

Arg Leu Ser Ser Val Lys Tyr Phe Phe Pro Ser Lys Val Tyr Trp Arg
 35 40 45

Arg Pro Lys Asn Ile Pro Ile Ala Ala Ser Glu Lys Pro Arg Trp Lys
 50 55 60

Phe Thr Ser Cys Pro Arg Tyr Pro Thr Thr Met Gly Glu Ile Lys Ala
 65 70 75 80

Pro Arg Leu Ile Pro Lys Thr Lys Ile Leu Lys Pro Ala Ser Arg Arg
 85 90 95

Glu Ser Phe Ser Pro Tyr Lys Leu Pro Thr Ile Ser Asp Thr Phe Gly
 100 105 110

Phe Asn Ser Pro Val Pro Arg Ile Ile Arg Ala Ile Glu Met Asn Arg
 115 120 125

GBS patentin.ST25

Ala Val
130

<210> 422

<211> 26

<212> PRT

<213> Streptococcus agalactiae

<400> 422

Ser Phe Pro Arg Ser Asn Asn Leu Cys Ala Phe Lys Asp Lys Phe Lys
1 5 10 15

Cys Arg Thr Ser Ser Arg Leu Asp Cys Leu
20 25

<210> 423

<211> 41

<212> PRT

<213> Streptococcus agalactiae

<400> 423

Ile His Ser Phe His Arg Arg Lys Leu Asn His His Gly Lys Leu Asn
1 5 10 15

Leu Tyr His Leu Val Leu Glu Lys Gln Pro Gly Leu Ser Ser Leu Leu
20 25 30

Ile Met Leu Tyr Gln Ser Pro Asp Leu
35 40

<210> 424

<211> 155

<212> PRT

<213> Streptococcus agalactiae

<400> 424

Leu Ser Phe Ser Ile Val Ser His Leu Leu Thr Thr Ile Ile Ile Pro
1 5 10 15

Leu Pro Ala Ser Cys Ala Asn Pro Ala Ile Arg Leu Ser Tyr Ser Arg
20 25 30

GBS patentin.ST25

Ile Pro Ser Ser Ala Leu Ile Thr Ile Arg Thr Thr Ser Glu Arg Ser
35 40 45

Met Ala Arg Ile Glu Arg Ile Thr Glu Tyr Phe Ser Val Phe Ser Tyr
50 55 60

Thr Leu Pro Asp Leu Arg Ile Pro Ala Val Ser Ile Ile Val Tyr Ser
65 70 75 80

Cys Pro Trp Leu Ser Thr Lys Leu Val Ser Ile Ala Ser Arg Val Val
85 90 95

Pro Ala Thr Gly Leu Ala Ile Thr Arg Ser Ser Pro Arg Met Ala Leu
100 105 110

Ile Lys Leu Asp Phe Pro Thr Phe Gly Arg Pro Ile Lys Leu Lys Arg
115 120 125

Ile Ile Ser Gly Phe Ser Phe Ser Ser Ser Thr Gly Arg Phe Ser Thr
130 135 140

Ile Ala Ser Asn Ile Ser Pro Val Pro Ile Pro
145 150 155

<210> 425

<211> 24

<212> PRT

<213> Streptococcus agalactiae

<400> 425

Cys Pro Ser Ser Asp Ile Ala Gly Ile Asn Phe Thr Lys Asn Ser Gly
1 5 10 15

Lys Ile Asp Lys Gln Thr Val Thr
20

<210> 426

<211> 32

<212> PRT

<213> Streptococcus agalactiae

<400> 426

Pro Phe Leu Arg Asn His Phe His Asn Asn Glu Thr Ser Thr Lys Phe
1 5 10 15

GBS patentin.ST25

Phe Ser Asp Ser Thr Lys Ser Arg Ile Gly Asn Thr Cys His Arg Cys
20 25 30

<210> 427

<211> 50

<212> PRT

<213> streptococcus agalactiae

<400> 427

Ala Ser Thr Gly Ser Ala Ala Asn Pro Gln Thr Thr Pro Gly Lys Leu
1 5 10 15

Leu Gln Ala Ser Ile Ala Pro Ile Pro Val Pro Gln Pro Val Ile Thr-
20 25 30

Lys Ser Ala Ala Pro Leu Leu Ser Lys Ile Ala Val Ser Lys Pro Phe
35 40 45

Cys Thr
50

<210> 428

<211> 47

<212> PRT

<213> Streptococcus agalactiae

<400> 428

Ala Met Pro Lys Arg Cys Phe Ile Pro Pro Glu Tyr Asp Glu Ile Phe
1 5 10 15

Phe Leu Pro Thr Ser Pro Lys Pro Thr Ser Ser Ser Asn Leu Gly Ile
20 25 30

Ser Cys Leu Ala Phe Phe Leu Ser Thr Pro Phe Lys Val Ala Ile
35 40 45

<210> 429

<211> 49

<212> PRT

<213> streptococcus agalactiae

GBS patentin.ST25

<400> 429

Leu Leu Leu Ile Leu Lys Asn Pro Asp Thr Thr His Asn Thr Thr Ile
1 5 10 15

Lys Arg Gln Pro Asn Lys Pro Pro Lys Val Leu Arg Lys Arg Thr Glu
20 25 30

Lys Lys Ser Ile Lys Leu Met Lys Arg Ile Pro Ile Asn His Val Ala
35 40 45

Pro

<210> 430

<211> 44

<212> PRT

<213> Streptococcus agalactiae

<400> 430

Asn Phe Lys Ala Arg Pro Pro Gly Val Val Ser Gly Leu Pro Asn Ile
1 5 10 15

Thr Pro Thr Phe Ser Leu Asn Trp Leu Ile Lys Ile Ala Ile Val Phe
20 25 30

Val Leu Leu Met Asp Ala Asp Asn Leu Arg Ile Ala
35 40

<210> 431

<211> 47

<212> PRT

<213> Streptococcus agalactiae

<400> 431

Lys Arg Val Gly Ile Cys His Ile Tyr His Val Ser Gln Ser Ser Cys
1 5 10 15

Phe His Asn Asn Lys Phe Ser Arg Tyr Phe Thr Gln Phe Ser Phe Asn
20 25 30

Ile Ile Val His Ser Ile Phe Leu Ser Gln Tyr Phe Ser Phe Trp
35 40 45

<210> 432

<211> 79

<212> PRT

<213> Streptococcus agalactiae

<400> 432

Asn Ser Thr Thr Ser Ala Ser Leu Ile Ser Gly Leu Ile Ser Ser Arg
 1 5 10 15

Ser Gly Arg Arg Val Asn Glu Pro Ser Ser Phe Ser Ala Ser Asn Asp
 20 25 30

Thr Lys Ala Gly Arg Pro Lys Val Ala Ser Thr Ala Ser Arg Ile Ala
 35 40 45

Gly Thr Phe Ile Asp Phe Ser Arg Thr Glu Ile Thr Cys Pro Gly Val
 50 55 60

Thr Arg Tyr Asp Gly Ile Ser Thr Arg Leu Pro Ser Thr Arg Ile
 65 70 75

<210> 433

<211> 37

<212> PRT

<213> Streptococcus agalactiae

<400> 433

Thr Arg Pro Leu Val Glu Ile Leu Val Asp Lys Leu Ala Pro Tyr Lys
 1 5 10 15

Glu Ala Asn Phe Ser Arg Asn Ser Cys Thr Leu Gly Tyr Leu Ala Phe
 20 25 30

Ala Val Thr Asn Ile
 35

<210> 434

<211> 287

<212> PRT

<213> Streptococcus agalactiae

<400> 434

Arg Thr Arg Asn Ala Ile Arg Tyr Pro Lys Ala Ser Ser Gly Asp Tyr
 1 5 10 15

GBS patentin.ST25

Gly Thr Lys Arg Glu Ile Ile Thr Ala Asn Lys Asp Lys Tyr Ser Ile
20 25 30

Ser Lys Met Cys Arg Trp Leu Asn Met Pro Arg Ser Ser Tyr Tyr Tyr
35 40 45

Gln Ala Val Glu Ser Val Ser Lys Thr Glu Phe Glu Glu Thr Ile Lys
50 55 60

Arg Ile Phe Leu Asp Ser Glu Ser Arg Tyr Gly Ser Arg Lys Ile Lys
65 70 75 80

Ile Cys Leu Asn Asn Glu Gly Ile Thr Leu Ser Arg Arg Arg Ile Arg
85 90 95

Arg Ile Met Lys Arg Leu Asn Leu Val Ser Val Tyr Gln Lys Ala Thr
100 105 110

Phe Lys Pro His Ser Arg Gly Lys Asn Glu Ala Pro Ile Pro Asn His
115 120 125

Leu Asp Arg Gln Phe Lys Gln Glu Arg Pro Leu Gln Ala Leu Val Thr
130 135 140

Asp Leu Thr Tyr Val Arg Val Gly Asn Arg Trp Ala Tyr Val Cys Leu
145 150 155 160

Ile Ile Asp Leu Tyr Asn Arg Glu Ile Ile Gly Leu Ser Leu Gly Trp
165 170 175

His Lys Thr Ala Glu Leu Val Lys Gln Ala Ile Gln Ser Ile Pro Tyr
180 185 190

Ala Leu Thr Lys Val Lys Met Phe His Ser Asp Arg Gly Lys Glu Phe
195 200 205

Asp Asn Gln Leu Ile Asp Glu Ile Leu Glu Ala Phe Gly Ile Thr Arg
210 215 220

Ser Leu Ser Gln Ala Gly Cys Pro Tyr Asp Asn Ala Val Ala Glu Ser
225 230 235 240

Thr Tyr Arg Ala Phe Lys Ile Glu Phe Val Tyr Gln Glu Thr Phe Gln
245 250 255

Ser Leu Glu Glu Leu Ala Leu Lys Thr Glu Lys Ala Thr Leu Phe Cys
260 265 270

Thr Thr Phe Ile Lys Cys Cys Leu Phe Arg Phe Leu Pro Met Leu
275 280 285

GBS patentin.ST25

<210> 435
 <211> 2367
 <212> DNA
 <213> Streptococcus agalactiae

<400> 435
 atggatgtat cgtctagtcc gaatattaca tttatgctgc aatacacaga ggctaatacct 60
 caatatgtgg actatactaa cagagaagag gctgtcaaaa ttgatgaaga attgtcctta 120
 gaaacgaaca ggcaaatgat tgaaggatta actgaagacg agttgactcg tattcaggaa 180
 gctgtccctg aaacgcagtt gaatttttagg gaatacattg attatatgaa ccgctcgtat 240
 gcaactgaag aacaatctaa agaactaaca gctatcttta ctcaagaagc agattatctt 300
 cagaaactac gattaatcga tctaaaaaat aagttggaat cagcttatca aaatgggttca 360
 cttctctggc aaggagttat ttcgtttgat aatgcttttc ttgcggaaca gggattgtat 420
 gatgttgcga ctggtcaagt tgatcaaaaa gcgattaagg cagtgatgcg tgatatgatg 480
 ccaacactta tccagaaaga gggcctttct gattctgctt tttggtgggg gaatatccat 540
 ctgaatacag ataatatcca tatccatttt gggctttctg aagttgaatc taaccgtgag 600
 aaaatattct atcagccacg tggacgtatg gagtacaaag gtaacttctc tcagaaaacc 660
 atcaaccggt ttaaaagtgg tgtgtatcat ggattgctga aagaagaaac aagatccaat 720
 cttctcagaa aagaacagat tttagctaata ctcaaagcgg acttcataac atctatttac 780
 cagaaggaca agattacttc ttcagctgaa aaaaattttt tggaacaagc ctacaatcat 840
 ttgccgctaa ataagaagtg gcgctatggt tctaatagcca gagattttgc ggttagtaag 900
 ttctttcttg atcgctatit agattcctat ttaaacaatg aaggtagtgc tgcctatcaa 960
 gaatttttga aagagactag agattttctt cagacttatg aaggggttta ttcagctgaa 1020
 aaaaataaaa tctatgaaaa actacgtaaa gttgatgggc aaacgatcag aacgcttgca 1080
 gaatcaaaag gatatgattt agaacatcat ttggcacgct gtgtaatgga tttagagag 1140
 cgtttagcca ataatatctt acgttcgttt agagaagctg caccctaaat tcaagacgtt 1200
 cagctggaaa aaaatttaga gagtttttct gttttgaacc agaagaaaat tttagaacaa 1260
 catcctgaag caagtgtggt aaaaagtcag aaagcttggc agaagttagg ctactttgtg 1320
 aaggctggag agcagccact tgaaattata aggccagtct ataaatctta tgataagcat 1380
 ggtaaaggta taggacggcc agaatttgta tcagatactg tttatgatat tagtcagcta 1440
 acagaaaata ttcagctgaa aagtctaacc ttgaaagacc tctctctggt ttcttctaac 1500
 gagttaaaag agttagtaga tgctgctaag ttaaagacta atccaacaga gagagaacgc 1560
 cgtgaattag gtacctatcg ttatgcgttg aaacttagca tattagaatc tagtcagaag 1620
 gaattgcagg ttcgtcaaaa gctactagaa caggtagcgc cactagcgtc tgatcaacca 1680

GBS patentin.ST25

tttttagatt	ttaagaaaca	gttaatagct	caggaattac	aagctatagc	gctacaattg	1740
actcctaatt	acaagctatc	agaagatgat	aaagccttga	aaaatcgatt	gaagaggcag	1800
tttgaagata	gtgttgcgct	acctgtttca	aaagctactc	ctggtgccat	acaacttcct	1860
attaggcaac	tttggactga	gctaggattg	gttcattcaca	ttcaagatga	aaacatttcta	1920
acgcttctga	aagggacatc	aacgacgaaa	caagcttata	tagaagaact	tcagactcat	1980
atctctatitt	ttcagttgaa	atatcagatt	aacaatagaa	acaagcagat	aagccagtta	2040
tcggatgaag	caacaataaa	ggagatgagg	atagctaattg	ctaaaggttt	ctctgagcta	2100
aaacgtctat	atgatacatt	acagccatca	gatgatggtc	aaaatcagat	tagtcaagct	2160
gtttctaaac	aattacaaga	acgaaaagtt	atcaaaaaag	ctcaattaca	acagacgcag	2220
agaagcggaa	aaatcaatac	agacttcatg	cgacaattga	cagcttctct	taatcgttca	2280
caacaagcaa	gtaaaaaagc	attgatggaa	cgtgcacgta	gtgatgaacg	tgaggaacaa	2340
gaagaacgta	ggcaagctca	acgttaa				2367

<210> 436

<211> 2802

<212> DNA

<213> Streptococcus agalactiae

<400> 436

atgaattcta	acacaaaagg	tcacggattt	ttccgcaagt	caaaagcata	cggcttagta	60
tgtgctattg	cattagcagg	tgcatttaca	ttagctacta	gtcaagtgtc	tgctgatcaa	120
gttacaactc	aagcaacaac	tcaaacagta	acgcaaaatc	aagcagaaac	agtaacatca	180
actcaacttg	ataaagcagt	agctacagct	aaaaaagcag	ctgtagctgt	tacaaccaca	240
cctgcagtta	atcatgcgac	aactactgat	gcacaagctg	atttagctaa	tcaaacacaa	300
gctgttaaag	atgttactgc	aaaagcacia	gctaatacac	aagctattaa	agatgctact	360
gctgaaaatg	caaaaattga	tgctgaaaac	aaagcagagg	cagagcgtgt	tgcaaaaagaa	420
aacaaggaag	gtcaagcagc	cgtagatgca	cgtaacaaag	caggtcaagc	agccgtagat	480
gcacgtaata	aagcgaaaca	gcaagcgcaa	gacgatcaaa	aagcaaaaat	tgatgctgaa	540
aacaaagcag	agtctcaacg	tgtaagtcag	ttaaattgcac	aaaataaagc	aaaaattgac	600
gcagaaaata	aagatgcgca	agctaaagca	aatgcgacta	atgcacaatt	acaaaaagat	660
tatcaagcta	aattagcgga	aatcaaatca	gttgaagctt	ataatgcagg	tgtacgtcaa	720
cgtaataaag	atgcacaagc	taaagcagat	gcgactaacg	cacagttaca	aaaagactat	780
caagctaaat	tagcacttta	taatcaagct	ctaaaagcta	aagcagaagc	agataaacag	840
tctattaata	atgttgcttt	tgatatcaaa	gctcaagcta	aagggtgttg	taacgctgaa	900
tatggaaact	caatcatgac	tgcaaaaact	aaacctgacg	gaagtttcga	gtttaaccat	960

GBS patentin.ST25

gatatgatcg atggtgtgaa gacaatcggc tatgggaaat tgacaggtaa agttaatcat	1020
cattatgttg ctaacaagga tggctctgtg acagcatttg ttgattctgt cactctttac	1080
aagtacgagt atcgtaatgt tgctcaaaat gctgctgtta accaaaatat tgtatttaga	1140
gttttaacaa aagatggtcg tcctatTTTT gaaaaagctc ataatggtaa caaaactttt	1200
gcagaaactt taaacaaaac tttaacaactc aatctttaa atgagcttaa accacatgct	1260
tccagcggta acgtcgaagt ctttaagatt catgatgact gggtagatga cacacatggg	1320
tctgcttttag tgtcttatgt taataataat gatgctgttc ctaatgtggc catcccagaa	1380
cggccaactc caccaaagcc agtgaaagt acacctgaag cagaaaaacc agtacctgaa	1440
aagccagttg agcctaaatt ggtaacgcct acattaaaaa cttatactcc agtcaaat	1500
attccgcgag aatacaaaacc agaaccaatc acccctgaga cgtttacccc tgagaaaatt	1560
actccagctc aaccaaaggt gaaaccacat gtgtctattc ctgaaaagat taactactca	1620
gttagtgctc atcctgtttt agttccagct gctaatacctt caaaagctgt cattgatgaa	1680
gcaggtcaat ctgttaatgg taaaaccgta ttaccaaatg caacattaga ctatgttgct	1740
aaacaaaact ttagtcaata caaaggatt aaagcttctg cagaagcgat cgcaaaaggt	1800
tttgcatttg tagatcaacc aaatgaagcg ttagctgaat tgactgttaa gtctatcaaa	1860
gcatctaatt gtgatgatgt atcaagcttg ttagaaatgc gtcattgttt atcaaaagat	1920
acttttagacc aaaaacttca atctcttatt aaagaggcag gaattagtcc agttggtag	1980
ttttacatgt ggactgcaaa agatccacaa gctttttata aagcttatgt tcaaaaagga	2040
ctagatatca cttataatct atccttttaa atcaaagcta actttactaa aggtcaaactc	2100
aaaaatggtg ttgcacagat tgattttggg aatggatata caggtaatat tgtagtcaat	2160
gatgttactg ttccagaagt acataaggat atacttgata aagaggatgg taaatcaatt	2220
aataatagta cggttaagtt aggtgatgaa gtgacctaca aacttgaagg atgggttgta	2280
ccagcaaacc gtggttacga tctttttgaa taaaaatttg tggatcaatt acaacacaca	2340
catgatcttt acttacgtga taaagtggc gctaaagttg atgtgacatt aaaagatgg	2400
acagtcatta aaaaaggac taatttagga gagtacacag aaacagttta caacaaaacg	2460
acaggtcatt atgagcttgc ctttaaaaaa gagtttttag ctaaggtttc tcgtgaatca	2520
gaatttggtg cagatgattt tattgtagtt aaacgtatta aggcaggatga tgtttacaat	2580
actgctgatt tatatgttaa tggatataaa gttaagtcag aagcagttgt gactcatact	2640
actgagaaat caaaaccagt tgaaccacaa aaagcaactc caaaagctcc agctaaagga	2700
ctgccatcaa ctggtgaagc tagtatgacg ccacttactg caattggagc aattatctta	2760
tcagctctag gcctcgcagg ctttaaaaag cgtcaaaaat aa	2802

<210> 437

<211> 3150

GBS patentin.ST25

<212> DNA

<213> Streptococcus agalactiae

<400> 437

atgttttagtt ggttggaagc tctttattac actctgatac aactggcaaa agtgaaccgg	60
ttgaatgctc ttttcttagt tagcgttgtg ggttatcttt gttaccaggg aataaaaactc	120
gtcagaaaaa ccataagaaa cttttttcag ctgatgaagg gtttcatagg tgatagagag	180
aacatcaaga aatgcatcaa aaacaagaaa gaggcactag tccattcttg gaaacatcgt	240
caagatattg attggaaatc aactggaaaa gataagagta aacagttatg gaatcttatg	300
aagcgacttg cgacagttgc tccttcattt ttgttcttat tattgggaaa tgttctcttt	360
cgtctcattt atcaactgcc ttttgtaaag caagacagaa agcgatttga caaggaaatg	420
aagcccttgc tctacttcaa gaactatcgt agttttgtgt tcatgggaat aggtttcagt	480
ttcatagcgt ttattctcac aaactatttt gtgacggttt taagggtgc tattcgtttt	540
ctatatttct caatcatgac gttaagagat aatagccaag tcgtagctt taacgttgat	600
agtttgctca tccagaattt attcaatgct aggggtattt tgatagctcc cattctagca	660
gtgccaatct ttctcattgg tttagtcgta gcttggcggg ctgcttgggt taactttgaa	720
cagtaccgtg attataatca taatgaagaa ggggatgac gctttgcgac tgtcaaagaa	780
atccaccagc aatataagaa agttcctaataaaaacggaaa cttatccagg tgaaggaggt	840
gtgcccgttc ttcataaaac aagaaagaat ttgacaggct taacgcttaa atctcaaagt	900
ctttggcaaa accgtacctt tagtcgctat ttaacgaatg cggaaaggat tttagggtc	960
ttatcgacgc cttcaggaga ttattacatc gatgatagca ccacaaactt gatcaccatg	1020
gggattactc ggtcaggtaa gggagaagct catattgccc ctattattga tattaatagc	1080
cgtgcggaaa ttcaaccgtc actgattatt gcagacccta aaggggaaca ttaccagtcc	1140
tcttataaaa ccatgcgtcg gcgtggctat gatgttaatg tcctttcttt ccaaaacatg	1200
gattgggtcca tgtcctataa cccttttagct cttgcgattg cagcagctaa gaagggttac	1260
tatgaaatga cacagacaag ggttaatgct gttgcagaag ccatttatcg taaaacgaaa	1320
cctggtagcg gtaatggcaa tgcaaaatac tgggaagata cctccatttc cctctttaat	1380
gccattgcta tggccttaat ggaccgtgct aatgaaaccg tcaggaatgg tgaaaccgat	1440
gcttgggata ccgttacagt tcgtaacatt gccaagtttt tgactgactt gggttctgaa	1500
gaagtctttg tcaatgattt tggagagatt gttgagaatc ctgataagaa ccaacaagt	1560
aagaagaaat ctaaaatcac ggtttacttt gataacttgc gtaaaatcaa tcaagaacaa	1620
ttttccaaat ttagagatat ggctgattta aacttttaggt cttctgactt cgcttcagaa	1680
gaaactaagg gaaatgtctt ctctagcatg atgtcaggta ttaacttatt cttgcaagat	1740
aatattgcta aactaacctc taaaaactct attgacctag aatcggttgg tttcccacgt	1800
cgcttgtcta tcaagtttcg ttctagttcc aatgtcgcta tgcgtaacga atacactcat	1860

GBS patentin.ST25

aagacggcta aggttaccat tactagtcaa gctgtttggg gtaaaaccac taaacaagtt	1920
atccacgtag atgctgcaac agctctgatt gatggtgaag gctatctaac ctatgtgatt	1980
gaaccccgagc ttcctgatca attcttggtta acaattgact ttaatcacga aaacaatggt	2040
ggttcagcta ttcgtcacaa aactttccaa ttctcagctg agaaagtcta taagaaacgt	2100
ggtaacgtta ttacgttggg tgactacacg aaaaaaccag ttttgatca tatcaaagtt	2160
actgtttctca acaagcaaga tgataacctt ctccagaaag aagatattga cctgatttat	2220
tcagataatc ctaaagtgat ttacttggtta acacctccaa ataggactga atataatagt	2280
attgtatctc tgtttttgga tcaattgttt aatgccatt atgagtttagc tctgtcaaat	2340
ggtcgcaagt gtgtcaatcg aattcttcat atcctcgatg aattcacaaa cattccagct	2400
attcctcaca tggataccaa gatttccatt ggtcttggtc aaaatattct ctactatctc	2460
tggattcaga acttgaaaca gttagtcagt gaatatggcg agaatacagc ggaaaccatt	2520
cgggagaact gttctttgaa agtttatatc aaatctactg cccagcgac caacgagtac	2580
ttcagtaaag agttggggac tcggaccatt acacgtcgca gaaggtaag taatattcta	2640
gatgaagcta atccaaatgt ttccattgaa aatcctagac aggaactctt aacaccgaca	2700
cagctctcga aactccaaga aggggaagcg gttattttgc gtggtgttaa aggtcgagac	2760
aatgcaggtc ggaaaatcac aacggatccg attttcttgc atgagaaaac gagccttcct	2820
tatcgctaca tgttcttaca agaagaattt gaccagtcga tggctttggc agatattcca	2880
gtggaaagtg ggcataggga ccttgacctg caagatatag cagtaggggc acaaagcact	2940
tttaataaga ttattgattg gcggatggct ctaactgacc gtatgagaac aaatgggaag	3000
atacctcaat tagcatcaag aaaacaaacg attaaagctc taagtcaatc tcaatttact	3060
tctccagcag acctaacaca agctgtgatt gcagaggtat ttgatgagga agatgatgac	3120
gatcttttct ttgtggatga tgtcatgtaa	3150

<210> 438

<211> 279

<212> DNA

<213> Streptococcus agalactiae

<400> 438

atgacagata atcgctttgc ccaattaaaa gaaaactttg aaaagggatc tcctaaaagg	60
cgagttccaa cgtctcgccc aatcgagct caaaaagcgc ctgagagcta taacaaaaag	120
ggacggtatc cattttcgct ccaccaagat gtgcgttatg ataaattaga agcattagta	180
gcttatcatg gagctaagtc tgcacagat tatctggaga ggttgattgt tcaggaatgg	240
gaaaagatgc agcggaagct taagaacaaa gaaaaataa	279

GBS patentin.ST25

<210> 439

<211> 384

<212> DNA

<213> Streptococcus agalactiae

<400> 439

atggcatatt tatcaaaatt atccgatttg gatccatcgt tgatggatgc ggattctgaa	60
caaatttata ttctaaagt cttgtttgag cataatgact ttaaaggctt gacctacaaa	120
gagattttat tatattcttt tttgttaa at cgtttaagag agccattaga ttttattcaa	180
aaaggctatg atgataatga agatacctat gttcacttta aggtcgaaga tttatgtgaa	240
ctactcaacc agagtaagac aaccgttatt tccttgaaga aaaggtagc tcaatatggt	300
ttgatagaag aagtgaagc aggtagtcac cagccgaatc gtatttattt aacagataaa	360
ttagttccat atattaaggg gtaa	384

<210> 440

<211> 1329

<212> DNA

<213> Streptococcus agalactiae

<400> 440

atgacaatct ttgatgaaag agagttaaaa gaacgattta ctcatgaaaa tagggtagt	60
ttttatgagt ttgtggctaa atatgatgct caaatggctt ctgtgatgaa agcaaagggc	120
tatcgatgta ttcatccaat ggagcgtaca gtgggttttta cttttgggga attcaccgatt	180
aggcgacgtc ggtggcaaaa aggagaacat tgggtggtgc cagttgatga aaagctagga	240
ctgaaaaaga atgttcgcta ctcttttagaa ttcattgtatc aaattgctag tttagcaacc	300
atgatgcctt atgaaaaagt gattaagggt gttcagatga tgtattgtat tgtgattacc	360
aaacctactg ttgtgaaggc cgttaagatt agtcgtgaat tgcttaaga aaaggaagcg	420
tatcgttttt ttgatgaaga tataccagta gataaagaac cagttgatat gatttatctt	480
gaaggagatg gagtcatggt caaagctcga gaagaaggat tagataatcg caatgttgat	540
ttgtctcatt tcgtggttca tacgggtagt cagaaagtag gaagcaatcg ctttgtctta	600
caaaataaaa aagagtttgt gtcccttgat aatcgtaaaa cgcgtaaaa gattttggac	660
tacctttaca atcattttta cattgcccc aacaccttgc ttattaccaa ttcagatgggt	720
ggccatggct ataccccata tgtttttaaa gagattgcga aagcactcaa agtgaagcaa	780
cacgaacact tttgggatag gtatcatgtc aatgaaaaga tcaaaagttt ttttaaaactc	840
tatccagtgg aactgatgac tggcgctttt cagagcatta aacagcatga taaagaaaag	900
cttagaactg ttttggatac gacagaagca ttgatactga tggaagaaga aatggaaggg	960

GBS patentin.ST25

tttaaccagt tcaaacgaaa gttgttaaac aattttcaat atactaaatc agctgaattg	1020
agaggtttca gtcgtgcagg aataggtggt atggagtcac aacatcgaaa aattacctat	1080
cggatgaaaa agcgcgggat gtattggaca attcagggag ctgagacgat gagtcaatta	1140
attgtcctat cgtatgaagg acagctaaga gatctcttct ttggttcttg gcgtgaagac	1200
tatcagaaat atcaagagct agaaaacctt agtgcgggaa aaatcaaaca tgaacagaat	1260
aaaatcaata agagatatga tctccagaca cttggtcggc ttaggtacgg taggcacgt	1320
aatttatag	1329

<210> 441

<211> 2367

<212> DNA

<213> Streptococcus agalactiae

<400> 441

atggatgtat cgtctagtc gaatattaca tttatgctgc aatacacaga ggctaatacct	60
caatatgtgg actataactaa cagagaagag gctgtcaaaa ttgatgaaga attgtcctta	120
gaaacgaaca ggcaaagtat tgaaggatta actgaagacg agttgactcg tattcaggaa	180
gctgtccctg aaacgcagtt gaattttagg gaatacattg attatatgaa ccgctcgtat	240
gcaactgaag aacaatctaa agaactaaca gctatcttta ctcaagaagc agattatctt	300
cagaaactac gattaatcga tctaaaaaat aagttggaat cagcttatca aaatggttca	360
cttctctggc aaggagttat ttcgtttgat aatgcttttc ttgcggaaca gggattgtat	420
gatgttgca ctggtcaagt tgatcaaaaa gcgattaagg cagtgatgcg tgatatgatg	480
ccaacactta tccagaaaga gggcctttct gattctgctt tttggtgggg gaatatccat	540
ctgaatacag ataatatcca tatccatttt gggctttctg aagttgaatc taaccgtgag	600
aaaatattct atcagccacg tggacgtatg gagtacaaag gtaacttctc tcagaaaacc	660
atcaaccggt ttaaaagtgg tgtgtatcat ggattgctga aagaagaaac aagatccaat	720
cttctcagaa aagaacagat tttagctaata ctcaaagcgg acttcataac atctatttac	780
cagaaggaca agattacttc ttcagctgaa aaaaattttt tggaacaagc ctacaatcat	840
ttgccgctaa ataagaagtg gcgctatggt tctaatacca gagattttgc ggtagtaag	900
ttctttcttg atcgctatatt agattcctat ttaacaatg aaggtagtgc tgcctatcaa	960
gaatttttga aagagactag agattttctt cagacttatg aaggggttta ttcagctgaa	1020
aaaaataaaa tctatgaaaa actacgtaaa gttgatgggc aaacgatcag aacgcttgca	1080
gaatcaaaag gatatgattt agaacatcat ttggcacgtc gtgtaatgga tttaaagagag	1140
cgtttagcca ataatatctt acgttcgttt agagaagctg caccctaaat tcaagacgtt	1200
cagctggaaa aaaattttaga gagtttttct gttttgaacc agaagaaaat tttagaacaa	1260

GBS patentin.ST25

catcctgaag	caagtgtggt	aaaaagtcag	aaagcttggc	agaagttagg	ctactttgtg	1320
aaggctggag	agcagccact	tgaaattata	aggccagtct	ataaatctta	tgataagcat	1380
ggtaaaggta	taggacggcc	agaatttgta	tcagatactg	tttatgatat	tagtcagcta	1440
acagaaaata	ttcagctgaa	aagtctaacc	ttgaaagacc	tctctctggt	ttcttctaac	1500
gagttaaaaag	agttagtaga	tgctgctaag	ttaaagacta	atccaacaga	gagagaacgc	1560
cgtgaattag	gtacctatcg	ttatgcgttg	aaacttagca	tattagaatc	tagtcagaag	1620
gaattgcagg	ttcgtcaaaa	gctactagaa	caggtagcgc	cactagcgtc	tgatcaacca	1680
tttttagatt	ttaagaaaca	gttaatagct	caggaattac	aagctatagc	gctacaattg	1740
actcctaatt	acaagctatc	agaagatgat	aaagccttga	aaaatcgatt	gaagaggcag	1800
tttgaagata	gtgttgcgct	acctgtttca	aaagctactc	ctggtgccat	acaacttcct	1860
attaggcaac	tttggactga	gctaggattg	gttcatacaca	ttcaagatga	aaacatttcta	1920
acgcttctga	aagggacatc	aacgacgaaa	caagcttata	tagaagaact	tcagactcat	1980
atctctatct	ttcagttgaa	atatcagatt	aacaatagaa	acaagcagat	aagccagtta	2040
tcggatgaag	caacaataaa	ggagatgagg	atagctaattg	ctaaagggtt	ctctgagcta	2100
aaacgtctat	atgatacatt	acagccatca	gatgatgggc	aaaatcagat	tagtcaagct	2160
gtttctaaac	aattacaaga	acgaaaagtt	atcaaaaaag	ctcaattaca	acagacgcag	2220
agaagcggaa	aaatcaatac	agacttcattg	cgacaattga	cagcttctct	taatcgttca	2280
caacaagcaa	gtaaaaaagc	attgatggaa	cgtgcacgta	gtgatgaacg	tgaggaacaa	2340
gaagaacgta	ggcaagctca	acgttaa				2367

<210> 442

<211> 2802

<212> DNA

<213> Streptococcus agalactiae

<400> 442

atgaattcta	acacaaaagg	tcacggattt	ttccgcaagt	caaaagcata	cggcttagta	60
tgtgctattg	cattagcagg	tgcatctaca	ttagctacta	gtcaagtgtc	tgctgatcaa	120
gttacaactc	aagcaacaac	tcaaacagta	acgcaaaatc	aagcagaaac	agtaacatca	180
actcaacttg	ataaagcagt	agctacagct	aaaaaagcag	ctgtagctgt	tacaaccaca	240
cctgcagtta	atcatgcgac	aactactgat	gcacaagctg	atttagctaa	tcaaacacaa	300
gctgttaaag	atgttactgc	aaaagcacaa	gctaatacac	aagctattaa	agatgctact	360
gctgaaaatg	caaaaattga	tgctgaaaac	aaagcagagg	cagagcgtgt	tgcaaaagaa	420
aacaaggaag	gtcaagcagc	cgtagatgca	cgtaacaaag	caggtcaagc	agccgtagat	480
gcacgtaata	aagcgaaaca	gcaagcgcaa	gacgatcaaa	aagcaaaaat	tgatgctgaa	540

GBS patentin.ST25

aacaaagcag agtctcaacg tgtaagtcag ttaaattgcac aaaataaagc aaaaattgac	600
gcagaaaata aagatgcgca agctaaagca aatgcgacta atgcacaatt acaaaaagat	660
tatcaagcta aattagcggg aatcaaatca gttgaagctt ataattgcagg tgtacgtcaa	720
cgtaataaag atgcacaagc taaagcagat gcgactaacg cacagttaca aaaagactat	780
caagctaaat tagcacttta taatcaagct ctaaaagcta aagcagaagc agataaacag	840
tctattaata atgttgcttt tgatatcaaa gctcaagcta aagggtgttg taacgctgaa	900
tatggaaact caatcatgac tgcaaaaact aaacctgacg gaagtttcga gtttaaccat	960
gatatgatcg atggtgtgaa gacaatcggc tatgggaaat tgacaggtaa agttaatcat	1020
cattatgttg ctaacaagga tggctctgtg acagcatttg ttgattctgt cactctttac	1080
aagtacgagt atcgtaatgt tgctcaaaat gctgctgtta accaaaatat tgtatttaga	1140
gttttaacaa aagatggctg tcctattttt gaaaaagctc ataattggtaa caaaactttt	1200
gcagaaactt taaacaaaac tttaacaact aatcttaaat atgagcttaa accacatgct	1260
tccagcggta acgtcgaagt ctttaagatt catgatgact ggggtacatga cacacatggg	1320
tctgctttag tgtcttatgt taataataat gatgctgttc ctaattgtgt catcccagaa	1380
cggccaactc caccaaagcc agtgaaagtt acacctgaag cagaaaaacc agtacctgaa	1440
aagccagttg agcctaaatt ggtaacgcct acattaaaaa cttatactcc agtcaaattt	1500
attccgcgag aatacaaac agaaccaatc acccctgaga cgtttaccct tgagaaattt	1560
actccagctc aaccaaaggt gaaaccacat gtgtctattc ctgaaaagat taactactca	1620
gttagtgctc atcctgtttt agttccagct gctaattcct caaaagctgt cattgatgaa	1680
gcagggtcaat ctgttaatgg taaaaccgta ttaccaaagc caacattaga ctatgttgct	1740
aaacaaaact ttagtcaata caaaggtatt aaagcttctg cagaagcgat cgcaaaaggt	1800
tttgcatctg tagatcaacc aatgaagcg ttagctgaat tgactgttaa gtctatcaaa	1860
gcatctaatt gtgatgatgt atcaagcttg ttagaaatgc gtcattgttt atcaaaagat	1920
actttagacc aaaaacttca atctcttatt aaagaggcag gaattagtcc agttgggtgag	1980
ttttacatgt ggactgcaaa agatccacaa gctttttata aagcttatgt tcaaaaagga	2040
ctagatatca cttataatct atccttttaa atcaaagcta actttactaa aggtcaaact	2100
aaaaatggtg ttgcacagat tgattttggg aatggatata caggtaatat tgtagtcaat	2160
gatgttactg ttccagaagt acataaggat atacttgata aagaggatgg taaatcaatt	2220
aataatagta cggttaagtt aggtgatgaa gtgacctaca aacttgaagg atgggttgta	2280
ccagcaaac gtggttacga tctttttgaa tacaattttg tggatcaatt acaacacaca	2340
catgatcttt acttacgtga taaagtgtc gctaaagttg atgtgacatt aaaagatggt	2400
acagtcatta aaaaaggac taatttagga gagtacacag aaacagttta caacaaaacg	2460
acaggtcatt atgagcttgc ctttaaaaaa gagtttttag ctaaggtttc tcgtgaatca	2520
gaatttggtg cagatgattt tattgtagtt aaacgtatta aggcagggtg tgtttacaat	2580

GBS patentin.ST25

actgctgatt tatatgttaa tggatataaa gttaagtcag aagcagttgt gactcatact	2640
actgagaaat caaaaccagt tgaaccacaa aaagcaactc caaaagctcc agctaaagga	2700
ctgccatcaa ctggtgaagc tagtatgacg ccacttactg caattggagc aattatctta	2760
tcagctctag gcctcgcagg ctttaaaaag cgtcaaaaat aa	2802

<210> 443

<211> 3150

<212> DNA

<213> Streptococcus agalactiae

<400> 443

atgttttagtt ggttggaagc tctttattac actctgatac aactggcaaa agtgaaccgg	60
ttgaatgctc ttttcttagt tagcgttgtg ggttatcttt gttaccaggg aataaaactc	120
gtcagaaaaa ccataagaaa cttttttcag ctgatgaagg gtttcatagg tgatagagag	180
aacatcaaga aatgcatcaa aaacaagaaa gaggcactag tccattcttg gaaacatcgt	240
caagatattg attggaaatc aactggaaaa gataagagta aacagttatg gaatcttatg	300
aagcgacttg cgacagttgc tccttcattt ttgttcttat tattgggaaa tgttctcttt	360
cgtctcattt atcaactgcc ttttgtaaag caagacagaa agcgatttga caaggaaatg	420
aagcccttgc tctacttcaa gaactatcgt agttttgtgt tcatgggaat aggtttcagt	480
ttcatagcgt ttattctcac aaactatttt gtgacgggtt taagggtgc tattcgtttt	540
ctatatttct caatcatgac gttaagagat aatagccaag tcgttagctt taacgttgat	600
agtttgctca tccagaattt attcaatgct agggtatattg tgatagctcc cattctagca	660
gtgccaatct ttctcattgg ttttagtcgta gcttggcggg ctgcttgggt taactttgaa	720
cagtaccgtg attataatca taatgaagaa ggggatgatc gctttgcgac tgtcaaagaa	780
atccaccagc aatataagaa agttcctaataaaaacggaaa cttatccagg tgaaggaggt	840
gtgcccgttc ttcatgaaac aagaaagaat ttgacaggct taacgcttaa atctcaaattg	900
ctttggcaaa accgtacctt tagtcgctat ttaacgaatg cggaaggat tttagggtc	960
ttatcgacgc cttcaggaga ttattacatc gatgatagca ccacaaactt gatcaccatg	1020
gggattactc ggtcaggtaa gggagaagct catattgccc ctattattga tattaatagc	1080
cgtgcggaaa ttcaaccgtc actgattatt gcagacccta aaggggaaca ttaccagtcc	1140
tcttataaaa ccatgcgtcg gcgtggctat gatgttaatg tcctttcttt ccaaaccatg	1200
gattgggtcca tgtcctataa cccttttagct cttgcgattg cagcagctaa gaagggttac	1260
tatgaaatga cacagacaag ggttaatgcg gttgcagaag ccatttatcg taaaacgaaa	1320
cctggtagcg gtaatggcaa tgcaaaatac tgggaagata cctccatttc cctctttaat	1380
gccattgcta tggccttaat ggaccgtgct aatgaaaccg tcaggaatgg tgaaaccgat	1440

GBS patentin.ST25

gcttgggata	ccgttacagt	tcgtaacatt	gccaaagtttt	tgactgactt	gggttctgaa	1500
gaagtctttg	tcaatgattt	tggagagatt	gttgagaatc	ctgataagaa	ccaacaagtg	1560
aagaagaaat	ctaaaatcac	ggttttacttt	gataacttgc	gtaaaatcaa	tcaagaacaa	1620
ttttccaaat	ttagagatat	ggctgattta	aacttttaggt	cttctgactt	cgcttcagaa	1680
gaaactaagg	gaaatgtctt	ctctagcatg	atgtcaggta	ttaacttatt	cttgcaagat	1740
aatattgcta	aactaacctc	taaaaactct	attgacctag	aatcggttgg	tttcccacgt	1800
cgcttgtcta	tcaagtttcg	ttctagtccc	aatgtcgcta	tgcgtaacga	atacactcat	1860
aagacggcta	aggttaccat	tactagtcaa	gctgtttggg	gtaaaaccac	taaacaagtt	1920
atccacgtag	atgctgcaac	agctctgatt	gatggtgaag	gctatctaac	ctatgtgatt	1980
gaaccccagc	ttcctgatca	attcttggtta	acaattgact	ttaatcacga	aaacaatggt	2040
ggttcagcta	ttcgtcacia	aactttccaa	ttctcagctg	agaaagtcta	taagaaacgt	2100
ggtaacgtta	ttacgttggg	tgactacacg	aaaaaaccag	ttttggatca	tatcaaagtt	2160
actgttctca	acaagcaaga	tgataacctt	ctccagaaag	aagatattga	cctgatttat	2220
tcagataatc	ctaaagtgat	ttacttggtta	acacctccaa	ataggactga	atataatagt	2280
attgtatctc	tgtttttggg	tcaattgttt	aatgccatt	atgagtttagc	tctgtcaaat	2340
ggtcgcaagt	gtgtcaatcg	aattcttcat	atcctcgatg	aattcacaaa	cattccagct	2400
attcctcaca	tggataccaa	gatttccatt	ggcttgggtc	aaaatattct	ctactatctc	2460
tggattcaga	acttgaaaca	gttagtcagt	gaatatggcg	agaatacagc	ggaaaccatt	2520
cgggagaact	gttctttgaa	agtttatatc	aaatctactg	ccccagcgac	caacgagtac	2580
ttcagtaaag	agttggggac	tcggaccatt	acacgtcgca	gaaggccaag	taatattcta	2640
gatgaagcta	atccaaatgt	ttccattgaa	aatcctagac	aggaactctt	aacaccgaca	2700
cagctctcga	aactccaaga	aggggaagcg	gttattttgc	gtggtgttaa	aggctcgagac	2760
aatgcaggtc	ggaaaatcac	aacggatccg	attttcttgc	atgagaaaac	gagccttcct	2820
tatcgctaca	tgttcttaca	agaagaattt	gaccagtcga	tggctttggc	agatattcca	2880
gtggaaagtg	ggcatagggg	ccttgacctg	caagatatag	cagtaggggc	acaaagcact	2940
tttaataaga	ttattgattg	gcggatggct	ctaactgacc	gtatgagaac	aaatgggaag	3000
atacctcaat	tagcatcaag	aaaacaaacg	attaaagctc	taagtcaatc	tcaatttact	3060
tctccagcag	acctaacaca	agctgtgatt	gcagaggtat	ttgatgagga	agatgatgac	3120
gatcttttct	ttgtggatga	tgtcatgtaa				3150

<210> 444

<211> 279

<212> DNA

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 444
atgacagata atcgctttgc ccaattaaaa gaaaactttg aaaagggatc tcctaaaagg 60
cgagttccaa cgtctcgcgc aatcgagct caaaaagcgc ctgagagcta taacaaaaag 120
ggacgggtatc ctttttcgct ccaccaagat gtgcgttatg ataaattaga agcattagta 180
gcttatcatg gagctaagtc tgcatacagat tatctggaga gggtgattgt tcaggaatgg 240
gaaaagatgc agcgggaagct taagaacaaa gaaaaataa 279

<210> 445

<211> 384

<212> DNA

<213> Streptococcus agalactiae

<400> 445
atggcatatt tatcaaaatt atccgatttg gatccatcgt tgatggatgc ggattctgaa 60
caaatttata ttctaaagt cttgtttgag cataatgact tttaaaggctt gacctacaaa 120
gagattttat tatattcttt ttgtttaaat cgtttaagag agccattaga ttttattcaa 180
aaaggctatg atgataatga agatacctat gttcacttta aggtcgaaga tttatgtgaa 240
ctactcaacc agagtaagac aaccgttatt tccttgaaga aaagggttagc tcaatatggg 300
ttgatagaag aagtgaagc aggtagtcac cagccgaatc gtatttattt aacagataaa 360
ttagttccat atattaaggg gtaa 384

<210> 446

<211> 1329

<212> DNA

<213> Streptococcus agalactiae

<400> 446
atgacaatct ttgatgaaag agagttaaaa gaacgattta ctcataaaaa taggggttagt 60
ttttatgagt ttgtggctaa atatgatgct caaatgggtc ctgtgatgaa agcaaagggc 120
tatcgatgta ttatttcaat ggagcgtaca gtgggttttta cttttgggga attcacgatt 180
aggcgacgtc ggtggcaaaa aggagaacat tgggtggtgc cagttgatga aaagctagga 240
ctgaaaaaga atgttcgcta ctcttttagaa ttcatgtatc aaattgctag ttttagcaacc 300
atgatgcctt atgaaaaagt gattaagggt gttcagatga tgtattgtat tgtgattacc 360
aaacctactg ttgtgaaggc cgtaagatt agtcgtgaat tgcttaaaga aaaggaagcg 420
tatcgttttt ttgatgaaga tataccagta gataaagaac cagttgatat gatttatctt 480
gaaggagatg gagtcatggg caaagctcga gaagaaggat tagataatcg caatgttgat 540

GBS patentin.ST25

ttgtctcatt	tcgtggttca	tacgggtagt	cagaaagtag	gaagcaatcg	ctttgtctta	600
caaaataaaa	aagagtttgt	gtcccttgat	aatcgtcaaa	cgcgtaaaa	gattttggac	660
tacctttaca	atcattttta	cattgcccc	aacaccttgc	ttattaccaa	ttcagatggg	720
ggccatggct	ataccccata	tgtttttaaa	gagattgcga	aagcactcaa	agtgaagcaa	780
cacgaacact	tttgggatag	gtatcatgtc	aatgaaaaga	tcaaaagttt	ttttaaactc	840
tatccagtgg	aactgatgac	tggcgctttt	cagagcatta	aacagcatga	taaagaaaag	900
cttagaactg	ttttggatac	gacagaagca	ttgatactga	tggaagaaga	aatggaaggg	960
tttaaccagt	tcaaacgaaa	gttggttaaac	aattttcaat	atactaaatc	agctgaattg	1020
agaggtttca	gtcgtgcagg	aataggtggt	atggagtcac	aacatcgaaa	aattacctat	1080
cggatgaaaa	agcgcgggat	gtattggaca	attcagggag	ctgagacgat	gagtcaatta	1140
attgtcctat	cgtatgaagg	acagctaaga	gatctcttct	ttggttcttg	gcgtgaagac	1200
tatcagaaat	atcaagagct	agaaaacctt	agtgcgggaa	aaatcaaaca	tgaacagaat	1260
aaaatcaata	agagatatga	tctccagaca	cttggtcggc	ttaggtacgg	taggcatcgt	1320
aatttatag						1329

<210> 447

<211> 1389

<212> DNA

<213> streptococcus agalactiae

<400> 447

atggctgtcg	aaattattat	gcctaaactc	ggggttgata	tgcaagaagg	cgaaatcctt	60
gagtggaaaa	aacaggtagg	tgatgttggt	aatgaagggt	acgtcctact	tgaaattatg	120
tcagataaaa	caaatatgga	gattgaagca	gaagactcag	gtgttttact	aaaaatcaca	180
catgggaatg	gagatgttgt	tcctgtaact	gagacaattg	gctatatcgg	tgctgaaggt	240
gaagaagtaa	cagaagcatc	ttcttctgaa	aatacatcag	ttgaagaaaa	cgcgacacaa	300
gtaacttcag	aaccagaaaa	agttgaagaa	acatcagaac	caagtgtgcc	agcagctaca	360
agtggtgaaa	aagtacgtgc	cactcctgca	gctcgtaaat	tagcaagaga	gatgtctatt	420
gaccttgac	tagtatctgg	aacaggggca	aatggctcgc	ttcacagaga	agatgttgaa	480
agcttcaagg	gtgctcaacc	acgtattaca	ccattggcac	gtcgaattgc	tgaagatcaa	540
ggagttgata	tagcagaaat	cactggcagt	ggtattcgtg	gtaaaattgt	taaaaatgat	600
gttttggtg	ctatgtcacc	gcaagcagca	gaggctcctg	tagaaacgaa	agctacacca	660
acaacagaag	aaaaacaatt	accagaaggt	gttgaagtca	ttaagatgtc	tgcaatgcgt	720
aaggctat	ctaaaggtat	gactaactct	tacctcactg	ctccaagctt	tacacttaac	780
tatgacattg	atatgactga	aatgatggct	cttcgcaaga	aattaattga	tccaatcatg	840

GBS patentin.ST25

gctaaaacag gcttgaaagt cagctttact gatttgattg gaatggccgt tgtaagaca 900
 ttgatgaaac cagagcatcg atacctaaat gcttcattaa ttaacgatgc acaagaaatt 960
 gagcttcata attttgtaa tattggaatc gcagttggtc ttgatgatgg cttgattggt 1020
 cctgttggtc acaatgctga tcaaatgtca ctttctgact ttgttatagc atctaaagat 1080
 gttattaaga aaactcaaga aggtaaatta aaatcagctg aaatgtcagg ttcaacattc 1140
 tcaattacta acttaggtat gtttggtact aagacgttta acccaattat caatcaaccg 1200
 aactcagcaa tccttggagt aggcgctact attccgactc caacagtggg tgatgggtgaa 1260
 attgtagctc gaccaatcat ggcaatgtgt ttaacaattg accaccgtat tgttgatgga 1320
 atgaatgggtg ctaagtttat ggttgatctt aagaacttaa tggaaaaccc atttggttta 1380
 cttatttga 1389

<210> 448

<211> 1596

<212> DNA

<213> Streptococcus agalactiae

<400> 448
 atgtctagtt ttaatagaaa aaaacttaag tttttgggta tatctttggc gactctaaca 60
 gccaccacag ttaccctggg tgccgtgggt aatgagtcaa agaactctgg agataataaa 120
 gttattaatt ggtatattcc tactgaaatc agtacattgg acatttcaaa gaatacagat 180
 gcttattcaa acttagctat aggtaattca ggcagcaatt tacttagaat tgataaagag 240
 ggcaaaccac aacccgattt agctaaaaaa gtatccgttt cttctgatgg tcttacttat 300
 actgctacac ttcgtgataa tttaaaatgg tcagatggaa gcaaactaag cgctgaagat 360
 tttgtttaca catggcggag aatagttgat cctaaaactg catctgaata tgcttacttg 420
 gcgacagaat cgcacctttt aaatgctgat aagattaatt ctggagatat taaagattta 480
 aataaacttg gtgtaacagc taaaggcaat caagtgacct ttaaattgac aagtccatgc 540
 cctcaattta aatattattt agccttctct aattttatgc ctcaaaaaca atcgtatggt 600
 gaaaaagttg gtaaagatta tggtaacaac tcaaaaaatc aaatttactc aggtccttac 660
 cttgttaagg attggaatgg ttcaaattgg aaatttaaat tagtcaaaaa taaatattat 720
 tgggattcta aacatgttaa aacaaatagt gtcatagttc aaactatcaa aaaaccagat 780
 actgcagttc aaatgtacaa gcaaggctcag attgattttg ctgaaatatc aggaacttct 840
 gctatttata accaaactgg ttcgggttaa gcattgacaa atcagaaaat taggcaagct 900
 ttgaatttag cgactgatcg taaagggtgtt gttaaagcgg cagttgatac aggttcaact 960
 cctgctgaat ctctgggtccc taaaaatta gccaaattac ctaatgggtga ggatctttcc 1020
 aagtatactg ccccagggtta tacgtataat acaagtaaag ctcaaaaact ttttaaagaa 1080

GBS patentin.ST25

ggtcttgctg aggttgggtca gtcattctctc aagttaacaa tcacagctga ttcggactct 1140
 ccagcagcta aaaatgctgt tgactatgtg aaatctacat gggagagtgc tttgcctggt 1200
 ctaactgttg aagaaaaatt tgttactttc aagcaacgcc ttgaagatgc aaaaaatgaa 1260
 aattttgatg tcgtgctctt ctcatgggga ggagattatc cagaaggatc aactttctat 1320
 gggttattca cgactaattc tgcgtataat tatggtaaatt tttcttctaa agagtatgac 1380
 aatgcctatc aaaaggcaat tactactgac gccttgaaac caggagatgc cgctaattgat 1440
 tacaaaactg ctgaaaaagc tttatttgat caatcatatt ataaccagc ttattaccta 1500
 gggaaaaaag gactccaaaa ttctaaatta aaggggttgg taagaaattc aactgggttg 1560
 aatgttgatt ttacttatgc ttataagaca gaataa 1596

<210> 449

<211> 788

<212> PRT

<213> Streptococcus agalactiae

<400> 449

Met Asp Val Ser Ser Ser Pro Asn Ile Thr Phe Met Leu Gln Tyr Thr
 1 5 10 15

Glu Ala Asn Pro Gln Tyr Val Asp Tyr Thr Asn Arg Glu Glu Ala Val
 20 25 30

Lys Ile Asp Glu Glu Leu Ser Leu Glu Thr Asn Arg Gln Met Ile Glu
 35 40 45

Gly Leu Thr Glu Asp Glu Leu Thr Arg Ile Gln Glu Ala Val Pro Glu
 50 55 60

Thr Gln Leu Asn Phe Arg Glu Tyr Ile Asp Tyr Met Asn Arg Ser Tyr
 65 70 75 80

Ala Thr Glu Glu Gln Ser Lys Glu Leu Thr Ala Ile Phe Thr Gln Glu
 85 90 95

Ala Asp Tyr Leu Gln Lys Leu Arg Leu Ile Asp Leu Lys Asn Lys Leu
 100 105 110

Glu Ser Ala Tyr Gln Asn Gly Ser Leu Leu Trp Gln Gly Val Ile Ser
 115 120 125

Phe Asp Asn Ala Phe Leu Ala Glu Gln Gly Leu Tyr Asp Val Ala Thr
 130 135 140

Gly Gln Val Asp Gln Lys Ala Ile Lys Ala Val Met Arg Asp Met Met
 145 150 155 160

Pro Thr Leu Ile Gln Lys Glu Gly Leu Ser Asp Ser Ala Phe Trp Trp
 165 170 175

Gly Asn Ile His Leu Asn Thr Asp Asn Ile His Ile His Phe Gly Leu
 180 185 190

Ser Glu Val Glu Ser Asn Arg Glu Lys Ile Phe Tyr Gln Pro Arg Gly
 195 200 205

Arg Met Glu Tyr Lys Gly Asn Phe Ser Gln Lys Thr Ile Asn Arg Phe
 210 215 220

Lys Ser Gly Val Tyr His Gly Leu Leu Lys Glu Glu Thr Arg Ser Asn
 225 230 235 240

Leu Leu Arg Lys Glu Gln Ile Leu Ala Asn Leu Lys Ala Asp Phe Ile
 245 250 255

Thr Ser Ile Tyr Gln Lys Asp Lys Ile Thr Ser Ser Ala Glu Lys Asn
 260 265 270

Phe Leu Glu Gln Ala Tyr Asn His Leu Pro Leu Asn Lys Lys Trp Arg
 275 280 285

Tyr Gly Ser Asn Ala Arg Asp Phe Ala Val Ser Lys Phe Phe Leu Asp
 290 295 300

Arg Tyr Leu Asp Ser Tyr Leu Asn Asn Glu Gly Ser Ala Ala Tyr Gln
 305 310 315 320

Glu Phe Leu Lys Glu Thr Arg Asp Phe Leu Gln Thr Tyr Glu Gly Val
 325 330 335

Tyr Ser Ala Glu Lys Asn Lys Ile Tyr Glu Lys Leu Arg Lys Val Asp
 340 345 350

Gly Gln Thr Ile Arg Thr Leu Ala Glu Ser Lys Gly Tyr Asp Leu Glu
 355 360 365

His His Leu Ala Arg Arg Val Met Asp Leu Arg Glu Arg Leu Ala Asn
 370 375 380

Asn Ile Leu Arg Ser Phe Arg Glu Ala Ala Pro Gln Ile Gln Asp Val
 385 390 395 400

Gln Leu Glu Lys Asn Leu Glu Ser Phe Ser Val Leu Asn Gln Lys Lys
 405 410 415

ile Leu Glu Gln His Pro Glu Ala Ser Val Val Lys Ser Gln Lys Ala
 420 425 430

Trp Gln Lys Leu Gly Tyr Phe Val Lys Ala Gly Glu Gln Pro Leu Glu
 435 440 445

Ile Ile Arg Pro Val Tyr Lys Ser Tyr Asp Lys His Gly Lys Gly Ile
 450 455 460

Gly Arg Pro Glu Phe Val Ser Asp Thr Val Tyr Asp Ile Ser Gln Leu
 465 470 475 480

Thr Glu Asn Ile Gln Leu Lys Ser Leu Thr Leu Lys Asp Leu Ser Leu
 485 490 495

Phe Ser Ser Asn Glu Leu Lys Glu Leu Val Asp Ala Ala Lys Leu Lys
 500 505 510

Thr Asn Pro Thr Glu Arg Glu Arg Arg Glu Leu Gly Thr Tyr Arg Tyr
 515 520 525

Ala Leu Lys Leu Ser Ile Leu Glu Ser Ser Gln Lys Glu Leu Gln Val
 530 535 540

Arg Gln Lys Leu Leu Glu Gln Val Gln Pro Leu Ala Ser Asp Gln Pro
 545 550 555 560

Phe Leu Asp Phe Lys Lys Gln Leu Ile Ala Gln Glu Leu Gln Ala Ile
 565 570 575

Ala Leu Gln Leu Thr Pro Asn Tyr Lys Leu Ser Glu Asp Asp Lys Ala
 580 585 590

Leu Lys Asn Arg Leu Lys Arg Gln Phe Glu Asp Ser Val Ala Leu Pro
 595 600 605

Val Ser Lys Ala Thr Pro Gly Ala Ile Gln Leu Pro Ile Arg Gln Leu
 610 615 620

Trp Thr Glu Leu Gly Leu Val His His Ile Gln Asp Glu Asn Ile Leu
 625 630 635 640

Thr Leu Leu Lys Gly Thr Ser Thr Thr Lys Gln Ala Tyr Ile Glu Glu
 645 650 655

Leu Gln Thr His Ile Ser Ile Phe Gln Leu Lys Tyr Gln Ile Asn Asn
 660 665 670

Arg Asn Lys Gln Ile Ser Gln Leu Ser Asp Glu Ala Thr Ile Lys Glu
 675 680 685

Met Arg Ile Ala Asn Ala Lys Gly Phe Ser Glu Leu Lys Arg Leu Tyr
 690 695 700

Asp Thr Leu Gln Pro Ser Asp Asp Gly Gln Asn Gln Ile Ser Gln Ala
 705 710 715 720

Val Ser Lys Gln Leu Gln Glu Arg Lys Val Ile Lys Lys Ala Gln Leu
 725 730 735

Gln Gln Thr Gln Arg Ser Gly Lys Ile Asn Thr Asp Phe Met Arg Gln
 740 745 750

Leu Thr Ala Ser Leu Asn Arg Ser Gln Gln Ala Ser Lys Lys Ala Leu
 755 760 765

Met Glu Arg Ala Arg Ser Asp Glu Arg Glu Glu Gln Glu Glu Arg Arg
 770 775 780

Gln Ala Gln Arg
 785

<210> 450

<211> 933

<212> PRT

<213> Streptococcus agalactiae

<400> 450

Met Asn Ser Asn Thr Lys Gly His Gly Phe Phe Arg Lys Ser Lys Ala
 1 5 10 15

Tyr Gly Leu Val Cys Ala Ile Ala Leu Ala Gly Ala Phe Thr Leu Ala
 20 25 30

Thr Ser Gln Val Ser Ala Asp Gln Val Thr Thr Gln Ala Thr Thr Gln
 35 40 45

Thr Val Thr Gln Asn Gln Ala Glu Thr Val Thr Ser Thr Gln Leu Asp
 50 55 60

Lys Ala Val Ala Thr Ala Lys Lys Ala Ala Val Ala Val Thr Thr Thr
 65 70 75 80

Pro Ala Val Asn His Ala Thr Thr Thr Asp Ala Gln Ala Asp Leu Ala
 85 90 95

Asn Gln Thr Gln Ala Val Lys Asp Val Thr Ala Lys Ala Gln Ala Asn
 100 105 110

Thr Gln Ala Ile Lys Asp Ala Thr ^{GBS patentin.ST25} Ala Glu Asn Ala Lys Ile Asp Ala
 115 120 125
 Glu Asn Lys Ala Glu Ala Glu Arg Val Ala Lys Glu Asn Lys Glu Gly
 130 135 140
 Gln Ala Ala Val Asp Ala Arg Asn Lys Ala Gly Gln Ala Ala Val Asp
 145 150 155 160
 Ala Arg Asn Lys Ala Lys Gln Gln Ala Gln Asp Asp Gln Lys Ala Lys
 165 170 175
 Ile Asp Ala Glu Asn Lys Ala Glu Ser Gln Arg Val Ser Gln Leu Asn
 180 185 190
 Ala Gln Asn Lys Ala Lys Ile Asp Ala Glu Asn Lys Asp Ala Gln Ala
 195 200 205
 Lys Ala Asn Ala Thr Asn Ala Gln Leu Gln Lys Asp Tyr Gln Ala Lys
 210 215 220
 Leu Ala Glu Ile Lys Ser Val Glu Ala Tyr Asn Ala Gly Val Arg Gln
 225 230 235 240
 Arg Asn Lys Asp Ala Gln Ala Lys Ala Asp Ala Thr Asn Ala Gln Leu
 245 250 255
 Gln Lys Asp Tyr Gln Ala Lys Leu Ala Leu Tyr Asn Gln Ala Leu Lys
 260 265 270
 Ala Lys Ala Glu Ala Asp Lys Gln Ser Ile Asn Asn Val Ala Phe Asp
 275 280 285
 Ile Lys Ala Gln Ala Lys Gly Val Asp Asn Ala Glu Tyr Gly Asn Ser
 290 295 300
 Ile Met Thr Ala Lys Thr Lys Pro Asp Gly Ser Phe Glu Phe Asn His
 305 310 315 320
 Asp Met Ile Asp Gly Val Lys Thr Ile Gly Tyr Gly Lys Leu Thr Gly
 325 330 335
 Lys Val Asn His His Tyr Val Ala Asn Lys Asp Gly Ser Val Thr Ala
 340 345 350
 Phe Val Asp Ser Val Thr Leu Tyr Lys Tyr Glu Tyr Arg Asn Val Ala
 355 360 365
 Gln Asn Ala Ala Val Asn Gln Asn Ile Val Phe Arg Val Leu Thr Lys
 370 375 380

GBS patentin.ST25

Asp Gly Arg Pro Ile Phe Glu Lys Ala His Asn Gly Asn Lys Thr Phe
 385 390 395 400

Ala Glu Thr Leu Asn Lys Thr Leu Gln Leu Asn Leu Lys Tyr Glu Leu
 405 410 415

Lys Pro His Ala Ser Ser Gly Asn Val Glu Val Phe Lys Ile His Asp
 420 425 430

Asp Trp Val His Asp Thr His Gly Ser Ala Leu Val Ser Tyr Val Asn
 435 440 445

Asn Asn Asp Ala Val Pro Asn Val Val Ile Pro Glu Arg Pro Thr Pro
 450 455 460

Pro Lys Pro Val Lys Val Thr Pro Glu Ala Glu Lys Pro Val Pro Glu
 465 470 475 480

Lys Pro Val Glu Pro Lys Leu Val Thr Pro Thr Leu Lys Thr Tyr Thr
 485 490 495

Pro Val Lys Phe Ile Pro Arg Glu Tyr Lys Pro Glu Pro Ile Thr Pro
 500 505 510

Glu Thr Phe Thr Pro Glu Lys Phe Thr Pro Ala Gln Pro Lys Val Lys
 515 520 525

Pro His Val Ser Ile Pro Glu Lys Ile Asn Tyr Ser Val Ser Val His
 530 535 540

Pro Val Leu Val Pro Ala Ala Asn Pro Ser Lys Ala Val Ile Asp Glu
 545 550 555 560

Ala Gly Gln Ser Val Asn Gly Lys Thr Val Leu Pro Asn Ala Thr Leu
 565 570 575

Asp Tyr Val Ala Lys Gln Asn Phe Ser Gln Tyr Lys Gly Ile Lys Ala
 580 585 590

Ser Ala Glu Ala Ile Ala Lys Gly Phe Ala Phe Val Asp Gln Pro Asn
 595 600 605

Glu Ala Leu Ala Glu Leu Thr Val Lys Ser Ile Lys Ala Ser Asn Gly
 610 615 620

Asp Asp Val Ser Ser Leu Leu Glu Met Arg His Val Leu Ser Lys Asp
 625 630 635 640

Thr Leu Asp Gln Lys Leu Gln Ser Leu Ile Lys Glu Ala Gly Ile Ser
 645 650 655

Pro Val Gly Glu Phe Tyr Met Trp Thr Ala Lys Asp Pro Gln Ala Phe
 660 665 670

Tyr Lys Ala Tyr Val Gln Lys Gly Leu Asp Ile Thr Tyr Asn Leu Ser
 675 680 685

Phe Lys Ile Lys Ala Asn Phe Thr Lys Gly Gln Ile Lys Asn Gly Val
 690 695 700

Ala Gln Ile Asp Phe Gly Asn Gly Tyr Thr Gly Asn Ile Val Val Asn
 705 710 715 720

Asp Val Thr Val Pro Glu Val His Lys Asp Ile Leu Asp Lys Glu Asp
 725 730 735

Gly Lys Ser Ile Asn Asn Ser Thr Val Lys Leu Gly Asp Glu Val Thr
 740 745 750

Tyr Lys Leu Glu Gly Trp Val Val Pro Ala Asn Arg Gly Tyr Asp Leu
 755 760 765

Phe Glu Tyr Lys Phe Val Asp Gln Leu Gln His Thr His Asp Leu Tyr
 770 775 780

Leu Arg Asp Lys Val Val Ala Lys Val Asp Val Thr Leu Lys Asp Gly
 785 790 795 800

Thr Val Ile Lys Lys Gly Thr Asn Leu Gly Glu Tyr Thr Glu Thr Val
 805 810 815

Tyr Asn Lys Thr Thr Gly His Tyr Glu Leu Ala Phe Lys Lys Glu Phe
 820 825 830

Leu Ala Lys Val Ser Arg Glu Ser Glu Phe Gly Ala Asp Asp Phe Ile
 835 840 845

Val Val Lys Arg Ile Lys Ala Gly Asp Val Tyr Asn Thr Ala Asp Leu
 850 855 860

Tyr Val Asn Gly Tyr Lys Val Lys Ser Glu Ala Val Val Thr His Thr
 865 870 875 880

Thr Glu Lys Ser Lys Pro Val Glu Pro Gln Lys Ala Thr Pro Lys Ala
 885 890 895

Pro Ala Lys Gly Leu Pro Ser Thr Gly Glu Ala Ser Met Thr Pro Leu
 900 905 910

Thr Ala Ile Gly Ala Ile Ile Leu Ser Ala Leu Gly Leu Ala Gly Phe
 915 920 925

GBS patentin.ST25

Lys Lys Arg Gln Lys
930

<210> 451

<211> 1049

<212> PRT

<213> streptococcus agalactiae

<400> 451

Met Phe Ser Trp Leu Glu Ala Leu Tyr Tyr Thr Leu Ile Gln Leu Ala
1 5 10 15

Lys Val Asn Arg Leu Asn Ala Leu Phe Leu Val Ser Val Val Gly Tyr
20 25 30

Leu Cys Tyr Gln Gly Ile Lys Leu Val Arg Lys Thr Ile Arg Asn Phe
35 40 45

Phe Gln Leu Met Lys Gly Phe Ile Gly Asp Arg Glu Asn Ile Lys Lys
50 55 60

Cys Ile Lys Asn Lys Lys Glu Ala Leu Val His Ser Trp Lys His Arg
65 70 75 80

Gln Asp Ile Asp Trp Lys Ser Thr Gly Lys Asp Lys Ser Lys Gln Leu
85 90 95

Trp Asn Leu Met Lys Arg Leu Ala Thr Val Ala Pro Ser Phe Leu Phe
100 105 110

Leu Leu Leu Gly Asn Val Leu Phe Arg Leu Ile Tyr Gln Leu Pro Phe
115 120 125

Val Lys Gln Asp Arg Lys Arg Phe Asp Lys Glu Met Lys Pro Leu Leu
130 135 140

Tyr Phe Lys Asn Tyr Arg Ser Phe Val Phe Met Gly Ile Gly Phe Ser
145 150 155 160

Phe Ile Ala Phe Ile Leu Thr Asn Tyr Phe Val Thr Val Leu Arg Ala
165 170 175

Ala Ile Arg Phe Leu Tyr Phe Ser Ile Met Thr Leu Arg Asp Asn Ser
180 185 190

Gln Val Val Ser Phe Asn Val Asp Ser Leu Leu Ile Gln Asn Leu Phe
195 200 205

Asn Ala Arg Val Phe Val Ile Ala ^{GBS patentin.ST25} Pro Ile Leu Ala Val Pro Ile Phe
 210 215 220
 Leu Ile Gly Leu Val Val Ala Trp Arg Ser Ala Trp Val Asn Phe Glu
 225 230 235 240
 Gln Tyr Arg Asp Tyr Asn His Asn Glu Glu Gly Asp Asp Arg Phe Ala
 245 250 255
 Thr Val Lys Glu Ile His Gln Gln Tyr Lys Lys Val Pro Asn Lys Thr
 260 265 270
 Glu Thr Tyr Pro Gly Glu Gly Gly Val Pro Val Leu His Glu Thr Arg
 275 280 285
 Lys Asn Leu Thr Gly Leu Thr Leu Lys Ser Gln Met Leu Trp Gln Asn
 290 295 300
 Arg Thr Phe Ser Arg Tyr Leu Thr Asn Ala Glu Arg Ile Leu Gly Leu
 305 310 315 320
 Leu Ser Thr Pro Ser Gly Asp Tyr Tyr Ile Asp Asp Ser Thr Thr Asn
 325 330 335
 Leu Ile Thr Met Gly Ile Thr Arg Ser Gly Lys Gly Glu Ala His Ile
 340 345 350
 Ala Pro Ile Ile Asp Ile Asn Ser Arg Ala Glu Ile Gln Pro Ser Leu
 355 360 365
 Ile Ile Ala Asp Pro Lys Gly Glu His Tyr Gln Ser Ser Tyr Lys Thr
 370 375 380
 Met Arg Arg Arg Gly Tyr Asp Val Asn Val Leu Ser Phe Gln Asn Met
 385 390 395 400
 Asp Trp Ser Met Ser Tyr Asn Pro Leu Ala Leu Ala Ile Ala Ala Ala
 405 410 415
 Lys Lys Gly Tyr Tyr Glu Met Thr Gln Thr Arg Val Asn Ala Val Ala
 420 425 430
 Glu Ala Ile Tyr Arg Lys Thr Lys Pro Gly Ser Gly Asn Gly Asn Ala
 435 440 445
 Lys Tyr Trp Glu Asp Thr Ser Ile Ser Leu Phe Asn Ala Ile Ala Met
 450 455 460
 Ala Leu Met Asp Arg Ala Asn Glu Thr Val Arg Asn Gly Glu Thr Asp
 465 470 475 480

Ala Trp Asp Thr Val Thr Val Arg Asn Ile Ala Lys Phe Leu Thr Asp
 485 490

Leu Gly Ser Glu Glu Val Phe Val Asn Asp Phe Gly Glu Ile Val Glu
 500 505 510

Asn Pro Asp Lys Asn Gln Gln Val Lys Lys Lys Ser Lys Ile Thr Val
 515 520 525

Tyr Phe Asp Asn Leu Arg Lys Ile Asn Gln Glu Gln Phe Ser Lys Phe
 530 535 540

Arg Asp Met Ala Asp Leu Asn Phe Arg Ser Ser Asp Phe Ala Ser Glu
 545 550 555 560

Glu Thr Lys Gly Asn Val Phe Ser Ser Met Met Ser Gly Ile Asn Leu
 565 570 575

Phe Leu Gln Asp Asn Ile Ala Lys Leu Thr Ser Lys Asn Ser Ile Asp
 580 585 590

Leu Glu Ser Val Gly Phe Pro Arg Arg Leu Ser Ile Lys Phe Arg Ser
 595 600 605

Ser Ser Asn Val Ala Met Arg Asn Glu Tyr Thr His Lys Thr Ala Lys
 610 615 620

Val Thr Ile Thr Ser Gln Ala Val Trp Gly Lys Thr Thr Lys Gln Val
 625 630 635 640

Ile His Val Asp Ala Ala Thr Ala Leu Ile Asp Gly Glu Gly Tyr Leu
 645 650 655

Thr Tyr Val Ile Glu Pro Gln Leu Pro Asp Gln Phe Leu Val Thr Ile
 660 665 670

Asp Phe Asn His Glu Asn Asn Gly Gly Ser Ala Ile Arg His Lys Thr
 675 680 685

Phe Gln Phe Ser Ala Glu Lys Val Tyr Lys Lys Arg Gly Asn Val Ile
 690 695 700

Thr Leu Asp Asp Tyr Thr Lys Lys Pro Val Leu Asp His Ile Lys Val
 705 710 715 720

Thr Val Leu Asn Lys Gln Asp Asp Asn Leu Leu Gln Lys Glu Asp Ile
 725 730 735

Asp Leu Ile Tyr Ser Asp Asn Pro Lys Val Ile Tyr Leu Val Thr Pro
 740 745 750

Pro Asn Arg Thr Glu Tyr Asn Ser Ile Val Ser Leu Phe Leu Asp Gln
 755 760 765
 Leu Phe Asn Ala Asn Tyr Glu Leu Ala Leu Ser Asn Gly Arg Lys Cys
 770 775 780
 Val Asn Arg Ile Leu His Ile Leu Asp Glu Phe Thr Asn Ile Pro Ala
 785 790 795 800
 Ile Pro His Met Asp Thr Lys Ile Ser Ile Gly Leu Gly Gln Asn Ile
 805 810 815
 Leu Tyr Tyr Leu Trp Ile Gln Asn Leu Lys Gln Leu Val Ser Glu Tyr
 820 825 830
 Gly Glu Asn Thr Ala Glu Thr Ile Arg Glu Asn Cys Ser Leu Lys Val
 835 840 845
 Tyr Ile Lys Ser Thr Ala Pro Ala Thr Asn Glu Tyr Phe Ser Lys Glu
 850 855 860
 Leu Gly Thr Arg Thr Ile Thr Arg Arg Arg Arg Ser Ser Asn Ile Leu
 865 870 875 880
 Asp Glu Ala Asn Pro Asn Val Ser Ile Glu Asn Pro Arg Gln Glu Leu
 885 890 895
 Leu Thr Pro Thr Gln Leu Ser Lys Leu Gln Glu Gly Glu Ala Val Ile
 900 905 910
 Leu Arg Gly Val Lys Gly Arg Asp Asn Ala Gly Arg Lys Ile Thr Thr
 915 920 925
 Asp Pro Ile Phe Leu His Glu Lys Thr Ser Leu Pro Tyr Arg Tyr Met
 930 935 940
 Phe Leu Gln Glu Glu Phe Asp Gln Ser Met Ala Leu Ala Asp Ile Pro
 945 950 955 960
 Val Glu Ser Gly His Arg Asp Leu Asp Leu Gln Asp Ile Ala Val Gly
 965 970 975
 Ala Gln Ser Thr Phe Asn Lys Ile Ile Asp Trp Arg Met Ala Leu Thr
 980 985 990
 Asp Arg Met Arg Thr Asn Gly Lys Ile Pro Gln Leu Ala Ser Arg Lys
 995 1000 1005
 Gln Thr Ile Lys Ala Leu Ser Gln Ser Gln Phe Thr Ser Pro Ala
 1010 1015 1020

GBS patentin.ST25

Asp Leu Thr Gln Ala Val Ile Ala Glu Val Phe Asp Glu Glu Asp
 1025 1030 1035

Asp Asp Asp Leu Phe Phe Val Asp Asp Val Met
 1040 1045

<210> 452

<211> 92

<212> PRT

<213> Streptococcus agalactiae

<400> 452

Met Thr Asp Asn Arg Phe Ala Gln Leu Lys Glu Asn Phe Glu Lys Gly
 1 5 10 15

Ser Pro Lys Arg Arg Val Pro Thr Ser Arg Pro Ile Ala Ala Gln Lys
 20 25 30

Ala Pro Glu Ser Tyr Asn Lys Lys Gly Arg Tyr Pro Phe Ser Leu His
 35 40 45

Gln Asp Val Arg Tyr Asp Lys Leu Glu Ala Leu Val Ala Tyr His Gly
 50 55 60

Ala Lys Ser Ala Ser Asp Tyr Leu Glu Arg Leu Ile Val Gln Glu Trp
 65 70 75 80

Glu Lys Met Gln Arg Lys Leu Lys Asn Lys Glu Lys
 85 90

<210> 453

<211> 127

<212> PRT

<213> Streptococcus agalactiae

<400> 453

Met Ala Tyr Leu Ser Lys Leu Ser Asp Leu Asp Pro Ser Leu Met Asp
 1 5 10 15

Ala Asp Ser Glu Gln Ile Tyr Ile Pro Lys Val Leu Phe Glu His Asn
 20 25 30

Asp Phe Lys Gly Leu Thr Tyr Lys Glu Ile Leu Leu Tyr Ser Phe Leu
 35 40 45

GBS patentin.ST25

Leu Asn Arg Leu Arg Glu pro Leu Asp Phe Ile Gln Lys Gly Tyr Asp
 50 55 60

Asp Asn Glu Asp Thr Tyr Val His Phe Lys Val Glu Asp Leu Cys Glu
 65 70 75 80

Leu Leu Asn Gln Ser Lys Thr Thr Val Ile Ser Leu Lys Lys Arg Leu
 85 90 95

Ala Gln Tyr Gly Leu Ile Glu Glu Val Lys Ala Gly Ser His Gln Pro
 100 105 110

Asn Arg Ile Tyr Leu Thr Asp Lys Leu Val Pro Tyr Ile Lys Gly
 115 120 125

<210> 454

<211> 442

<212> PRT

<213> Streptococcus agalactiae

<400> 454

Met Thr Ile Phe Asp Glu Arg Glu Leu Lys Glu Arg Phe Thr His Glu
 1 5 10 15

Asn Arg Val Ser Phe Tyr Glu Phe Val Ala Lys Tyr Asp Ala Gln Met
 20 25 30

Val Pro Val Met Lys Ala Lys Gly Tyr Arg Cys Ile His Ser Met Glu
 35 40 45

Arg Thr Val Val Phe Thr Phe Gly Glu Phe Thr Ile Arg Arg Arg Arg
 50 55 60

Trp Gln Lys Gly Glu His Trp Val Val Pro Val Asp Glu Lys Leu Gly
 65 70 75 80

Leu Lys Lys Asn Val Arg Tyr Ser Leu Glu Phe Met Tyr Gln Ile Ala
 85 90 95

Ser Leu Ala Thr Met Met Pro Tyr Glu Lys Val Ile Lys Val Val Gln
 100 105 110

Met Met Tyr Cys Ile Val Ile Thr Lys Pro Thr Val Val Lys Ala Val
 115 120 125

Lys Ile Ser Arg Glu Leu Leu Lys Glu Lys Glu Ala Tyr Arg Phe Phe
 130 135 140

GBS patentin.ST25

Asp Glu Asp Ile Pro Val Asp Lys Glu Pro Val Asp Met Ile Tyr Leu
 145 150 155 160
 Glu Gly Asp Gly Val Met Val Lys Ala Arg Glu Glu Gly Leu Asp Asn
 165 170 175
 Arg Asn Val Asp Leu Ser His Phe Val Val His Thr Gly Ser Gln Lys
 180 185 190
 Val Gly Ser Asn Arg Phe Val Leu Gln Asn Lys Lys Glu Phe Val Ser
 195 200 205
 Leu Asp Asn Arg Gln Thr Arg Gln Lys Ile Leu Asp Tyr Leu Tyr Asn
 210 215 220
 His Phe Tyr Ile Ala Pro Asn Thr Leu Leu Ile Thr Asn Ser Asp Gly
 225 230 235 240
 Gly His Gly Tyr Thr Pro Tyr Val Phe Lys Glu Ile Ala Lys Ala Leu
 245 250 255
 Lys Val Lys Gln His Glu His Phe Trp Asp Arg Tyr His Val Asn Glu
 260 265 270
 Lys Ile Lys Ser Phe Phe Lys Leu Tyr Pro Val Glu Leu Met Thr Gly
 275 280 285
 Ala Phe Gln Ser Ile Lys Gln His Asp Lys Glu Lys Leu Arg Thr Val
 290 295 300
 Leu Asp Thr Thr Glu Ala Leu Ile Leu Met Glu Glu Glu Met Glu Gly
 305 310 315 320
 Phe Asn Gln Phe Lys Arg Lys Leu Leu Asn Asn Phe Gln Tyr Thr Lys
 325 330 335
 Ser Ala Glu Leu Arg Gly Phe Ser Arg Ala Gly Ile Gly Val Met Glu
 340 345 350
 Ser Gln His Arg Lys Ile Thr Tyr Arg Met Lys Lys Arg Gly Met Tyr
 355 360 365
 Trp Thr Ile Gln Gly Ala Glu Thr Met Ser Gln Leu Ile Val Leu Ser
 370 375 380
 Tyr Glu Gly Gln Leu Arg Asp Leu Phe Phe Gly Ser Trp Arg Glu Asp
 385 390 395 400
 Tyr Gln Lys Tyr Gln Glu Leu Glu Asn Leu Ser Ala Gly Lys Ile Lys
 405 410 415

His Glu Gln Asn Lys Ile Asn Lys Arg Tyr Asp Leu Gln Thr Leu Gly
 420 425 430

Arg Leu Arg Tyr Gly Arg His Arg Asn Leu
 435 440

<210> 455

<211> 788

<212> PRT

<213> streptococcus agalactiae

<400> 455

Met Asp Val Ser Ser Ser Pro Asn Ile Thr Phe Met Leu Gln Tyr Thr
 1 5 10 15

Glu Ala Asn Pro Gln Tyr Val Asp Tyr Thr Asn Arg Glu Glu Ala Val
 20 25 30

Lys Ile Asp Glu Glu Leu Ser Leu Glu Thr Asn Arg Gln Met Ile Glu
 35 40 45

Gly Leu Thr Glu Asp Glu Leu Thr Arg Ile Gln Glu Ala Val Pro Glu
 50 55 60

Thr Gln Leu Asn Phe Arg Glu Tyr Ile Asp Tyr Met Asn Arg Ser Tyr
 65 70 75 80

Ala Thr Glu Glu Gln Ser Lys Glu Leu Thr Ala Ile Phe Thr Gln Glu
 85 90 95

Ala Asp Tyr Leu Gln Lys Leu Arg Leu Ile Asp Leu Lys Asn Lys Leu
 100 105 110

Glu Ser Ala Tyr Gln Asn Gly Ser Leu Leu Trp Gln Gly Val Ile Ser
 115 120 125

Phe Asp Asn Ala Phe Leu Ala Glu Gln Gly Leu Tyr Asp Val Ala Thr
 130 135 140

Gly Gln Val Asp Gln Lys Ala Ile Lys Ala Val Met Arg Asp Met Met
 145 150 155 160

Pro Thr Leu Ile Gln Lys Glu Gly Leu Ser Asp Ser Ala Phe Trp Trp
 165 170 175

Gly Asn Ile His Leu Asn Thr Asp Asn Ile His Ile His Phe Gly Leu
 180 185 190

GBS patentin.ST25

Ser Glu Val Glu Ser Asn Arg Glu Lys Ile Phe Tyr Gln Pro Arg Gly
195 200 205

Arg Met Glu Tyr Lys Gly Asn Phe Ser Gln Lys Thr Ile Asn Arg Phe
210 215 220

Lys Ser Gly Val Tyr His Gly Leu Leu Lys Glu Glu Thr Arg Ser Asn
225 230 235 240

Leu Leu Arg Lys Glu Gln Ile Leu Ala Asn Leu Lys Ala Asp Phe Ile
245 250 255

Thr Ser Ile Tyr Gln Lys Asp Lys Ile Thr Ser Ser Ala Glu Lys Asn
260 265 270

Phe Leu Glu Gln Ala Tyr Asn His Leu Pro Leu Asn Lys Lys Trp Arg
275 280 285

Tyr Gly Ser Asn Ala Arg Asp Phe Ala Val Ser Lys Phe Phe Leu Asp
290 295 300

Arg Tyr Leu Asp Ser Tyr Leu Asn Asn Glu Gly Ser Ala Ala Tyr Gln
305 310 315 320

Glu Phe Leu Lys Glu Thr Arg Asp Phe Leu Gln Thr Tyr Glu Gly Val
325 330 335

Tyr Ser Ala Glu Lys Asn Lys Ile Tyr Glu Lys Leu Arg Lys Val Asp
340 345 350

Gly Gln Thr Ile Arg Thr Leu Ala Glu Ser Lys Gly Tyr Asp Leu Glu
355 360 365

His His Leu Ala Arg Arg Val Met Asp Leu Arg Glu Arg Leu Ala Asn
370 375 380

Asn Ile Leu Arg Ser Phe Arg Glu Ala Ala Pro Gln Ile Gln Asp Val
385 390 395 400

Gln Leu Glu Lys Asn Leu Glu Ser Phe Ser Val Leu Asn Gln Lys Lys
405 410 415

Ile Leu Glu Gln His Pro Glu Ala Ser Val Val Lys Ser Gln Lys Ala
420 425 430

Trp Gln Lys Leu Gly Tyr Phe Val Lys Ala Gly Glu Gln Pro Leu Glu
435 440 445

Ile Ile Arg Pro Val Tyr Lys Ser Tyr Asp Lys His Gly Lys Gly Ile
450 455 460

GBS patentin.ST25

Gly Arg Pro Glu Phe Val Ser Asp Thr Val Tyr Asp Ile Ser Gln Leu
465 470 475 480

Thr Glu Asn Ile Gln Leu Lys Ser Leu Thr Leu Lys Asp Leu Ser Leu
485 490 495

Phe Ser Ser Asn Glu Leu Lys Glu Leu Val Asp Ala Ala Lys Leu Lys
500 505 510

Thr Asn Pro Thr Glu Arg Glu Arg Arg Glu Leu Gly Thr Tyr Arg Tyr
515 520 525

Ala Leu Lys Leu Ser Ile Leu Glu Ser Ser Gln Lys Glu Leu Gln Val
530 535 540

Arg Gln Lys Leu Leu Glu Gln Val Gln Pro Leu Ala Ser Asp Gln Pro
545 550 555 560

Phe Leu Asp Phe Lys Lys Gln Leu Ile Ala Gln Glu Leu Gln Ala Ile
565 570 575

Ala Leu Gln Leu Thr Pro Asn Tyr Lys Leu Ser Glu Asp Asp Lys Ala
580 585 590

Leu Lys Asn Arg Leu Lys Arg Gln Phe Glu Asp Ser Val Ala Leu Pro
595 600 605

Val Ser Lys Ala Thr Pro Gly Ala Ile Gln Leu Pro Ile Arg Gln Leu
610 615 620

Trp Thr Glu Leu Gly Leu Val His His Ile Gln Asp Glu Asn Ile Leu
625 630 635 640

Thr Leu Leu Lys Gly Thr Ser Thr Thr Lys Gln Ala Tyr Ile Glu Glu
645 650 655

Leu Gln Thr His Ile Ser Ile Phe Gln Leu Lys Tyr Gln Ile Asn Asn
660 665 670

Arg Asn Lys Gln Ile Ser Gln Leu Ser Asp Glu Ala Thr Ile Lys Glu
675 680 685

Met Arg Ile Ala Asn Ala Lys Gly Phe Ser Glu Leu Lys Arg Leu Tyr
690 695 700

Asp Thr Leu Gln Pro Ser Asp Asp Gly Gln Asn Gln Ile Ser Gln Ala
705 710 715 720

Val Ser Lys Gln Leu Gln Glu Arg Lys Val Ile Lys Lys Ala Gln Leu
725 730 735

GBS patentin.ST25
 Gln Gln Thr Gln Arg Ser Gly Lys Ile Asn Thr Asp Phe Met Arg Gln
 740 745 750

Leu Thr Ala Ser Leu Asn Arg Ser Gln Gln Ala Ser Lys Lys Ala Leu
 755 760 765

Met Glu Arg Ala Arg Ser Asp Glu Arg Glu Glu Gln Glu Glu Arg Arg
 770 775 780

Gln Ala Gln Arg
 785

<210> 456

<211> 933

<212> PRT

<213> Streptococcus agalactiae

<400> 456

Met Asn Ser Asn Thr Lys Gly His Gly Phe Phe Arg Lys Ser Lys Ala
 1 5 10 15

Tyr Gly Leu Val Cys Ala Ile Ala Leu Ala Gly Ala Phe Thr Leu Ala
 20 25 30

Thr Ser Gln Val Ser Ala Asp Gln Val Thr Thr Gln Ala Thr Thr Gln
 35 40 45

Thr Val Thr Gln Asn Gln Ala Glu Thr Val Thr Ser Thr Gln Leu Asp
 50 55 60

Lys Ala Val Ala Thr Ala Lys Lys Ala Ala Val Ala Val Thr Thr Thr
 65 70 75 80

Pro Ala Val Asn His Ala Thr Thr Thr Asp Ala Gln Ala Asp Leu Ala
 85 90 95

Asn Gln Thr Gln Ala Val Lys Asp Val Thr Ala Lys Ala Gln Ala Asn
 100 105 110

Thr Gln Ala Ile Lys Asp Ala Thr Ala Glu Asn Ala Lys Ile Asp Ala
 115 120 125

Glu Asn Lys Ala Glu Ala Glu Arg Val Ala Lys Glu Asn Lys Glu Gly
 130 135 140

Gln Ala Ala Val Asp Ala Arg Asn Lys Ala Gly Gln Ala Ala Val Asp
 145 150 155 160

Ala Arg Asn Lys Ala Lys Gln Gln GBS patentin.ST25
 165 170 175
 Ile Asp Ala Glu Asn Lys Ala Glu Ser Gln Arg Val Ser Gln Leu Asn
 180 185 190
 Ala Gln Asn Lys Ala Lys Ile Asp Ala Glu Asn Lys Asp Ala Gln Ala
 195 200 205
 Lys Ala Asn Ala Thr Asn Ala Gln Leu Gln Lys Asp Tyr Gln Ala Lys
 210 215 220
 Leu Ala Glu Ile Lys Ser Val Glu Ala Tyr Asn Ala Gly Val Arg Gln
 225 230 235 240
 Arg Asn Lys Asp Ala Gln Ala Lys Ala Asp Ala Thr Asn Ala Gln Leu
 245 250 255
 Gln Lys Asp Tyr Gln Ala Lys Leu Ala Leu Tyr Asn Gln Ala Leu Lys
 260 265 270
 Ala Lys Ala Glu Ala Asp Lys Gln Ser Ile Asn Asn Val Ala Phe Asp
 275 280 285
 Ile Lys Ala Gln Ala Lys Gly Val Asp Asn Ala Glu Tyr Gly Asn Ser
 290 295 300
 Ile Met Thr Ala Lys Thr Lys Pro Asp Gly Ser Phe Glu Phe Asn His
 305 310 315 320
 Asp Met Ile Asp Gly Val Lys Thr Ile Gly Tyr Gly Lys Leu Thr Gly
 325 330 335
 Lys Val Asn His His Tyr Val Ala Asn Lys Asp Gly Ser Val Thr Ala
 340 345 350
 Phe Val Asp Ser Val Thr Leu Tyr Lys Tyr Glu Tyr Arg Asn Val Ala
 355 360 365
 Gln Asn Ala Ala Val Asn Gln Asn Ile Val Phe Arg Val Leu Thr Lys
 370 375 380
 Asp Gly Arg Pro Ile Phe Glu Lys Ala His Asn Gly Asn Lys Thr Phe
 385 390 395 400
 Ala Glu Thr Leu Asn Lys Thr Leu Gln Leu Asn Leu Lys Tyr Glu Leu
 405 410 415
 Lys Pro His Ala Ser Ser Gly Asn Val Glu Val Phe Lys Ile His Asp
 420 425 430

GBS patentin.ST25

Asp Trp Val His Asp Thr His Gly Ser Ala Leu Val Ser Tyr Val Asn
435 440 445

Asn Asn Asp Ala Val Pro Asn Val Val Ile Pro Glu Arg Pro Thr Pro
450 455 460

Pro Lys Pro Val Lys Val Thr Pro Glu Ala Glu Lys Pro Val Pro Glu
465 470 475 480

Lys Pro Val Glu Pro Lys Leu Val Thr Pro Thr Leu Lys Thr Tyr Thr
485 490 495

Pro Val Lys Phe Ile Pro Arg Glu Tyr Lys Pro Glu Pro Ile Thr Pro
500 505 510

Glu Thr Phe Thr Pro Glu Lys Phe Thr Pro Ala Gln Pro Lys Val Lys
515 520 525

Pro His Val Ser Ile Pro Glu Lys Ile Asn Tyr Ser Val Ser Val His
530 535 540

Pro Val Leu Val Pro Ala Ala Asn Pro Ser Lys Ala Val Ile Asp Glu
545 550 555 560

Ala Gly Gln Ser Val Asn Gly Lys Thr Val Leu Pro Asn Ala Thr Leu
565 570 575

Asp Tyr Val Ala Lys Gln Asn Phe Ser Gln Tyr Lys Gly Ile Lys Ala
580 585 590

Ser Ala Glu Ala Ile Ala Lys Gly Phe Ala Phe Val Asp Gln Pro Asn
595 600 605

Glu Ala Leu Ala Glu Leu Thr Val Lys Ser Ile Lys Ala Ser Asn Gly
610 615 620

Asp Asp Val Ser Ser Leu Leu Glu Met Arg His Val Leu Ser Lys Asp
625 630 635 640

Thr Leu Asp Gln Lys Leu Gln Ser Leu Ile Lys Glu Ala Gly Ile Ser
645 650 655

Pro Val Gly Glu Phe Tyr Met Trp Thr Ala Lys Asp Pro Gln Ala Phe
660 665 670

Tyr Lys Ala Tyr Val Gln Lys Gly Leu Asp Ile Thr Tyr Asn Leu Ser
675 680 685

Phe Lys Ile Lys Ala Asn Phe Thr Lys Gly Gln Ile Lys Asn Gly Val
690 695 700

Ala Gln Ile Asp Phe Gly Asn Gly Tyr Thr Gly Asn Ile Val Val Asn
 705 710 715 720
 Asp Val Thr Val Pro Glu Val His Lys Asp Ile Leu Asp Lys Glu Asp
 725 730 735
 Gly Lys Ser Ile Asn Asn Ser Thr Val Lys Leu Gly Asp Glu Val Thr
 740 745 750
 Tyr Lys Leu Glu Gly Trp Val Val Pro Ala Asn Arg Gly Tyr Asp Leu
 755 760 765
 Phe Glu Tyr Lys Phe Val Asp Gln Leu Gln His Thr His Asp Leu Tyr
 770 775 780
 Leu Arg Asp Lys Val Val Ala Lys Val Asp Val Thr Leu Lys Asp Gly
 785 790 795 800
 Thr Val Ile Lys Lys Gly Thr Asn Leu Gly Glu Tyr Thr Glu Thr Val
 805 810 815
 Tyr Asn Lys Thr Thr Gly His Tyr Glu Leu Ala Phe Lys Lys Glu Phe
 820 825 830
 Leu Ala Lys Val Ser Arg Glu Ser Glu Phe Gly Ala Asp Asp Phe Ile
 835 840 845
 Val Val Lys Arg Ile Lys Ala Gly Asp Val Tyr Asn Thr Ala Asp Leu
 850 855 860
 Tyr Val Asn Gly Tyr Lys Val Lys Ser Glu Ala Val Val Thr His Thr
 865 870 875 880
 Thr Glu Lys Ser Lys Pro Val Glu Pro Gln Lys Ala Thr Pro Lys Ala
 885 890 895
 Pro Ala Lys Gly Leu Pro Ser Thr Gly Glu Ala Ser Met Thr Pro Leu
 900 905 910
 Thr Ala Ile Gly Ala Ile Ile Leu Ser Ala Leu Gly Leu Ala Gly Phe
 915 920 925
 Lys Lys Arg Gln Lys
 930

<210> 457

<211> 1049

<212> PRT

<213> Streptococcus agalactiae

GBS patentin.ST25

<400> 457

Met Phe Ser Trp Leu Glu Ala Leu Tyr Tyr Thr Leu Ile Gln Leu Ala
1 5 10 15
Lys Val Asn Arg Leu Asn Ala Leu Phe Leu Val Ser Val Val Gly Tyr
20 25 30
Leu Cys Tyr Gln Gly Ile Lys Leu Val Arg Lys Thr Ile Arg Asn Phe
35 40 45
Phe Gln Leu Met Lys Gly Phe Ile Gly Asp Arg Glu Asn Ile Lys Lys
50 55 60
Cys Ile Lys Asn Lys Lys Glu Ala Leu Val His Ser Trp Lys His Arg
65 70 75 80
Gln Asp Ile Asp Trp Lys Ser Thr Gly Lys Asp Lys Ser Lys Gln Leu
85 90 95
Trp Asn Leu Met Lys Arg Leu Ala Thr Val Ala Pro Ser Phe Leu Phe
100 105 110
Leu Leu Leu Gly Asn Val Leu Phe Arg Leu Ile Tyr Gln Leu Pro Phe
115 120 125
Val Lys Gln Asp Arg Lys Arg Phe Asp Lys Glu Met Lys Pro Leu Leu
130 135 140
Tyr Phe Lys Asn Tyr Arg Ser Phe Val Phe Met Gly Ile Gly Phe Ser
145 150 155 160
Phe Ile Ala Phe Ile Leu Thr Asn Tyr Phe Val Thr Val Leu Arg Ala
165 170 175
Ala Ile Arg Phe Leu Tyr Phe Ser Ile Met Thr Leu Arg Asp Asn Ser
180 185 190
Gln Val Val Ser Phe Asn Val Asp Ser Leu Leu Ile Gln Asn Leu Phe
195 200 205
Asn Ala Arg Val Phe Val Ile Ala Pro Ile Leu Ala Val Pro Ile Phe
210 215 220
Leu Ile Gly Leu Val Val Ala Trp Arg Ser Ala Trp Val Asn Phe Glu
225 230 235 240
Gln Tyr Arg Asp Tyr Asn His Asn Glu Glu Gly Asp Asp Arg Phe Ala
245 250 255

Thr Val Lys Glu Ile His Gln Gln Tyr Lys Lys Val Pro Asn Lys Thr
 260 265 270

Glu Thr Tyr Pro Gly Glu Gly Gly Val Pro Val Leu His Glu Thr Arg
 275 280 285

Lys Asn Leu Thr Gly Leu Thr Leu Lys Ser Gln Met Leu Trp Gln Asn
 290 295 300

Arg Thr Phe Ser Arg Tyr Leu Thr Asn Ala Glu Arg Ile Leu Gly Leu
 305 310 315 320

Leu Ser Thr Pro Ser Gly Asp Tyr Tyr Ile Asp Asp Ser Thr Thr Asn
 325 330 335

Leu Ile Thr Met Gly Ile Thr Arg Ser Gly Lys Gly Glu Ala His Ile
 340 345 350

Ala Pro Ile Ile Asp Ile Asn Ser Arg Ala Glu Ile Gln Pro Ser Leu
 355 360 365

Ile Ile Ala Asp Pro Lys Gly Glu His Tyr Gln Ser Ser Tyr Lys Thr
 370 375 380

Met Arg Arg Arg Gly Tyr Asp Val Asn Val Leu Ser Phe Gln Asn Met
 385 390 395 400

Asp Trp Ser Met Ser Tyr Asn Pro Leu Ala Leu Ala Ile Ala Ala Ala
 405 410 415

Lys Lys Gly Tyr Tyr Glu Met Thr Gln Thr Arg Val Asn Ala Val Ala
 420 425 430

Glu Ala Ile Tyr Arg Lys Thr Lys Pro Gly Ser Gly Asn Gly Asn Ala
 435 440 445

Lys Tyr Trp Glu Asp Thr Ser Ile Ser Leu Phe Asn Ala Ile Ala Met
 450 455 460

Ala Leu Met Asp Arg Ala Asn Glu Thr Val Arg Asn Gly Glu Thr Asp
 465 470 475 480

Ala Trp Asp Thr Val Thr Val Arg Asn Ile Ala Lys Phe Leu Thr Asp
 485 490 495

Leu Gly Ser Glu Glu Val Phe Val Asn Asp Phe Gly Glu Ile Val Glu
 500 505 510

Asn Pro Asp Lys Asn Gln Gln Val Lys Lys Lys Ser Lys Ile Thr Val
 515 520 525

GBS patentin.ST25

Tyr Phe Asp Asn Leu Arg Lys Ile Asn Gln Glu Gln Phe Ser Lys Phe
 530 535 540

Arg Asp Met Ala Asp Leu Asn Phe Arg Ser Ser Asp Phe Ala Ser Glu
 545 550 555 560

Glu Thr Lys Gly Asn Val Phe Ser Ser Met Met Ser Gly Ile Asn Leu
 565 570 575

Phe Leu Gln Asp Asn Ile Ala Lys Leu Thr Ser Lys Asn Ser Ile Asp
 580 585 590

Leu Glu Ser Val Gly Phe Pro Arg Arg Leu Ser Ile Lys Phe Arg Ser
 595 600 605

Ser Ser Asn Val Ala Met Arg Asn Glu Tyr Thr His Lys Thr Ala Lys
 610 615 620

Val Thr Ile Thr Ser Gln Ala Val Trp Gly Lys Thr Thr Lys Gln Val
 625 630 635 640

Ile His Val Asp Ala Ala Thr Ala Leu Ile Asp Gly Glu Gly Tyr Leu
 645 650 655

Thr Tyr Val Ile Glu Pro Gln Leu Pro Asp Gln Phe Leu Val Thr Ile
 660 665 670

Asp Phe Asn His Glu Asn Asn Gly Gly Ser Ala Ile Arg His Lys Thr
 675 680 685

Phe Gln Phe Ser Ala Glu Lys Val Tyr Lys Lys Arg Gly Asn Val Ile
 690 695 700

Thr Leu Asp Asp Tyr Thr Lys Lys Pro Val Leu Asp His Ile Lys Val
 705 710 715 720

Thr Val Leu Asn Lys Gln Asp Asp Asn Leu Leu Gln Lys Glu Asp Ile
 725 730 735

Asp Leu Ile Tyr Ser Asp Asn Pro Lys Val Ile Tyr Leu Val Thr Pro
 740 745 750

Pro Asn Arg Thr Glu Tyr Asn Ser Ile Val Ser Leu Phe Leu Asp Gln
 755 760 765

Leu Phe Asn Ala Asn Tyr Glu Leu Ala Leu Ser Asn Gly Arg Lys Cys
 770 775 780

Val Asn Arg Ile Leu His Ile Leu Asp Glu Phe Thr Asn Ile Pro Ala
 785 790 795 800

GBS patentin.ST25

Ile Pro His Met Asp Thr Lys Ile Ser Ile Gly Leu Gly Gln Asn Ile
805 810 815

Leu Tyr Tyr Leu Trp Ile Gln Asn Leu Lys Gln Leu Val Ser Glu Tyr
820 825 830

Gly Glu Asn Thr Ala Glu Thr Ile Arg Glu Asn Cys Ser Leu Lys Val
835 840 845

Tyr Ile Lys Ser Thr Ala Pro Ala Thr Asn Glu Tyr Phe Ser Lys Glu
850 855 860

Leu Gly Thr Arg Thr Ile Thr Arg Arg Arg Arg Ser Ser Asn Ile Leu
865 870 875 880

Asp Glu Ala Asn Pro Asn Val Ser Ile Glu Asn Pro Arg Gln Glu Leu
885 890 895

Leu Thr Pro Thr Gln Leu Ser Lys Leu Gln Glu Gly Glu Ala Val Ile
900 905 910

Leu Arg Gly Val Lys Gly Arg Asp Asn Ala Gly Arg Lys Ile Thr Thr
915 920 925

Asp Pro Ile Phe Leu His Glu Lys Thr Ser Leu Pro Tyr Arg Tyr Met
930 935 940

Phe Leu Gln Glu Glu Phe Asp Gln Ser Met Ala Leu Ala Asp Ile Pro
945 950 955 960

Val Glu Ser Gly His Arg Asp Leu Asp Leu Gln Asp Ile Ala Val Gly
965 970 975

Ala Gln Ser Thr Phe Asn Lys Ile Ile Asp Trp Arg Met Ala Leu Thr
980 985 990

Asp Arg Met Arg Thr Asn Gly Lys Ile Pro Gln Leu Ala Ser Arg Lys
995 1000 1005

Gln Thr Ile Lys Ala Leu Ser Gln Ser Gln Phe Thr Ser Pro Ala
1010 1015 1020

Asp Leu Thr Gln Ala Val Ile Ala Glu Val Phe Asp Glu Glu Asp
1025 1030 1035

Asp Asp Asp Leu Phe Phe Val Asp Asp Val Met
1040 1045

<210> 458

<211> 92

GBS patentin.ST25

<212> PRT

<213> Streptococcus agalactiae

<400> 458

Met Thr Asp Asn Arg Phe Ala Gln Leu Lys Glu Asn Phe Glu Lys Gly
 1 5 10 15
 Ser Pro Lys Arg Arg Val Pro Thr Ser Arg Pro Ile Ala Ala Gln Lys
 20 25 30
 Ala Pro Glu Ser Tyr Asn Lys Lys Gly Arg Tyr Pro Phe Ser Leu His
 35 40 45
 Gln Asp Val Arg Tyr Asp Lys Leu Glu Ala Leu Val Ala Tyr His Gly
 50 55 60
 Ala Lys Ser Ala Ser Asp Tyr Leu Glu Arg Leu Ile Val Gln Glu Trp
 65 70 75 80
 Glu Lys Met Gln Arg Lys Leu Lys Asn Lys Glu Lys
 85 90

<210> 459

<211> 127

<212> PRT

<213> Streptococcus agalactiae

<400> 459

Met Ala Tyr Leu Ser Lys Leu Ser Asp Leu Asp Pro Ser Leu Met Asp
 1 5 10 15
 Ala Asp Ser Glu Gln Ile Tyr Ile Pro Lys Val Leu Phe Glu His Asn
 20 25 30
 Asp Phe Lys Gly Leu Thr Tyr Lys Glu Ile Leu Leu Tyr Ser Phe Leu
 35 40 45
 Leu Asn Arg Leu Arg Glu Pro Leu Asp Phe Ile Gln Lys Gly Tyr Asp
 50 55 60
 Asp Asn Glu Asp Thr Tyr Val His Phe Lys Val Glu Asp Leu Cys Glu
 65 70 75 80
 Leu Leu Asn Gln Ser Lys Thr Thr Val Ile Ser Leu Lys Lys Arg Leu
 85 90 95

Ala Gln Tyr Gly Leu Ile Glu Glu Val Lys Ala Gly Ser His Gln Pro
 100 105 110

Asn Arg Ile Tyr Leu Thr Asp Lys Leu Val Pro Tyr Ile Lys Gly
 115 120 125

<210> 460

<211> 442

<212> PRT

<213> Streptococcus agalactiae

<400> 460

Met Thr Ile Phe Asp Glu Arg Glu Leu Lys Glu Arg Phe Thr His Glu
 1 5 10 15

Asn Arg Val Ser Phe Tyr Glu Phe Val Ala Lys Tyr Asp Ala Gln Met
 20 25 30

Val Pro Val Met Lys Ala Lys Gly Tyr Arg Cys Ile His Ser Met Glu
 35 40 45

Arg Thr Val Val Phe Thr Phe Gly Glu Phe Thr Ile Arg Arg Arg Arg
 50 55 60

Trp Gln Lys Gly Glu His Trp Val Val Pro Val Asp Glu Lys Leu Gly
 65 70 75 80

Leu Lys Lys Asn Val Arg Tyr Ser Leu Glu Phe Met Tyr Gln Ile Ala
 85 90 95

Ser Leu Ala Thr Met Met Pro Tyr Glu Lys Val Ile Lys Val Val Gln
 100 105 110

Met Met Tyr Cys Ile Val Ile Thr Lys Pro Thr Val Val Lys Ala Val
 115 120 125

Lys Ile Ser Arg Glu Leu Leu Lys Glu Lys Glu Ala Tyr Arg Phe Phe
 130 135 140

Asp Glu Asp Ile Pro Val Asp Lys Glu Pro Val Asp Met Ile Tyr Leu
 145 150 155 160

Glu Gly Asp Gly Val Met Val Lys Ala Arg Glu Glu Gly Leu Asp Asn
 165 170 175

Arg Asn Val Asp Leu Ser His Phe Val Val His Thr Gly Ser Gln Lys
 180 185 190

Val Gly Ser Asn Arg Phe Val Leu Gln Asn Lys Lys Glu Phe Val Ser
 195 200 205
 Leu Asp Asn Arg Gln Thr Arg Gln Lys Ile Leu Asp Tyr Leu Tyr Asn
 210 215 220
 His Phe Tyr Ile Ala Pro Asn Thr Leu Leu Ile Thr Asn Ser Asp Gly
 225 230 235 240
 Gly His Gly Tyr Thr Pro Tyr Val Phe Lys Glu Ile Ala Lys Ala Leu
 245 250 255
 Lys Val Lys Gln His Glu His Phe Trp Asp Arg Tyr His Val Asn Glu
 260 265 270
 Lys Ile Lys Ser Phe Phe Lys Leu Tyr Pro Val Glu Leu Met Thr Gly
 275 280 285
 Ala Phe Gln Ser Ile Lys Gln His Asp Lys Glu Lys Leu Arg Thr Val
 290 295 300
 Leu Asp Thr Thr Glu Ala Leu Ile Leu Met Glu Glu Glu Met Glu Gly
 305 310 315 320
 Phe Asn Gln Phe Lys Arg Lys Leu Leu Asn Asn Phe Gln Tyr Thr Lys
 325 330 335
 Ser Ala Glu Leu Arg Gly Phe Ser Arg Ala Gly Ile Gly Val Met Glu
 340 345 350
 Ser Gln His Arg Lys Ile Thr Tyr Arg Met Lys Lys Arg Gly Met Tyr
 355 360 365
 Trp Thr Ile Gln Gly Ala Glu Thr Met Ser Gln Leu Ile Val Leu Ser
 370 375 380
 Tyr Glu Gly Gln Leu Arg Asp Leu Phe Phe Gly Ser Trp Arg Glu Asp
 385 390 395 400
 Tyr Gln Lys Tyr Gln Glu Leu Glu Asn Leu Ser Ala Gly Lys Ile Lys
 405 410 415
 His Glu Gln Asn Lys Ile Asn Lys Arg Tyr Asp Leu Gln Thr Leu Gly
 420 425 430
 Arg Leu Arg Tyr Gly Arg His Arg Asn Leu
 435 440

<210> 461

<211> 462

<212> PRT

<213> Streptococcus agalactiae

<400> 461

Met Ala Val Glu Ile Ile Met Pro Lys Leu Gly Val Asp Met Gln Glu
 1 5 10 15
 Gly Glu Ile Leu Glu Trp Lys Lys Gln Val Gly Asp Val Val Asn Glu
 20 25 30
 Gly Asp Val Leu Leu Glu Ile Met Ser Asp Lys Thr Asn Met Glu Ile
 35 40 45
 Glu Ala Glu Asp Ser Gly Val Leu Leu Lys Ile Thr His Gly Asn Gly
 50 55 60
 Asp Val Val Pro Val Thr Glu Thr Ile Gly Tyr Ile Gly Ala Glu Gly
 65 70 75 80
 Glu Glu Val Thr Glu Ala Ser Ser Ser Glu Asn Thr Ser Val Glu Glu
 85 90 95
 Asn Ala Thr Gln Val Thr Ser Glu Pro Glu Lys Val Glu Glu Thr Ser
 100 105 110
 Glu Pro Ser Val Pro Ala Ala Thr Ser Gly Glu Lys Val Arg Ala Thr
 115 120 125
 Pro Ala Ala Arg Lys Leu Ala Arg Glu Met Ser Ile Asp Leu Ala Leu
 130 135 140
 Val Ser Gly Thr Gly Ala Asn Gly Arg Val His Arg Glu Asp Val Glu
 145 150 155 160
 Ser Phe Lys Gly Ala Gln Pro Arg Ile Thr Pro Leu Ala Arg Arg Ile
 165 170 175
 Ala Glu Asp Gln Gly Val Asp Ile Ala Glu Ile Thr Gly Ser Gly Ile
 180 185 190
 Arg Gly Lys Ile Val Lys Asn Asp Val Leu Ala Ala Met Ser Pro Gln
 195 200 205
 Ala Ala Glu Ala Pro Val Glu Thr Lys Ala Thr Pro Thr Thr Glu Glu
 210 215 220
 Lys Gln Leu Pro Glu Gly Val Glu Val Ile Lys Met Ser Ala Met Arg
 225 230 235 240

Lys Ala Ile Ser Lys Gly Met Thr GBS patentin.ST25
 245 Asn Ser Tyr Leu Thr Ala Pro Ser
 250 255
 Phe Thr Leu Asn Tyr Asp Ile Asp Met Thr Glu Met Met Ala Leu Arg
 260 265 270
 Lys Lys Leu Ile Asp Pro Ile Met Ala Lys Thr Gly Leu Lys Val Ser
 275 280 285
 Phe Thr Asp Leu Ile Gly Met Ala Val Val Lys Thr Leu Met Lys Pro
 290 295 300
 Glu His Arg Tyr Leu Asn Ala Ser Leu Ile Asn Asp Ala Gln Glu Ile
 305 310 315 320
 Glu Leu His Asn Phe Val Asn Ile Gly Ile Ala Val Gly Leu Asp Asp
 325 330 335
 Gly Leu Ile Val Pro Val Val His Asn Ala Asp Gln Met Ser Leu Ser
 340 345 350
 Asp Phe Val Ile Ala Ser Lys Asp Val Ile Lys Lys Thr Gln Glu Gly
 355 360 365
 Lys Leu Lys Ser Ala Glu Met Ser Gly Ser Thr Phe Ser Ile Thr Asn
 370 375 380
 Leu Gly Met Phe Gly Thr Lys Thr Phe Asn Pro Ile Ile Asn Gln Pro
 385 390 395 400
 Asn Ser Ala Ile Leu Gly Val Gly Ala Thr Ile Pro Thr Pro Thr Val
 405 410 415
 Val Asp Gly Glu Ile Val Ala Arg Pro Ile Met Ala Met Cys Leu Thr
 420 425 430
 Ile Asp His Arg Ile Val Asp Gly Met Asn Gly Ala Lys Phe Met Val
 435 440 445
 Asp Leu Lys Asn Leu Met Glu Asn Pro Phe Gly Leu Leu Ile
 450 455 460

<210> 462

<211> 531

<212> PRT

<213> Streptococcus agalactiae

<400> 462

GBS patentin.ST25

Met Ser Ser Phe Asn Arg Lys Lys Leu Lys Phe Leu Gly Ile Ser Leu
 1 5 10 15

Ala Thr Leu Thr Ala Thr Thr Val Thr Leu Val Ala Cys Gly Asn Glu
 20 25 30

Ser Lys Asn Ser Gly Asp Asn Lys Val Ile Asn Trp Tyr Ile Pro Thr
 35 40 45

Glu Ile Ser Thr Leu Asp Ile Ser Lys Asn Thr Asp Ala Tyr Ser Asn
 50 55 60

Leu Ala Ile Gly Asn Ser Gly Ser Asn Leu Leu Arg Ile Asp Lys Glu
 65 70 75 80

Gly Lys Pro Lys Pro Asp Leu Ala Lys Lys Val Ser Val Ser Ser Asp
 85 90 95

Gly Leu Thr Tyr Thr Ala Thr Leu Arg Asp Asn Leu Lys Trp Ser Asp
 100 105 110

Gly Ser Lys Leu Ser Ala Glu Asp Phe Val Tyr Thr Trp Arg Arg Ile
 115 120 125

Val Asp Pro Lys Thr Ala Ser Glu Tyr Ala Tyr Leu Ala Thr Glu Ser
 130 135 140

His Leu Leu Asn Ala Asp Lys Ile Asn Ser Gly Asp Ile Lys Asp Leu
 145 150 155 160

Asn Lys Leu Gly Val Thr Ala Lys Gly Asn Gln Val Thr Phe Lys Leu
 165 170 175

Thr Ser Pro Cys Pro Gln Phe Lys Tyr Tyr Leu Ala Phe Ser Asn Phe
 180 185 190

Met Pro Gln Lys Gln Ser Tyr Val Glu Lys Val Gly Lys Asp Tyr Gly
 195 200 205

Thr Thr Ser Lys Asn Gln Ile Tyr Ser Gly Pro Tyr Leu Val Lys Asp
 210 215 220

Trp Asn Gly Ser Asn Gly Lys Phe Lys Leu Val Lys Asn Lys Tyr Tyr
 225 230 235 240

Trp Asp Ser Lys His Val Lys Thr Asn Ser Val Ile Val Gln Thr Ile
 245 250 255

Lys Lys Pro Asp Thr Ala Val Gln Met Tyr Lys Gln Gly Gln Ile Asp
 260 265 270

GBS patentin.ST25

Phe Ala Glu Ile Ser Gly Thr Ser Ala Ile Tyr Asn Gln Thr Gly Ser
275 280 285

Val Lys Ala Leu Thr Asn Gln Lys Ile Arg Gln Ala Leu Asn Leu Ala
290 295 300

Thr Asp Arg Lys Gly Val Val Lys Ala Ala Val Asp Thr Gly Ser Thr
305 310 315 320

Pro Ala Glu Ser Leu Val Pro Lys Lys Leu Ala Lys Leu Pro Asn Gly
325 330 335

Glu Asp Leu Ser Lys Tyr Thr Ala Pro Gly Tyr Thr Tyr Asn Thr Ser
340 345 350

Lys Ala Gln Lys Leu Phe Lys Glu Gly Leu Ala Glu Val Gly Gln Ser
355 360 365

Ser Leu Lys Leu Thr Ile Thr Ala Asp Ser Asp Ser Pro Ala Ala Lys
370 375 380

Asn Ala Val Asp Tyr Val Lys Ser Thr Trp Glu Ser Ala Leu Pro Gly
385 390 395 400

Leu Thr Val Glu Glu Lys Phe Val Thr Phe Lys Gln Arg Leu Glu Asp
405 410 415

Ala Lys Asn Glu Asn Phe Asp Val Val Leu Phe Ser Trp Gly Gly Asp
420 425 430

Tyr Pro Glu Gly Ser Thr Phe Tyr Gly Leu Phe Thr Thr Asn Ser Ala
435 440 445

Tyr Asn Tyr Gly Lys Phe Ser Ser Lys Glu Tyr Asp Asn Ala Tyr Gln
450 455 460

Lys Ala Ile Thr Thr Asp Ala Leu Lys Pro Gly Asp Ala Ala Asn Asp
465 470 475 480

Tyr Lys Thr Ala Glu Lys Ala Leu Phe Asp Gln Ser Tyr Tyr Asn Pro
485 490 495

Val Tyr Tyr Leu Gly Lys Lys Gly Leu Gln Asn Ser Lys Leu Lys Gly
500 505 510

Leu Val Arg Asn Ser Thr Gly Leu Asn Val Asp Phe Thr Tyr Ala Tyr
515 520 525

Lys Thr Glu
530